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WO 2004/030615 A2

(54) Title: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

(57) Abstract: The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

WO 2004/030615

PCT/US2003/028547

COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FIELD OF THE INVENTION

The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

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BACKGROUND OF THE INVENTION

Malignant tumors (cancers) are the second leading cause of death in the United States, after heart disease (Boring et al., *CA Cancer J. Clin.* 43:7 (1993)). Cancer is characterized by the increase in the number of abnormal, or neoplastic, cells derived from a normal tissue which proliferate to form a tumor mass, the invasion of adjacent tissues by these neoplastic tumor cells, and the generation of malignant cells which eventually spread via the blood or lymphatic system to regional lymph nodes and to distant sites via a process called metastasis. In a cancerous state, a cell proliferates under conditions in which normal cells would not grow. Cancer manifests itself in a wide variety of forms, characterized by different degrees of invasiveness and aggressiveness.

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In attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify transmembrane or otherwise membrane-associated polypeptides that are specifically expressed on the surface of one or more particular type(s) of cancer cell as compared to on one or more normal non-cancerous cell(s). Often, such membrane-associated polypeptides are more abundantly expressed on the surface of the cancer cells as compared to on the surface of the non-cancerous cells. The identification of such tumor-associated cell surface antigen polypeptides has given rise to the ability to specifically target cancer cells for destruction via antibody-based therapies. In this regard, it is noted that antibody-based therapy has proved very effective in the treatment of certain cancers. For example, HERCEPTIN® and RITUXAN® (both from Genentech Inc., South San Francisco, California) are antibodies that have been used successfully to treat breast cancer and non-Hodgkin's lymphoma, respectively. More specifically, HERCEPTIN® is a recombinant DNA-derived humanized monoclonal antibody that selectively binds to the extracellular domain of the human epidermal growth factor receptor 2 (HER2) proto-oncogene. HER2 protein overexpression is observed in 25-30% of primary breast cancers. RITUXAN® is a genetically engineered chimeric murine/human monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes. Both these antibodies are recombinantly produced in CHO cells.

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In other attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify (1) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (2) polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (3) polypeptides whose expression is specifically limited

WO 2004/030615

PCT/US2003/028547

to only a single (or very limited number of different) tissue type(s) in both the cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue). Such polypeptides may remain intracellularly located or may be secreted by the cancer cell. Moreover, such polypeptides may be expressed not by the cancer cell itself, but rather by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Such secreted polypeptides are often proteins that provide cancer cells with a growth advantage over normal cells and include such things as, for example, angiogenic factors, cellular adhesion factors, growth factors, and the like. Identification of antagonists of such non-membrane associated polypeptides would be expected to serve as effective therapeutic agents for the treatment of such cancers. Furthermore, identification of the expression pattern of such polypeptides would be useful for the diagnosis of particular cancers in mammals.

Despite the above identified advances in mammalian cancer therapy, there is a great need for additional diagnostic and therapeutic agents capable of detecting the presence of tumor in a mammal and for effectively inhibiting neoplastic cell growth, respectively. Accordingly, it is an objective of the present invention to identify: (1) cell membrane-associated polypeptides that are more abundantly expressed on one or more type(s) of cancer cell(s) as compared to on normal cells or on other different cancer cells, (2) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) (or by other cells that produce polypeptides having a potentiating effect on the growth of cancer cells) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (3) non-membrane-associated polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (4) polypeptides whose expression is specifically limited to only a single (or very limited number of different) tissue type(s) in both a cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue), and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals. It is also an objective of the present invention to identify cell membrane-associated, secreted or intracellular polypeptides whose expression is limited to a single or very limited number of tissues, and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals.

SUMMARY OF THE INVENTION

A. Embodiments

In the present specification, Applicants describe for the first time the identification of various cellular polypeptides (and their encoding nucleic acids or fragments thereof) which are expressed to a greater degree on the surface of or by one or more types of cancer cell(s) as compared to on the surface of or by one or more types of normal non-cancer cells. Alternatively, such polypeptides are expressed by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Again alternatively, such polypeptides may not be overexpressed by tumor cells as compared to normal cells of the same tissue type, but rather may be specifically expressed by both tumor cells and normal cells of only a single or very limited

WO 2004/030615

PCT/US2003/028547

number of tissue types (preferably tissues which are not essential for life, e.g., prostate, etc.). All of the above polypeptides are herein referred to as Tumor-associated Antigenic Target polypeptides ("TAT" polypeptides) and are expected to serve as effective targets for cancer therapy and diagnosis in mammals.

Accordingly, in one embodiment of the present invention, the invention provides an isolated nucleic acid molecule having a nucleotide sequence that encodes a tumor-associated antigenic target polypeptide or fragment thereof (a "TAT" polypeptide).

In certain aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule encoding a full-length TAT polypeptide having an amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule comprising the coding sequence of a full-length TAT polypeptide cDNA as disclosed herein, the coding sequence of a TAT polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In further aspects, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule that encodes the same mature polypeptide encoded by the full-length coding region of any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect of the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide(s) are disclosed herein. Therefore, soluble extracellular domains of the herein described TAT polypeptides are contemplated.

In other aspects, the present invention is directed to isolated nucleic acid molecules which hybridize to (a) a nucleotide sequence encoding a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular

WO 2004/030615

PCT/US2003/028547

domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the nucleotide sequence of (a). In this regard, an embodiment of the present invention is directed to fragments of a full-length TAT polypeptide coding sequence, or the complement thereof, as disclosed herein, that may find use as, for example, hybridization probes useful as, for example, diagnostic probes, antisense oligonucleotide probes, or for encoding fragments of a full-length TAT polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-TAT polypeptide antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide. Such nucleic acid fragments are usually at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a TAT polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the TAT polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which TAT polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such novel fragments of TAT polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the TAT polypeptide fragments encoded by these nucleotide molecule fragments, preferably those TAT polypeptide fragments that comprise a binding site for an anti-TAT antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide.

In another embodiment, the invention provides isolated TAT polypeptides encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated TAT polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity, to a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide protein, with or without the signal peptide, as disclosed herein, an amino acid sequence encoded by any of the nucleic acid sequences disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated TAT polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid

WO 2004/030615

PCT/US2003/028547

sequence identity, to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated TAT polypeptide without the N-terminal signal sequence and/or without the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

Another aspect of the invention provides an isolated TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cells comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides isolated chimeric polypeptides comprising any of the herein described TAT polypeptides fused to a heterologous (non-TAT) polypeptide. Example of such chimeric molecules comprise any of the herein described TAT polypeptides fused to a heterologous polypeptide such as, for example, an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, single-chain antibody or antibody that competitively inhibits the binding of an anti-TAT polypeptide antibody to its respective antigenic epitope. Antibodies of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the antibodies of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described antibodies. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described antibodies is further provided and comprises culturing host cells under conditions suitable for expression of the desired antibody and recovering the desired antibody from the cell culture.

In another embodiment, the invention provides oligopeptides ("TAT binding oligopeptides") which

WO 2004/030615

PCT/US2003/028547

bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding oligopeptides of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding oligopeptides of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding oligopeptides of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described TAT binding oligopeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described TAT binding oligopeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired oligopeptide and recovering the desired oligopeptide from the cell culture.

In another embodiment, the invention provides small organic molecules ("TAT binding organic molecules") which bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding organic molecules of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding organic molecules of the present invention preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding organic molecules of the present invention may be detectably labeled, attached to a solid support, or the like.

In a still further embodiment, the invention concerns a composition of matter comprising a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

In yet another embodiment, the invention concerns an article of manufacture comprising a container and a composition of matter contained within the container, wherein the composition of matter may comprise a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein. The article may further optionally comprise a label affixed to the container, or a package insert included with the container, that refers to the use of the composition of matter for the therapeutic treatment or diagnostic detection of a tumor.

Another embodiment of the present invention is directed to the use of a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT polypeptide antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, for the preparation of a medicament useful in the treatment of a condition which is responsive to the TAT polypeptide, chimeric TAT polypeptide, anti-TAT polypeptide antibody, TAT binding oligopeptide, or TAT

WO 2004/030615

PCT/US2003/028547

binding organic molecule.

B. Additional Embodiments

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cell that expresses a TAT polypeptide, wherein the method comprises contacting the cell with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, and wherein the binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes inhibition of the growth of the cell expressing the TAT polypeptide. In preferred embodiments, the cell is a cancer cell and binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes death of the cell expressing the TAT polypeptide. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of determining the presence of a TAT polypeptide in a sample suspected of containing the TAT polypeptide, wherein the method comprises exposing the sample to an antibody, oligopeptide or small organic molecule that binds to the TAT polypeptide and determining binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide in the sample, wherein the presence of such binding is indicative of the presence of the TAT polypeptide in the sample. Optionally, the sample may contain cells (which may be cancer cells) suspected of expressing the TAT polypeptide. The antibody, TAT binding oligopeptide or TAT binding organic molecule employed in the method may optionally be detectably labeled, attached to a solid support, or the like.

A further embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises detecting the level of expression of a gene encoding a TAT polypeptide (a) in a test sample of tissue cells obtained from said mammal, and (b) in a control sample of known normal non-cancerous cells of the same tissue origin or type, wherein a higher level of expression of the

WO 2004/030615

PCT/US2003/028547

TAT polypeptide in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

Another embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises (a) contacting a test sample comprising tissue cells obtained from the mammal with an antibody, oligopeptide or small organic molecule that binds to a TAT polypeptide and
5 (b) detecting the formation of a complex between the antibody, oligopeptide or small organic molecule and the TAT polypeptide in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in the mammal. Optionally, the antibody, TAT binding oligopeptide or TAT binding organic molecule employed is detectably labeled, attached to a solid support, or the like, and/or the test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

10 Yet another embodiment of the present invention is directed to a method for treating or preventing a cell proliferative disorder associated with altered, preferably increased, expression or activity of a TAT polypeptide, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a TAT polypeptide. Preferably, the cell proliferative disorder is cancer and the antagonist of the TAT polypeptide is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic
15 molecule or antisense oligonucleotide. Effective treatment or prevention of the cell proliferative disorder may be a result of direct killing or growth inhibition of cells that express a TAT polypeptide or by antagonizing the cell growth potentiating activity of a TAT polypeptide.

Yet another embodiment of the present invention is directed to a method of binding an antibody, oligopeptide or small organic molecule to a cell that expresses a TAT polypeptide, wherein the method
20 comprises contacting a cell that expresses a TAT polypeptide with said antibody, oligopeptide or small organic molecule under conditions which are suitable for binding of the antibody, oligopeptide or small organic molecule to said TAT polypeptide and allowing binding therebetween.

Other embodiments of the present invention are directed to the use of (a) a TAT polypeptide, (b) a nucleic acid encoding a TAT polypeptide or a vector or host cell comprising that nucleic acid, (c) an anti-TAT
25 polypeptide antibody, (d) a TAT-binding oligopeptide, or (e) a TAT-binding small organic molecule in the preparation of a medicament useful for (i) the therapeutic treatment or diagnostic detection of a cancer or tumor, or (ii) the therapeutic treatment or prevention of a cell proliferative disorder.

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cancer cell, wherein the growth of said cancer cell is at least in part dependent upon the growth potentiating
30 effect(s) of a TAT polypeptide (wherein the TAT polypeptide may be expressed either by the cancer cell itself or a cell that produces polypeptide(s) that have a growth potentiating effect on cancer cells), wherein the method comprises contacting the TAT polypeptide with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth-potentiating activity of the TAT polypeptide and, in turn, inhibiting the growth of the cancer cell. Preferably the growth of the cancer cell is completely inhibited.
35 Even more preferably, binding of the antibody, oligopeptide or small organic molecule to the TAT polypeptide induces the death of the cancer cell. Optionally, the antibody is a monoclonal antibody, antibody fragment,

WO 2004/030615

PCT/US2003/028547

chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth potentiating activity of said TAT polypeptide and resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet further embodiments of the present invention will be evident to the skilled artisan upon a reading of the present specification.

BRIEF DESCRIPTION OF THE DRAWINGS

In the list of figures for the present application, specific cDNA sequences which are upregulated in certain tumor tissues as compared to their normal tissue counterparts are individually identified with a designation beginning with the letters "DNA" followed by a specific numerical designation. A full or partial length protein sequence that is encoded by a cDNA sequence identified and shown herein is individually identified with a designation beginning with the letters "PRO" followed by a specific numerical designation. Figures showing encoded amino acid sequences immediately follow the figure showing the cDNA sequence encoding that specific amino acid sequence. If start and/or stop codons have been identified in a cDNA sequence shown in the attached figures, they are shown in bold and underlined font.

WO 2004/030615

PCT/US2003/028547

List of Figures

Figure 1: DNA323717, XM_059201, gen.XM_059201
 Figure 2: DNA323718, XM_117159, gen.XM_117159
 Figure 3: DNA323719, XM_114062, gen.XM_114062
 Figure 4: DNA323720, XM_086178, gen.XM_086178
 Figure 5: PRO80480
 Figure 6: DNA323721, XM_051556, gen.XM_051556
 Figure 7: PRO80481
 Figure 8: DNA323722, NM_017891, gen.NM_017891
 Figure 9: PRO80482
 Figure 10: DNA323723, NM_018188, gen.NM_018188
 Figure 11: PRO80483
 Figure 12: DNA323724, NM_002617, gen.NM_002617
 Figure 13: PRO23746
 Figure 14: DNA323725, XM_049742, gen.XM_049742
 Figure 15: DNA323726, NM_033534, gen.NM_033534
 Figure 16: PRO80484
 Figure 17: DNA323727, NM_014188, gen.NM_014188
 Figure 18: PRO80485
 Figure 19: DNA323728, XM_086180, gen.XM_086180
 Figure 20: DNA323729, XM_166599, gen.XM_166599
 Figure 21: PRO80487
 Figure 22: DNA323730, NM_017900, gen.NM_017900
 Figure 23: PRO80488
 Figure 24: DNA323731, XM_001589, gen.XM_001589
 Figure 25: PRO80489
 Figure 26: DNA323732, NM_016176, gen.NM_016176
 Figure 27: PRO80490
 Figure 28: DNA323733, XM_117692, gen.XM_117692
 Figure 29: DNA323734, XM_086360, gen.XM_086360
 Figure 30: PRO80492
 Figure 31: DNA287173, NM_001428, gen.NM_001428
 Figure 32: PRO69463
 Figure 33: DNA323735, XM_001299, gen.XM_001299
 Figure 34: DNA323736, NM_000983, gen.NM_000983
 Figure 35: PRO80493
 Figure 36A-B: DNA227821, NM_014851, gen.NM_014851
 Figure 37: PRO38284
 Figure 38A-B: DNA323737, XM_086204, gen.XM_086204
 Figure 39: PRO80494
 Figure 40: DNA323738, XM_030920, gen.XM_030920
 Figure 41: DNA323739, NM_018948, gen.NM_018948
 Figure 42: DNA273712, NM_007262, gen.NM_007262
 Figure 43: PRO61679
 Figure 44: DNA151148, NM_004781, gen.NM_004781
 Figure 45: PRO12618
 Figure 46: DNA323740, XM_086151, gen.XM_086151
 Figure 47: PRO80497
 Figure 48: DNA171408, NM_004401, gen.NM_004401
 Figure 49: PRO20136
 Figure 50: DNA323741, NM_003132, gen.NM_003132
 Figure 51: PRO80498
 Figure 52: DNA323742, XM_086586, gen.XM_086586
 Figure 53: PRO80499
 Figure 54: DNA323743, XM_086587, gen.XM_086587
 Figure 55: DNA323744, XM_059230, gen.XM_059230
 Figure 56: PRO80501
 Figure 57A-B: DNA323745, XM_048780, gen.XM_048780
 Figure 58: DNA323746, XM_053183, gen.XM_053183
 Figure 59: DNA323747, XM_165442, gen.XM_165442
 Figure 60: DNA323748, NM_033440, gen.NM_033440
 Figure 61: PRO2269
 Figure 62: DNA323749, NM_024329, gen.NM_024329
 Figure 63: PRO80505
 Figure 64: DNA323750, XM_018205, gen.XM_018205
 Figure 65: PRO80506
 Figure 66: DNA323751, XM_011650, gen.XM_011650
 Figure 67: DNA323752, XM_017315, gen.XM_017315
 Figure 68A-B: DNA323753, XM_030470, gen.XM_030470
 Figure 69: DNA323754, NM_004930, gen.NM_004930
 Figure 70: PRO80510
 Figure 71: DNA323755, NM_003689, gen.NM_003689
 Figure 72: PRO80511
 Figure 73: DNA323756, NM_016183, gen.NM_016183
 Figure 74: PRO80512
 Figure 75: DNA323757, XM_015234, gen.XM_015234
 Figure 76A-B: DNA323758, XM_027916, gen.XM_027916
 Figure 77: DNA323759, XM_033683, gen.XM_033683
 Figure 78: DNA323760, XM_001826, gen.XM_001826
 Figure 79: DNA323761, XM_033654, gen.XM_033654
 Figure 80: PRO80517
 Figure 81: DNA323762, NM_001791, gen.NM_001791
 Figure 82: PRO26194
 Figure 83: DNA323763, NM_005826, gen.NM_005826
 Figure 84: PRO60815
 Figure 85: DNA323764, XM_086357, gen.XM_086357
 Figure 86: PRO80518
 Figure 87: DNA323765, NM_000975, gen.NM_000975
 Figure 88: PRO80519
 Figure 89: DNA323766, NM_007260, gen.NM_007260
 Figure 90: PRO61250
 Figure 91: DNA323767, NM_017761, gen.NM_017761
 Figure 92: PRO80520
 Figure 93: DNA323768, NM_006625, gen.NM_006625
 Figure 94: PRO22196
 Figure 95: DNA323769, NM_054016, gen.NM_054016
 Figure 96: PRO80521
 Figure 97: DNA323770, XM_086375, gen.XM_086375
 Figure 98: DNA323771, XM_006290, gen.XM_006290
 Figure 99: DNA323772, NM_015484, gen.NM_015484
 Figure 100: PRO80524
 Figure 101A-B: DNA323773, XM_001616, gen.XM_001616
 Figure 102: DNA323774, XM_058240,

WO 2004/030615

PCT/US2003/028547

gen.XM.058240
Figure 103: DNA323775, XM.059117,
gen.XM.059117
Figure 104: PRO80527
Figure 105: DNA226262, NM.005563,
gen.NM.005563
Figure 106: PRO36725
Figure 107: DNA323776, NM.022778,
gen.NM.022778
Figure 108: PRO80528
Figure 109: DNA323777, XM.017846,
gen.XM.017846
Figure 110: DNA323778, NM.005517,
gen.NM.005517
Figure 111: PRO80530
Figure 112A-C: DNA323779, XM.046918,
gen.XM.046918
Figure 113: DNA323780, XM.002114,
gen.XM.002114
Figure 114: DNA323781, XM.059066,
gen.XM.059066
Figure 115: PRO80533
Figure 116: DNA323782, NM.018066,
gen.NM.018066
Figure 117: PRO80534
Figure 118: DNA323783, NM.006600,
gen.NM.006600
Figure 119: PRO80535
Figure 120: DNA323784, XM.059067,
gen.XM.059067
Figure 121: PRO80536
Figure 122: DNA323785, NM.032872,
gen.NM.032872
Figure 123: PRO80537
Figure 124: DNA196349, NM.006990,
gen.NM.006990
Figure 125: PRO24856
Figure 126: DNA323788, XM.001640,
gen.XM.001640
Figure 127: DNA323789, NM.002946,
gen.NM.002946
Figure 128: PRO59099
Figure 129: DNA323790, XM.114044,
gen.XM.114044
Figure 130: DNA323791, XM.059088,
gen.XM.059088
Figure 131: DNA323792, NM.031459,
gen.NM.031459
Figure 132: PRO80542
Figure 133: DNA323793, XM.010664,
gen.XM.010664
Figure 134: DNA323794, XM.001812,
gen.XM.001812
Figure 135: DNA323795, XM.001807,
gen.XM.001807
Figure 136: DNA323796, XM.086444,

gen.XM.086444
Figure 137: DNA323797, NM.024640,
gen.NM.024640
Figure 138: PRO80547
Figure 139A-B: DNA323798, XM.049310,
gen.XM.049310
Figure 140: DNA323799, XM.113374,
gen.XM.113374
Figure 141: DNA323800, XM.002105,
gen.XM.002105
Figure 142: DNA323801, NM.014571,
gen.NM.014571
Figure 143: PRO80550
Figure 144: DNA323802, XM.165438,
gen.XM.165438
Figure 145: DNA323803, XM.029844,
gen.XM.029844
Figure 146: DNA188748, NM.006559,
gen.NM.006559
Figure 147: PRO22304
Figure 148: DNA323804, NM.003757,
gen.NM.003757
Figure 149: PRO80553
Figure 150: DNA323805, NM.004964,
gen.NM.004964
Figure 151: PRO80554
Figure 152: DNA323806, NM.023009,
gen.NM.023009
Figure 153: PRO80555
Figure 154: DNA323807, XM.030423,
gen.XM.030423
Figure 155A-B: DNA323808, XM.036299,
gen.XM.036299
Figure 156: PRO80557
Figure 157: DNA227213, NM.003680,
gen.NM.003680
Figure 158: PRO37676
Figure 159: DNA323809, NM.006112,
gen.NM.006112
Figure 160: PRO80558
Figure 161: DNA323810, XM.018136,
gen.XM.018136
Figure 162: PRO80559
Figure 163: DNA323811, XM.117184,
gen.XM.117184
Figure 164: PRO80560
Figure 165: DNA323812, NM.017825,
gen.NM.017825
Figure 166: PRO80561
Figure 167: DNA189315, NM.014408,
gen.NM.014408
Figure 168: PRO22262
Figure 169A-B: DNA323813, XM.029031,
gen.XM.029031
Figure 170: PRO80562
Figure 171: DNA323814, XM.059171,

WO 2004/030615

PCT/US2003/028547

gen.XM_059171
Figure 172: PRO80563
Figure 173: DNA83085, NM_000760, gen.NM_000760
Figure 174: PRO2583
Figure 175: DNA323815, XM_165984, gen.XM_165984
Figure 176: DNA323816, XM_029842, gen.XM_029842
Figure 177: PRO2851
Figure 178: DNA323817, XM_086384, gen.XM_086384
Figure 179: PRO80565
Figure 180A-C: DNA274487, NM_014747, gen.NM_014747
Figure 181: PRO62389
Figure 182: DNA323818, XM_010712, gen.XM_010712
Figure 183: DNA323819, NM_024664, gen.NM_024664
Figure 184: PRO80567
Figure 185: DNA323820, XM_059214, gen.XM_059214
Figure 186: PRO80568
Figure 187: DNA323821, XM_046349, gen.XM_046349
Figure 188: DNA103253, NM_006516, gen.NM_006516
Figure 189: PRO4583
Figure 190: DNA323822, XM_086543, gen.XM_086543
Figure 191: PRO80570
Figure 192: DNA274745, NM_006824, gen.NM_006824
Figure 193: PRO62518
Figure 194: DNA273060, NM_001255, gen.NM_001255
Figure 195: PRO61125
Figure 196: DNA323823, NM_030587, gen.NM_030587
Figure 197: PRO80571
Figure 198: DNA323824, XM_097649, gen.XM_097649
Figure 199: DNA256503, NM_003780, gen.NM_003780
Figure 200: PRO51539
Figure 201: DNA323825, XM_046450, gen.XM_046450
Figure 202A-B: DNA272024, NM_014663, gen.NM_014663
Figure 203: PRO60298
Figure 204: DNA323826, XM_046565, gen.XM_046565
Figure 205: PRO80574
Figure 206: DNA323827, NM_024602, gen.NM_024602
Figure 207: PRO80575

Figure 208: DNA323828, XM_046557, gen.XM_046557
Figure 209: PRO80576
Figure 210: DNA323829, NM_001012, gen.NM_001012
Figure 211: PRO10760
Figure 212: DNA323830, XM_046551, gen.XM_046551
Figure 213A-B: DNA323831, XM_027983, gen.XM_027983
Figure 214: DNA323832, XM_086324, gen.XM_086324
Figure 215: PRO80579
Figure 216: DNA323833, XM_032391, gen.XM_032391
Figure 217: PRO80580
Figure 218: DNA103214, NM_006066, gen.NM_006066
Figure 219: PRO4544
Figure 220: DNA304686, NM_002574, gen.NM_002574
Figure 221: PRO71112
Figure 222: DNA323834, NM_032756, gen.NM_032756
Figure 223: PRO80581
Figure 224: DNA323835, XM_059133, gen.XM_059133
Figure 225: PRO80582
Figure 226: DNA323836, XM_027313, gen.XM_027313
Figure 227: PRO80583
Figure 228: DNA323837, XM_054868, gen.XM_054868
Figure 229: DNA323838, NM_001262, gen.NM_001262
Figure 230: PRO59546
Figure 231: DNA323839, XM_086391, gen.XM_086391
Figure 232: PRO80584
Figure 233: DNA323840, XM_114798, gen.XM_114798
Figure 234: PRO80585
Figure 235: DNA272748, NM_002979, gen.NM_002979
Figure 236: PRO60860
Figure 237: DNA323841, XM_038911, gen.XM_038911
Figure 238: PRO80586
Figure 239: DNA323842, NM_018070, gen.NM_018070
Figure 240: PRO80587
Figure 241: DNA323843, NM_024603, gen.NM_024603
Figure 242: PRO80588
Figure 243: DNA323844, XM_086389, gen.XM_086389

WO 2004/030615

PCT/US2003/028547

Figure 244: DNA323845, XM_038852,
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Figure 245: DNA323846, NM_032864,
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Figure 246: PRO80591
Figure 247: DNA323847, NM_024586,
gen.NM_024586
Figure 248: PRO80592
Figure 249A-B: DNA323848, XM_097565,
gen.XM_097565
Figure 250: DNA323849, XM_001472,
gen.XM_001472
Figure 251A-C: DNA323850, XM_055481,
gen.XM_055481
Figure 252: PRO80593
Figure 253: DNA323851, XM_010615,
gen.XM_010615
Figure 254A-B: DNA323852, XM_089138,
gen.XM_089138
Figure 255: PRO80595
Figure 256A-B: DNA323853, XM_059180,
gen.XM_059180
Figure 257: DNA323854, XM_015717,
gen.XM_015717
Figure 258: PRO80597
Figure 259: DNA323855, XM_114125,
gen.XM_114125
Figure 260: DNA323856, NM_015640,
gen.NM_015640
Figure 261: PRO80599
Figure 262: DNA323857, NM_017768,
gen.NM_017768
Figure 263: PRO80600
Figure 264: DNA323858, XM_165977,
gen.XM_165977
Figure 265: DNA323859, XM_086343,
gen.XM_086343
Figure 266: PRO80602
Figure 267: DNA269708, NM_007034,
gen.NM_007034
Figure 268: PRO58118
Figure 269: DNA323860, NM_001554,
gen.NM_001554
Figure 270: PRO80603
Figure 271: DNA226260, NM_006769,
gen.NM_006769
Figure 272: PRO36723
Figure 273: DNA323861, NM_004261,
gen.NM_004261
Figure 274: PRO80604
Figure 275: DNA323862, XM_165983,
gen.XM_165983
Figure 276: DNA323863, XM_016164,
gen.XM_016164
Figure 277: DNA323864, XM_086164,
gen.XM_086164

Figure 278: PRO80607
Figure 279: DNA323865, XM_086165,
gen.XM_086165
Figure 280: DNA323866, XM_086167,
gen.XM_086167
Figure 281: DNA323867, XM_086166,
gen.XM_086166
Figure 282: DNA323868, XM_086138,
gen.XM_086138
Figure 283: PRO80611
Figure 284: DNA323869, NM_000969,
gen.NM_000969
Figure 285: PRO80612
Figure 286: DNA323870, XM_088863,
gen.XM_088863
Figure 287: PRO80613
Figure 288: DNA271003, NM_003729,
gen.NM_003729
Figure 289: PRO59332
Figure 290: DNA323871, XM_165981,
gen.XM_165981
Figure 291: PRO80614
Figure 292: DNA275139, NM_013296,
gen.NM_013296
Figure 293: PRO62849
Figure 294: DNA323872, XM_058702,
gen.XM_058702
Figure 295: DNA323873, XM_054978,
gen.XM_054978
Figure 296: DNA323874, NM_032636,
gen.NM_032636
Figure 297: PRO80617
Figure 298: DNA323875, NM_006513,
gen.NM_006513
Figure 299: PRO80618
Figure 300: DNA323876, NM_006621,
gen.NM_006621
Figure 301: PRO80619
Figure 302A-B: DNA323877, NM_007158,
gen.NM_007158
Figure 303: PRO80620
Figure 304: DNA323878, XM_086132,
gen.XM_086132
Figure 305: PRO80621
Figure 306: DNA323879, NM_004000,
gen.NM_004000
Figure 307: PRO80622
Figure 308: DNA323880, NM_001688,
gen.NM_001688
Figure 309: PRO80623
Figure 310: DNA323881, NM_019099,
gen.NM_019099
Figure 311: PRO80624
Figure 312A-B: DNA323882, NM_000701,
gen.NM_000701
Figure 313: PRO80625

WO 2004/030615

PCT/US2003/028547

Figure 314A-B: DNA323883, XM_018332,
gen.XM_018332
Figure 315A-B: DNA323884, XM_040709,
gen.XM_040709
Figure 316: PRO80627
Figure 317: DNA323885, XM_086518,
gen.XM_086518
Figure 318A-D: DNA323886, XM_034671,
gen.XM_034671
Figure 319: DNA323887, XM_034662,
gen.XM_034662
Figure 320: PRO80630
Figure 321: DNA323888, XM_039721,
gen.XM_039721
Figure 322: PRO80631
Figure 323A-B: DNA323889, XM_086397,
gen.XM_086397
Figure 324A-B: DNA323890, XM_086515,
gen.XM_086515
Figure 325: PRO80633
Figure 326: DNA323891, XM_016480,
gen.XM_016480
Figure 327: DNA323892, XM_165975,
gen.XM_165975
Figure 328: DNA323893, NM_016361,
gen.NM_016361
Figure 329: PRO231
Figure 330: DNA323894, XM_059210,
gen.XM_059210
Figure 331: DNA323895, XM_086296,
gen.XM_086296
Figure 332: DNA323896, NM_030920,
gen.NM_030920
Figure 333: PRO80638
Figure 334: DNA323897, NM_016022,
gen.NM_016022
Figure 335: PRO80639
Figure 336: DNA323898, NM_031901,
gen.NM_031901
Figure 337: PRO80640
Figure 338A-B: DNA323899, XM_088788,
gen.XM_088788
Figure 339: PRO80641
Figure 340: DNA274759, NM_005620,
gen.NM_005620
Figure 341: PRO62529
Figure 342: DNA323900, XM_001468,
gen.XM_001468
Figure 343: PRO49642
Figure 344: DNA323901, NM_006862,
gen.NM_006862
Figure 345: PRO80642
Figure 346: DNA227529, NM_002796,
gen.NM_002796
Figure 347: PRO37992
Figure 348: DNA323902, NM_002810,

gen.NM_002810
Figure 349: PRO61638
Figure 350: DNA290284, NM_005997,
gen.NM_005997
Figure 351: PRO70433
Figure 352: DNA323903, XM_097639,
gen.XM_097639
Figure 353: DNA323904, XM_041879,
gen.XM_041879
Figure 354: DNA323905, XM_041884,
gen.XM_041884
Figure 355: PRO80644
Figure 356: DNA225809, NM_000396,
gen.NM_000396
Figure 357: PRO36272
Figure 358: DNA323906, NM_025150,
gen.NM_025150
Figure 359: PRO80645
Figure 360: DNA323907, XM_114098,
gen.XM_114098
Figure 361: DNA323908, XM_113369,
gen.XM_113369
Figure 362: PRO80646
Figure 363: DNA323909, XM_099467,
gen.XM_099467
Figure 364: DNA323910, NM_002965,
gen.NM_002965
Figure 365: PRO80648
Figure 366: DNA323911, XM_086400,
gen.XM_086400
Figure 367: DNA210134, NM_014624,
gen.NM_014624
Figure 368: PRO33679
Figure 369: DNA304666, NM_002961,
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Figure 370: PRO71093
Figure 371: DNA304720, NM_019554,
gen.NM_019554
Figure 372: PRO71146
Figure 373: DNA323912, XM_165976,
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Figure 374: DNA227577, NM_006271,
gen.NM_006271
Figure 375: PRO38040
Figure 376: DNA323913, XM_114097,
gen.XM_114097
Figure 377: DNA323914, XM_040009,
gen.XM_040009
Figure 378: PRO80651
Figure 379: DNA323915, NM_024330,
gen.NM_024330
Figure 380: PRO703
Figure 381: DNA323916, NM_012437,
gen.NM_012437
Figure 382: PRO80652
Figure 383: DNA323917, XM_086271,

WO 2004/030615

PCT/US2003/028547

gen.XM_086271
Figure 384: DNA323918, XM_114055,
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Figure 385: PRO37535
Figure 386: DNA323919, XM_113360,
gen.XM_113360
Figure 387: PRO80654
Figure 388: DNA323920, XM_086564,
gen.XM_086564
Figure 389: DNA323921, NM_005973,
gen.NM_005973
Figure 390: PRO80656
Figure 391: DNA323922, XM_044077,
gen.XM_044077
Figure 392: DNA323923, NM_001878,
gen.NM_001878
Figure 393: PRO80657
Figure 394: DNA323924, NM_021948,
gen.NM_021948
Figure 395: PRO6018
Figure 396: DNA273088, NM_006365,
gen.NM_006365
Figure 397: PRO61146
Figure 398: DNA323925, XM_044127,
gen.XM_044127
Figure 399: PRO80658
Figure 400: DNA323926, XM_053245,
gen.XM_053245
Figure 401: PRO80659
Figure 402: DNA257916, NM_032323,
gen.NM_032323
Figure 403: PRO52449
Figure 404: DNA323927, NM_005572,
gen.NM_005572
Figure 405: PRO80660
Figure 406: DNA323928, XM_044166,
gen.XM_044166
Figure 407: PRO80661
Figure 408: DNA323929, XM_044128,
gen.XM_044128
Figure 409: DNA226125, NM_003145,
gen.NM_003145
Figure 410: PRO36588
Figure 411A-B: DNA323930, XM_044172,
gen.XM_044172
Figure 412: DNA323931, NM_032292,
gen.NM_032292
Figure 413: PRO80664
Figure 414: DNA323932, NM_004632,
gen.NM_004632
Figure 415: PRO80665
Figure 416: DNA323933, XM_044075,
gen.XM_044075
Figure 417: PRO80666
Figure 418: DNA323934, NM_018253,
gen.NM_018253

Figure 419: PRO80667
Figure 420: DNA323935, NM_018116,
gen.NM_018116
Figure 421: PRO80668
Figure 422: DNA323936, NM_002004,
gen.NM_002004
Figure 423: PRO80669
Figure 424: DNA323937, NM_005698,
gen.NM_005698
Figure 425: PRO80670
Figure 426: DNA323938, NM_052837,
gen.NM_052837
Figure 427: PRO80671
Figure 428: DNA194600, NM_006589,
gen.NM_006589
Figure 429: PRO23942
Figure 430: DNA323939, XM_086567,
gen.XM_086567
Figure 431: PRO80672
Figure 432: DNA323940, XM_086552,
gen.XM_086552
Figure 433: DNA323941, XM_036744,
gen.XM_036744
Figure 434: DNA323942, NM_130898,
gen.NM_130898
Figure 435: PRO80675
Figure 436: DNA226793, NM_006694,
gen.NM_006694
Figure 437: PRO37256
Figure 438: DNA294794, NM_002870,
gen.NM_002870
Figure 439: PRO70754
Figure 440: DNA323943, NM_001030,
gen.NM_001030
Figure 441: PRO80676
Figure 442: DNA323944, XM_036829,
gen.XM_036829
Figure 443: PRO80677
Figure 444: DNA323945, NM_015449,
gen.NM_015449
Figure 445: PRO80678
Figure 446: DNA323946, NM_014847,
gen.NM_014847
Figure 447: PRO80679
Figure 448: DNA323947, XM_036934,
gen.XM_036934
Figure 449: PRO80680
Figure 450A-B: DNA323948, XM_036845,
gen.XM_036845
Figure 451: DNA323949, XM_010636,
gen.XM_010636
Figure 452: DNA323950, NM_006556,
gen.NM_006556
Figure 453: PRO62574
Figure 454: DNA323951, XM_034082,
gen.XM_034082

WO 2004/030615

PCT/US2003/028547

Figure 455: DNA323952, NM_025207,
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Figure 456: PRO80684
Figure 457: DNA103436, NM_003815,
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Figure 458: PRO4763
Figure 459: DNA323953, NM_003516,
gen.NM_003516
Figure 460: PRO80685
Figure 461: DNA323954, NM_005850,
gen.NM_005850
Figure 462: PRO59725
Figure 463A-B: DNA323955, NM_014849,
gen.NM_014849
Figure 464: PRO80686
Figure 465: DNA323956, XM_059094,
gen.XM_059094
Figure 466: DNA323957, XM_058247,
gen.XM_058247
Figure 467: PRO80688
Figure 468: DNA323958, NM_003779,
gen.NM_003779
Figure 469: PRO80689
Figure 470: DNA323959, NM_004550,
gen.NM_004550
Figure 471: PRO58974
Figure 472: DNA323960, XM_085581,
gen.XM_085581
Figure 473: DNA323961, XM_113379,
gen.XM_113379
Figure 474: DNA226619, NM_003564,
gen.NM_003564
Figure 475: PRO37082
Figure 476A-B: DNA323962, XM_049680,
gen.XM_049680
Figure 477: DNA323963, XM_165443,
gen.XM_165443
Figure 478: PRO80693
Figure 479: DNA323964, XM_086381,
gen.XM_086381
Figure 480: PRO80694
Figure 481A-B: DNA323965, NM_002857,
gen.NM_002857
Figure 482: PRO80695
Figure 483A-B: DNA323966, XM_049690,
gen.XM_049690
Figure 484: DNA323967, XM_114153,
gen.XM_114153
Figure 485: DNA323968, XM_086378,
gen.XM_086378
Figure 486: DNA323969, XM_001897,
gen.XM_001897
Figure 487: PRO10002
Figure 488: DNA323970, NM_052862,
gen.NM_052862
Figure 489: PRO80699

Figure 490: DNA323971, XM_086481,
gen.XM_086481
Figure 491: PRO80700
Figure 492: DNA323972, XM_059191,
gen.XM_059191
Figure 493: DNA323973, XM_086485,
gen.XM_086485
Figure 494: DNA323974, XM_086484,
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Figure 495: DNA323975, XM_047479,
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Figure 496: PRO80704
Figure 497: DNA323976, NM_003617,
gen.NM_003617
Figure 498: PRO37806
Figure 499: DNA254298, NM_025226,
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Figure 500: PRO49409
Figure 501: DNA323977, XM_034000,
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Figure 502: PRO80705
Figure 503: DNA323978, NM_032738,
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Figure 504: PRO329
Figure 505: DNA323979, NM_000569,
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Figure 506: PRO80706
Figure 507: DNA323980, XM_088945,
gen.XM_088945
Figure 508: PRO80707
Figure 509: DNA323981, XM_060331,
gen.XM_060331
Figure 510: PRO80708
Figure 511: DNA323982, NM_004905,
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Figure 512: PRO80709
Figure 513: DNA323983, NM_017847,
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Figure 514: PRO80710
Figure 515A-B: DNA323984, XM_051877,
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Figure 516: PRO62077
Figure 517: DNA323985, NM_005717,
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Figure 518: PRO80711
Figure 519A-B: DNA271986, NM_014837,
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Figure 520: PRO60261
Figure 521A-B: DNA323986, XM_056923,
gen.XM_056923
Figure 522: DNA323987, XM_046464,
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Figure 523: DNA323988, XM_002068,
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Figure 524A-B: DNA323989, XM_001289,
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WO 2004/030615

PCT/US2003/028547

Figure 525: DNA323990, XM_114109,
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Figure 527: DNA323991, NM_022371,
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Figure 528: PRO80715
Figure 529: DNA323992, NM_004673,
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Figure 530: PRO188
Figure 531: DNA323993, XM_060517,
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Figure 532: DNA323994, XM_165978,
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Figure 533: PRO80717
Figure 534: DNA323995, XM_117181,
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Figure 535: DNA323996, NM_018122,
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Figure 536: PRO80719
Figure 537: DNA323997, XM_042967,
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Figure 538: DNA323998, XM_086494,
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Figure 539: PRO80720
Figure 540: DNA290234, NM_002923,
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Figure 541: PRO70333
Figure 542: DNA323999, XM_086328,
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Figure 543: DNA324000, XM_086282,
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Figure 544: DNA324001, XM_053633,
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Figure 545: DNA256905, NM_138391,
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Figure 546: PRO51836
Figure 547: DNA324002, XM_015434,
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Figure 548: DNA324003, NM_006763,
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Figure 549: PRO80725
Figure 550: DNA227246, NM_005686,
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Figure 551: PRO37709
Figure 552: DNA324004, XM_058405,
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Figure 553A-B: DNA226005, NM_000228,
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Figure 554: PRO36468
Figure 555: DNA324005, NM_015714,
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Figure 556: PRO11582
Figure 557: DNA324006, XM_086142,
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Figure 558: DNA83046, NM_000574, gen.NM_000574
Figure 559: PRO2569

Figure 560A-B: DNA324007, XM_114030,
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Figure 561: DNA324008, XM_097519,
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Figure 562: DNA324009, XM_059120,
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Figure 563: PRO80730
Figure 564: DNA324010, NM_016456,
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Figure 565: PRO1248
Figure 566: DNA324011, XM_036556,
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Figure 567: DNA324012, XM_001914,
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Figure 568: DNA324013, XM_001916,
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Figure 569: DNA324014, NM_018085,
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Figure 570: PRO80734
Figure 571: DNA324015, NM_006335,
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Figure 572: PRO80735
Figure 573: DNA324016, XM_036500,
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Figure 574: PRO80736
Figure 575: DNA324017, XM_036507,
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Figure 576: DNA196344, NM_004767,
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Figure 577: PRO24851
Figure 578: DNA247474, NM_014176,
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Figure 579: PRO44999
Figure 580A-B: DNA324018, XM_084055,
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Figure 581: DNA324019, XM_010682,
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Figure 582: DNA324020, XM_117185,
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Figure 583: DNA324021, XM_055880,
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Figure 584: PRO80740
Figure 585: DNA193882, NM_014184,
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Figure 586: PRO23300
Figure 587: DNA324022, NM_018212,
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Figure 588: PRO80741
Figure 589: DNA324023, XM_086431,
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Figure 590: PRO80742
Figure 591: DNA324024, XM_037329,
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Figure 592: DNA324025, XM_086432,
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Figure 593A-B: DNA324026, XM_010732,

WO 2004/030615

PCT/US2003/028547

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Figure 594: DNA227504, NM_000447,
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Figure 599A-B: DNA324029, XM_001958,
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Figure 600: DNA324030, XM_016199,
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Figure 601: DNA324031, XM_086244,
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Figure 602: DNA324032, XM_086245,
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Figure 603: DNA254346, NM_024709,
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Figure 604: PRO49457
Figure 605: DNA324033, XM_088107,
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Figure 606: DNA324034, NM_032890,
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Figure 607: PRO80752
Figure 608: DNA324035, XM_052974,
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Figure 609: PRO80753
Figure 610: DNA324036, XM_047499,
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Figure 611: PRO80754
Figure 612: DNA324037, NM_000858,
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Figure 613: PRO80755
Figure 614: DNA324038, NM_024319,
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Figure 615: PRO80756
Figure 616: DNA324039, XM_047545,
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Figure 617: PRO4914
Figure 618A-B: DNA324040, XM_056884,
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Figure 619: DNA324041, XM_098599,
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Figure 620: DNA324042, XM_165439,
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Figure 621: PRO80759
Figure 622: DNA324043, XM_089030,
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Figure 623: PRO80760
Figure 624: DNA82328, NM_000029, gen.NM_000029
Figure 625: PRO1707
Figure 626: DNA324044, NM_014236,
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Figure 627: PRO80761
Figure 628: DNA324045, XM_056970,

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Figure 629: PRO80762
Figure 630: DNA324046, NM_032324,
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Figure 631: PRO80763
Figure 632: DNA324047, XM_086257,
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Figure 633: PRO80764
Figure 634: DNA324048, XM_114137,
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Figure 635: PRO80765
Figure 636: DNA324049, NM_000143,
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Figure 637: PRO62607
Figure 638: DNA324050, XM_090833,
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Figure 639: DNA324051, NM_130398,
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Figure 640: PRO80767
Figure 641: DNA324052, XM_117196,
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Figure 642: DNA324053, XM_018041,
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Figure 643: DNA324054, NM_001011,
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Figure 644: PRO10692
Figure 645: DNA324055, NM_024027,
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Figure 646: PRO1182
Figure 647: DNA324056, NM_016030,
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Figure 648: PRO80770
Figure 649: DNA103217, NM_003310,
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Figure 650: PRO4547
Figure 651: DNA275195, NM_001034,
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Figure 652: PRO62893
Figure 653: DNA324057, XM_059368,
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Figure 654: PRO80771
Figure 655: DNA324058, NM_006826,
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Figure 656: PRO70258
Figure 657: DNA324059, NM_005378,
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Figure 658: PRO80772
Figure 659: DNA324060, NM_002539,
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Figure 660: PRO80773
Figure 661: DNA324061, XM_096149,
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Figure 662: DNA275049, NM_004939,
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Figure 663: PRO62770
Figure 664A-B: DNA324062, XM_036450,

WO 2004/030615

PCT/US2003/028547

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Figure 665: DNA324063, XM_103946,
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Figure 667: DNA324064, NM_014713,
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Figure 668: PRO80776
Figure 669: DNA324065, XM_087206,
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Figure 670: DNA324066, NM_106552,
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Figure 671: PRO80778
Figure 672: DNA324067, XM_092135,
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Figure 673: PRO80779
Figure 674: DNA324068, NM_017910,
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Figure 675: PRO80780
Figure 676: DNA324069, XM_092517,
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Figure 677: PRO80781
Figure 678A-B: DNA324070, NM_025203,
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Figure 679: PRO80782
Figure 680: DNA324071, XM_002480,
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Figure 681: DNA324072, NM_002707,
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Figure 682: PRO12199
Figure 683: DNA324073, XM_087151,
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Figure 684: DNA227165, NM_014748,
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Figure 685: PRO37628
Figure 686: DNA324074, NM_015636,
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Figure 687: PRO80785
Figure 688: DNA273800, NM_001521,
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Figure 689: PRO61761
Figure 690: DNA324075, XM_047175,
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Figure 691: PRO80786
Figure 692A-B: DNA324076, NM_004341,
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Figure 693: PRO80787
Figure 694: DNA324077, NM_016085,
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Figure 695: PRO80788
Figure 696: DNA324078, NM_080592,
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Figure 697: PRO80789
Figure 698: DNA227545, NM_021095,
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Figure 699: PRO38008
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Figure 701: DNA324080, NM_000221,
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Figure 702: PRO80790
Figure 703: DNA271243, NM_006488,
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Figure 704: PRO59558
Figure 705: DNA324081, NM_007046,
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Figure 706: PRO9886
Figure 707: DNA324082, NM_021831,
gen.NM_021831
Figure 708: PRO80791
Figure 709: DNA324083, NM_020134,
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Figure 710: PRO80792
Figure 711: DNA103593, NM_000183,
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Figure 712: PRO4917
Figure 713: DNA324084, NM_000182,
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Figure 714: PRO80793
Figure 715: DNA324085, XM_097976,
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Figure 716A-B: DNA324086, XM_039712,
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Figure 717: DNA324087, NM_022552,
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Figure 718: PRO80796
Figure 719: DNA324088, NM_024572,
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Figure 720: PRO80797
Figure 721: DNA324089, NM_018607,
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Figure 722: PRO80798
Figure 723: DNA324090, XM_165448,
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Figure 724: PRO80799
Figure 725: DNA324091, XM_087195,
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Figure 726: DNA324092, XM_087193,
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Figure 727: DNA324093, NM_138801,
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Figure 728: PRO80802
Figure 729: DNA324094, XM_098004,
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Figure 730: PRO80803
Figure 731: DNA324095, XM_031519,
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Figure 732: PRO80804
Figure 733A-B: DNA324096, XM_031527,
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Figure 734: DNA324097, XM_038576,
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Figure 735: PRO80806

WO 2004/030615

PCT/US2003/028547

Figure 736: DNA324098, XM_117264,
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Figure 738A-B: DNA324099, XM_031626,
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Figure 739: PRO80808
Figure 740: DNA324100, XM_057664,
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Figure 741: DNA226428, NM_000251,
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Figure 742: PRO36891
Figure 743: DNA324101, XM_087211,
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Figure 744A-B: DNA275066, NM_000179,
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Figure 745: PRO62786
Figure 746A-C: DNA270154, NM_003128,
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Figure 747: PRO58543
Figure 748: DNA324102, XM_087051,
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Figure 749: DNA324103, NM_002954,
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Figure 750: PRO62239
Figure 751: DNA271060, NM_002453,
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Figure 752: PRO59384
Figure 753: DNA324104, XM_048088,
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Figure 754: PRO80811
Figure 755: DNA324105, XM_010886,
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Figure 756: PRO80812
Figure 757: DNA324106, XM_045283,
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Figure 758: PRO80813
Figure 759: DNA324107, NM_006430,
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Figure 760: PRO80814
Figure 761A-B: DNA324108, NM_003400,
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Figure 762: PRO59544
Figure 763: DNA324109, XM_018301,
gen.XM_018301
Figure 764: DNA324110, NM_005917,
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Figure 765: PRO4918
Figure 766: DNA324111, XM_016843,
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Figure 767: PRO80816
Figure 768: DNA324112, XM_088638,
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Figure 769: PRO80817
Figure 770: DNA324113, XM_002647,
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Figure 771: DNA324114, XM_010881,

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Figure 772: DNA324115, XM_087069,
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Figure 773: DNA324116, XM_016625,
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Figure 774: PRO80820
Figure 775: DNA324117, XM_087068,
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Figure 776: DNA324118, XM_002674,
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Figure 777: DNA324119, XM_065884,
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Figure 778: PRO80823
Figure 779A-B: DNA324120, XM_002739,
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Figure 780: DNA324121, XM_031596,
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Figure 781: PRO61325
Figure 782: DNA324122, XM_031585,
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Figure 783: DNA324123, XM_031586,
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Figure 784: DNA324124, XM_018039,
gen.XM_018039
Figure 785: DNA324125, NM_032822,
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Figure 786: PRO80827
Figure 787A-B: DNA324126, XM_096172,
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Figure 788A-B: DNA324127, XM_002727,
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Figure 789: DNA324128, NM_003124,
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Figure 790: PRO80830
Figure 791: DNA324129, XM_086980,
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Figure 792: DNA227795, NM_006429,
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Figure 793: PRO38258
Figure 794: DNA287167, NM_006636,
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Figure 795: PRO59136
Figure 796: DNA324130, NM_033046,
gen.NM_033046
Figure 797: PRO80832
Figure 798: DNA324131, NM_133637,
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Figure 799: PRO80833
Figure 800: DNA324132, XM_035220,
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Figure 801: DNA324133, NM_013247,
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Figure 802: PRO80835
Figure 803: DNA227528, NM_021103,
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Figure 804: PRO37991

WO 2004/030615

PCT/US2003/028547

Figure 805: DNA324134, XM_086920,
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Figure 806: DNA150725, NM_001747,
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Figure 807: PRO12792
Figure 808: DNA324135, NM_005911,
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Figure 809: PRO80837
Figure 810: DNA324136, NM_032827,
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Figure 811: PRO80838
Figure 812: DNA324137, NM_017952,
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Figure 813: PRO80839
Figure 814: DNA227190, NM_006839,
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Figure 815: PRO37653
Figure 816: DNA324138, XM_114215,
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Figure 817: DNA324139, XM_052989,
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Figure 818: DNA324140, XM_049116,
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Figure 819: PRO80842
Figure 820A-B: DNA324141, XM_049108,
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Figure 821: PRO80843
Figure 822: DNA324142, XM_049113,
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Figure 823: DNA324143, XM_002611,
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Figure 824A-B: DNA324144, XM_114247,
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Figure 825: DNA324145, NM_017789,
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Figure 826: PRO80846
Figure 827: DNA324146, NM_001862,
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Figure 828: PRO80847
Figure 829: DNA324147, NM_005783,
gen.NM_005783
Figure 830: PRO80848
Figure 831A-B: DNA324148, XM_037108,
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Figure 832: DNA324149, NM_000993,
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Figure 833: PRO11197
Figure 834: DNA324150, NM_017546,
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Figure 835: PRO80850
Figure 836: DNA324151, NM_001450,
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Figure 837: PRO80851
Figure 838: DNA324152, XM_114229,
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Figure 839: DNA324153, XM_087122,

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Figure 840: PRO80853
Figure 841: DNA324154, XM_018540,
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Figure 842: DNA324155, XM_087040,
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Figure 843: DNA324156, NM_032212,
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Figure 844: PRO80856
Figure 845: DNA324157, XM_002217,
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Figure 846: PRO80857
Figure 847: DNA324158, NM_000576,
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Figure 848: PRO65
Figure 849: DNA324159, XM_086923,
gen.XM_086923
Figure 850: DNA324160, XM_086925,
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Figure 851A-B: DNA324161, XM_114266,
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Figure 852: PRO80860
Figure 853: DNA324162, XM_002704,
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Figure 854: DNA194740, NM_005291,
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Figure 855: PRO24028
Figure 856A-B: DNA324163, XM_114267,
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Figure 857: DNA324164, XM_034952,
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Figure 858: DNA324165, XM_086950,
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Figure 859A-B: DNA255531, NM_017751,
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Figure 860: PRO50596
Figure 861: DNA324166, XM_017698,
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Figure 862: DNA324167, XM_030529,
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Figure 863: PRO80866
Figure 864: DNA275240, NM_005915,
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Figure 865: PRO62927
Figure 866: DNA324168, XM_043173,
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Figure 867: DNA324169, XM_092489,
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Figure 868: PRO80868
Figure 869: DNA324170, XM_115672,
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Figure 870: PRO80869
Figure 871: DNA324171, NM_020548,
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Figure 872: PRO60753
Figure 873: DNA324172, XM_037101,

WO 2004/030615

PCT/US2003/028547

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Figure 875: DNA324173, NM_032390,
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Figure 876: PRO80871
Figure 877: DNA324174, XM_002447,
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Figure 878: DNA324175, NM_033416,
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Figure 879: PRO80873
Figure 880: DNA324176, XM_016288,
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Figure 881: DNA272127, NM_003937,
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Figure 882: PRO60397
Figure 883: DNA324177, XM_030582,
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Figure 884: PRO80875
Figure 885: DNA324178, NM_015702,
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Figure 886: PRO80876
Figure 887: DNA324179, NM_016838,
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Figure 888: PRO80877
Figure 889: DNA324180, NM_016839,
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Figure 890: PRO80878
Figure 891: DNA324181, XM_087118,
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Figure 892: PRO80879
Figure 893: DNA324182, XM_165998,
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Figure 894: DNA324183, NM_001935,
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Figure 895: PRO80881
Figure 896: DNA324184, NM_020675,
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Figure 897: PRO80882
Figure 898: DNA88051, NM_000079, gen.NM_000079
Figure 899: PRO2146
Figure 900: DNA324185, XM_166008,
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Figure 901: DNA324186, XM_087240,
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Figure 902: PRO11403
Figure 903: DNA324187, NM_013341,
gen.NM_013341
Figure 904: PRO80883
Figure 905: DNA304805, NM_031942,
gen.NM_031942
Figure 906: PRO69531
Figure 907: DNA324188, XM_059465,
gen.XM_059465
Figure 908: PRO80884
Figure 909: DNA324189, XM_015920,
gen.XM_015920

Figure 910: DNA324190, XM_166007,
gen.XM_166007
Figure 911: DNA324191, XM_015922,
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Figure 912: DNA324192, XM_087061,
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Figure 913: PRO80888
Figure 914: DNA324193, XM_087062,
gen.XM_087062
Figure 915: PRO80889
Figure 916: DNA324194, NM_001463,
gen.NM_001463
Figure 917: PRO80890
Figure 918: DNA324195, XM_092158,
gen.XM_092158
Figure 919: PRO80891
Figure 920: DNA324196, XM_059351,
gen.XM_059351
Figure 921A-B: DNA324197, NM_000090,
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Figure 922: PRO2665
Figure 923: DNA324198, NM_014585,
gen.NM_014585
Figure 924: PRO37675
Figure 925: DNA324199, XM_010778,
gen.XM_010778
Figure 926: DNA324200, XM_086961,
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Figure 927: DNA324201, XM_165994,
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Figure 928: DNA324202, XM_045170,
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Figure 929: DNA324203, XM_113390,
gen.XM_113390
Figure 930: DNA299899, NM_002157,
gen.NM_002157
Figure 931: PRO62760
Figure 932: DNA324204, XM_087045,
gen.XM_087045
Figure 933: DNA324205, XM_086944,
gen.XM_086944
Figure 934: DNA271608, NM_014670,
gen.NM_014670
Figure 935: PRO59895
Figure 936: DNA324206, XM_027963,
gen.XM_027963
Figure 937: PRO80900
Figure 938: DNA324207, XM_010852,
gen.XM_010852
Figure 939: PRO80901
Figure 940: DNA324208, XM_028034,
gen.XM_028034
Figure 941: DNA324209, NM_015934,
gen.NM_015934
Figure 942: DNA324210, XM_087028,
gen.XM_087028

WO 2004/030615

PCT/US2003/028547

Figure 943: PRO80903
Figure 944: DNA324211, XM_092346,
gen.XM_092346
Figure 945: PRO80904
Figure 946: DNA324212, XM_002669,
gen.XM_002669
Figure 947: PRO80905
Figure 948: DNA324213, NM_021121,
gen.NM_021121
Figure 949: PRO23124
Figure 950: DNA324214, NM_001959,
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Figure 951: PRO23124
Figure 952: DNA324215, XM_030834,
gen.XM_030834
Figure 953: PRO80906
Figure 954A-C: DNA324216, XM_055254,
gen.XM_055254
Figure 955: DNA324217, NM_004044,
gen.NM_004044
Figure 956: PRO80908
Figure 957: DNA324218, XM_114298,
gen.XM_114298
Figure 958: DNA324219, NM_021141,
gen.NM_021141
Figure 959: PRO59313
Figure 960A-B: DNA324220, XM_098048,
gen.XM_098048
Figure 961: PRO80910
Figure 962: DNA324221, XM_098047,
gen.XM_098047
Figure 963: PRO80911
Figure 964: DNA324222, XM_002636,
gen.XM_002636
Figure 965: DNA324223, XM_087181,
gen.XM_087181
Figure 966: DNA324224, NM_000998,
gen.NM_000998
Figure 967: PRO10498
Figure 968: DNA324225, XM_059422,
gen.XM_059422
Figure 969: PRO9984
Figure 970: DNA324226, XM_092545,
gen.XM_092545
Figure 971: DNA324227, XM_059461,
gen.XM_059461
Figure 972: PRO80915
Figure 973: DNA324228, NM_018674,
gen.NM_018674
Figure 974: PRO80916
Figure 975: DNA324229, XM_050962,
gen.XM_050962
Figure 976: PRO80917
Figure 977: DNA194827, NM_012100,
gen.NM_012100
Figure 978: PRO24091

Figure 979: DNA324230, XM_050638,
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Figure 980A-B: DNA324231, NM_002846,
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Figure 981: PRO2610
Figure 982: DNA324232, NM_006000,
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Figure 983: PRO26228
Figure 984: DNA324233, XM_050891,
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Figure 985: DNA324234, XM_087162,
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Figure 986: DNA324235, XM_058098,
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Figure 987: PRO80920
Figure 988: DNA324236, NM_022453,
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Figure 989: PRO80921
Figure 990: DNA324237, NM_032726,
gen.NM_032726
Figure 991: PRO70675
Figure 992: DNA324238, XM_010866,
gen.XM_010866
Figure 993: DNA324239, XM_087166,
gen.XM_087166
Figure 994: DNA254204, NM_001087,
gen.NM_001087
Figure 995: PRO49316
Figure 996: DNA324240, NM_005731,
gen.NM_005731
Figure 997: PRO80924
Figure 998: DNA189697, NM_004846,
gen.NM_004846
Figure 999: PRO23123
Figure 1000: DNA324241, NM_025202,
gen.NM_025202
Figure 1001: PRO80925
Figure 1002: DNA324242, XM_115825,
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Figure 1003: PRO80926
Figure 1004: DNA324243, XM_010858,
gen.XM_010858
Figure 1005: PRO80927
Figure 1006: DNA324244, XM_002540,
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Figure 1007: DNA324245, XM_048690,
gen.XM_048690
Figure 1008: PRO80929
Figure 1009: DNA324246, NM_030926,
gen.NM_030926
Figure 1010: PRO80930
Figure 1011: DNA324247, XM_087218,
gen.XM_087218
Figure 1012: DNA324248, NM_004509,
gen.NM_004509
Figure 1013: PRO80932

WO 2004/030615

PCT/US2003/028547

Figure 1014: DNA324249, NM_004510, gen.NM_004510
Figure 1015: PRO80933
Figure 1016: DNA324250, NM_080424, gen.NM_080424
Figure 1017: PRO80934
Figure 1018: DNA324251, NM_018410, gen.NM_018410
Figure 1019: PRO80935
Figure 1020: DNA324252, NM_017974, gen.NM_017974
Figure 1021: PRO80936
Figure 1022A-B: DNA324253, XM_096169, gen.XM_096169
Figure 1023: PRO80937
Figure 1024: DNA150884, NM_005855, gen.NM_005855
Figure 1025: PRO12520
Figure 1026A-B: DNA324254, NM_004735, gen.NM_004735
Figure 1027: PRO80938
Figure 1028A-C: DNA324255, XM_030203, gen.XM_030203
Figure 1029: DNA324256, XM_059372, gen.XM_059372
Figure 1030: DNA324257, NM_002712, gen.NM_002712
Figure 1031: PRO80941
Figure 1032A-B: DNA324258, XM_042326, gen.XM_042326
Figure 1033: PRO80942
Figure 1034: DNA324259, NM_004404, gen.NM_004404
Figure 1035: PRO80943
Figure 1036: DNA324260, XM_002742, gen.XM_002742
Figure 1037: DNA324261, NM_138483, gen.NM_138483
Figure 1038: PRO80945
Figure 1039: DNA324262, XM_115706, gen.XM_115706
Figure 1040: DNA324263, XM_115722, gen.XM_115722
Figure 1041: DNA324264, XM_084141, gen.XM_084141
Figure 1042: DNA324265, XM_005086, gen.XM_005086
Figure 1043: DNA324266, NM_015453, gen.NM_015453
Figure 1044: PRO80949
Figure 1045: DNA324267, NM_022485, gen.NM_022485
Figure 1046: PRO80950
Figure 1047A-B: DNA324268, XM_054520, gen.XM_054520
Figure 1048: PRO80951

Figure 1049: DNA324269, NM_006354, gen.NM_006354
Figure 1050: PRO80952
Figure 1051: DNA324270, NM_133480, gen.NM_133480
Figure 1052: PRO80953
Figure 1053: DNA324271, NM_133481, gen.NM_133481
Figure 1054: PRO80954
Figure 1055: DNA324272, NM_005718, gen.NM_005718
Figure 1056: PRO80955
Figure 1057: DNA324273, NM_015644, gen.NM_015644
Figure 1058: PRO80956
Figure 1059: DNA324274, XM_059561, gen.XM_059561
Figure 1060: DNA324275, XM_052310, gen.XM_052310
Figure 1061: PRO80958
Figure 1062: DNA269910, NM_006395, gen.NM_006395
Figure 1063: PRO58308
Figure 1064: DNA324276, NM_000994, gen.NM_000994
Figure 1065: PRO80959
Figure 1066: DNA151017, NM_004844, gen.NM_004844
Figure 1067: PRO12841
Figure 1068: DNA324277, XM_059557, gen.XM_059557
Figure 1069: PRO80960
Figure 1070A-B: DNA324278, XM_042860, gen.XM_042860
Figure 1071: PRO80961
Figure 1072: DNA324279, XM_042841, gen.XM_042841
Figure 1073: PRO80962
Figure 1074: DNA324280, XM_053712, gen.XM_053712
Figure 1075: DNA324281, XM_087284, gen.XM_087284
Figure 1076: DNA324282, NM_002948, gen.NM_002948
Figure 1077: PRO6360
Figure 1078: DNA324283, XM_053323, gen.XM_053323
Figure 1079A-B: DNA324284, NM_001068, gen.NM_001068
Figure 1080: PRO80966
Figure 1081: DNA252367, NM_017801, gen.NM_017801
Figure 1082: PRO48357
Figure 1083: DNA324285, XM_093624, gen.XM_093624
Figure 1084: PRO80967

WO 2004/030615

PCT/US2003/028547

Figure 1085: DNA324286, XM_046401,
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Figure 1086: DNA324287, NM_022461,
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Figure 1087: PRO80969
Figure 1088: DNA324288, XM_113410,
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Figure 1089: DNA88100, NM_000404,
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Figure 1090: PRO2172
Figure 1091: DNA324289, XM_091076,
gen.XM_091076
Figure 1092: PRO80970
Figure 1093A-B: DNA271187, NM_005109,
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Figure 1094: PRO59504
Figure 1095: DNA324290, NM_002468,
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Figure 1096: PRO36735
Figure 1097: DNA269930, NM_001607,
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Figure 1098: PRO58328
Figure 1099: DNA270401, NM_003149,
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Figure 1100: PRO58784
Figure 1101: DNA324291, XM_087370,
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Figure 1102: PRO80971
Figure 1103: DNA324292, XM_098158,
gen.XM_098158
Figure 1104: PRO80972
Figure 1105: DNA324293, XM_017364,
gen.XM_017364
Figure 1106: DNA324294, XM_087349,
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Figure 1107: PRO80974
Figure 1108: DNA226547, NM_002295,
gen.NM_002295
Figure 1109: PRO37010
Figure 1110: DNA324295, NM_003973,
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Figure 1111: PRO80975
Figure 1112: DNA324296, XM_030417,
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Figure 1113: DNA324297, NM_020347,
gen.NM_020347
Figure 1114: PRO80977
Figure 1115: DNA324298, XM_087346,
gen.XM_087346
Figure 1116: PRO80978
Figure 1117: DNA324299, XM_096198,
gen.XM_096198
Figure 1118: PRO80979
Figure 1119: DNA324300, XM_003222,
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Figure 1120: DNA324301, XM_087588,

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Figure 1121: DNA324302, XM_166011,
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Figure 1122A-B: DNA324303, XM_114364,
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Figure 1123A-B: DNA324304, XM_033294,
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Figure 1124: PRO80983
Figure 1125: DNA324305, NM_138614,
gen.NM_138614
Figure 1126: PRO80984
Figure 1127: DNA324306, XM_002899,
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Figure 1128: DNA225910, NM_004345,
gen.NM_004345
Figure 1129: PRO36373
Figure 1130: DNA324307, XM_010953,
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Figure 1131: DNA324308, XM_051518,
gen.XM_051518
Figure 1132A-D: DNA324309, NM_001407,
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Figure 1133: PRO50095
Figure 1134: DNA324310, NM_003365,
gen.NM_003365
Figure 1135: PRO80988
Figure 1136: DNA324311, XM_003245,
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Figure 1137: DNA324312, XM_047561,
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Figure 1138: PRO80990
Figure 1139: DNA324313, XM_116853,
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Figure 1140A-B: DNA324314, XM_113405,
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Figure 1141: DNA324315, XM_114323,
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Figure 1142: PRO80993
Figure 1143: DNA324316, XM_002828,
gen.XM_002828
Figure 1144: PRO80994
Figure 1145: DNA150976, NM_022171,
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Figure 1146: PRO12565
Figure 1147: DNA324317, XM_041507,
gen.XM_041507
Figure 1148: PRO71103
Figure 1149: DNA103505, NM_004636,
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Figure 1150: PRO4832
Figure 1151: DNA324318, NM_006764,
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Figure 1152: PRO80995
Figure 1153: DNA150562, NM_007275,
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Figure 1154: PRO12779

WO 2004/030615

PCT/US2003/028547

Figure 1155: DNA254582, NM_004635,
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Figure 1157: DNA324319, NM_052859,
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Figure 1159: DNA324320, NM_001064,
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Figure 1160: PRO80997
Figure 1161: DNA324321, XM_041211,
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Figure 1162: DNA324322, XM_003213,
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Figure 1163A-C: DNA324323, XM_037423,
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Figure 1164: PRO80999
Figure 1165A-B: DNA227307, NM_007184,
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Figure 1166: PRO37770
Figure 1167: DNA324324, NM_000688,
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Figure 1168: PRO81000
Figure 1169: DNA324325, XM_067715,
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Figure 1170: DNA324326, NM_000992,
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Figure 1171: PRO62153
Figure 1172: DNA324327, NM_000666,
gen.NM_000666
Figure 1173: PRO81002
Figure 1174: DNA324328, NM_032750,
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Figure 1175: PRO81003
Figure 1176: DNA324329, NM_033008,
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Figure 1177: PRO81004
Figure 1178: DNA324330, NM_033010,
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Figure 1179: PRO81005
Figure 1180: DNA324331, NM_020418,
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Figure 1181: PRO81006
Figure 1182: DNA273919, NM_004704,
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Figure 1183: PRO61870
Figure 1184A-B: DNA324332, XM_087448,
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Figure 1185: PRO81007
Figure 1186: DNA324333, XM_002855,
gen.XM_002855
Figure 1187: DNA324334, XM_002854,
gen.XM_002854
Figure 1188: DNA0, NM_002854, gen.NM_002854
Figure 1189: PRO
Figure 1190: DNA324335, XM_096195,
gen.XM_096195

Figure 1191: PRO81010
Figure 1192: DNA324336, XM_166015,
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Figure 1193: DNA324337, XM_113395,
gen.XM_113395
Figure 1194: PRO81012
Figure 1195: DNA269730, NM_014814,
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Figure 1196: PRO58140
Figure 1197: DNA324338, XM_036938,
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Figure 1198: DNA324339, XM_029369,
gen.XM_029369
Figure 1199: DNA324340, XM_076414,
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Figure 1200: PRO81015
Figure 1201: DNA324341, XM_093546,
gen.XM_093546
Figure 1202: DNA324342, XM_113409,
gen.XM_113409
Figure 1203: DNA324343, XM_087268,
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Figure 1204: DNA324344, XM_116071,
gen.XM_116071
Figure 1205: DNA324345, XM_116072,
gen.XM_116072
Figure 1206: DNA324346, NM_000986,
gen.NM_000986
Figure 1207: PRO10602
Figure 1208: DNA324347, XM_015462,
gen.XM_015462
Figure 1209: DNA324348, XM_167366,
gen.XM_167366
Figure 1210: PRO81022
Figure 1211: DNA324349, XM_087331,
gen.XM_087331
Figure 1212: PRO81023
Figure 1213: DNA324350, XM_039952,
gen.XM_039952
Figure 1214: DNA324351, XM_045290,
gen.XM_045290
Figure 1215: PRO81025
Figure 1216A-B: DNA324352, NM_007085,
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Figure 1217: PRO2077
Figure 1218: DNA324353, NM_004547,
gen.NM_004547
Figure 1219: PRO81026
Figure 1220: DNA324354, XM_027161,
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Figure 1221A-B: DNA324355, XM_032269,
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Figure 1222: PRO81028
Figure 1223: DNA88547, NM_006810,
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Figure 1224: PRO2837

WO 2004/030615

PCT/US2003/028547

Figure 1225: DNA324356, XM_114301,
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Figure 1226: PRO81029
Figure 1227: DNA324357, XM_098173,
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Figure 1228: PRO81030
Figure 1229: DNA324358, XM_042618,
gen.XM_042618
Figure 1230: PRO81031
Figure 1231: DNA324359, XM_084129,
gen.XM_084129
Figure 1232: DNA324360, XM_098154,
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Figure 1233: PRO81033
Figure 1234: DNA324361, XM_050552,
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Figure 1235: DNA324362, NM_032343,
gen.NM_032343
Figure 1236: PRO81034
Figure 1237: DNA324363, XM_051264,
gen.XM_051264
Figure 1238A-B: DNA324364, NM_013336,
gen.NM_013336
Figure 1239: PRO1314
Figure 1240: DNA324365, XM_067264,
gen.XM_067264
Figure 1241: PRO81036
Figure 1242: DNA324366, XM_114309,
gen.XM_114309
Figure 1243: DNA324367, XM_084111,
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Figure 1244: DNA324368, XM_113397,
gen.XM_113397
Figure 1245: DNA324369, XM_098111,
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Figure 1246: DNA324370, NM_004637,
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Figure 1247: PRO81040
Figure 1248: DNA324371, NM_020701,
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Figure 1249: PRO81041
Figure 1250: DNA324372, NM_003418,
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Figure 1251: PRO81042
Figure 1252: DNA324373, XM_059583,
gen.XM_059583
Figure 1253: PRO81043
Figure 1254: DNA324374, XM_113417,
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Figure 1255: DNA324375, XM_093487,
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Figure 1256A-B: DNA324376, XM_030812,
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Figure 1257: PRO58177
Figure 1258A-B: DNA324377, XM_039805,
gen.XM_039805

Figure 1259: PRO81046
Figure 1260: DNA324378, NM_000532,
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Figure 1261: PRO81047
Figure 1262: DNA324379, XM_036118,
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Figure 1263: DNA324380, XM_084123,
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Figure 1264: DNA324381, XM_018149,
gen.XM_018149
Figure 1265: DNA324382, XM_087342,
gen.XM_087342
Figure 1266: DNA324383, XM_059516,
gen.XM_059516
Figure 1267: DNA324384, XM_087341,
gen.XM_087341
Figure 1268: DNA324385, XM_165451,
gen.XM_165451
Figure 1269: PRO81053
Figure 1270: DNA269858, NM_004766,
gen.NM_004766
Figure 1271: PRO58259
Figure 1272: DNA324386, NM_030921,
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Figure 1273: PRO51109
Figure 1274: DNA324387, XM_002859,
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Figure 1275: DNA324388, XM_166014,
gen.XM_166014
Figure 1276: DNA324389, NM_013363,
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Figure 1277: PRO287
Figure 1278: DNA324390, XM_058267,
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Figure 1279: PRO81056
Figure 1280A-B: DNA324391, NM_032383,
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Figure 1281: PRO81057
Figure 1282: DNA324392, NM_015472,
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Figure 1283: PRO81058
Figure 1284: DNA324393, NM_014445,
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Figure 1285: PRO11048
Figure 1286: DNA324394, XM_042168,
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Figure 1287: PRO81059
Figure 1288A-B: DNA324395, XM_114356,
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Figure 1289: DNA324396, XM_105236,
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Figure 1290: DNA324397, XM_010978,
gen.XM_010978
Figure 1291: DNA324398, XM_017356,
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Figure 1292A-B: DNA324399, XM_039796,

WO 2004/030615

PCT/US2003/028547

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Figure 1294: DNA324400, XM_016334,
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Figure 1295: DNA324401, XM_116058,
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Figure 1296: DNA324402, XM_113408,
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Figure 1297: DNA324403, NM_002492,
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Figure 1298: PRO81068
Figure 1299: DNA324404, XM_037381,
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Figure 1300: DNA324405, XM_037377,
gen.XM_037377
Figure 1301: PRO69681
Figure 1302A-B: DNA324406, XM_087254,
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Figure 1303: PRO81070
Figure 1304: DNA324407, XM_037600,
gen.XM_037600
Figure 1305: PRO81071
Figure 1306: DNA324408, NM_018023,
gen.NM_018023
Figure 1307: PRO81072
Figure 1308: DNA324409, XM_093423,
gen.XM_093423
Figure 1309: PRO81073
Figure 1310: DNA324410, XM_029136,
gen.XM_029136
Figure 1311: PRO81074
Figure 1312: DNA324411, XM_087322,
gen.XM_087322
Figure 1313A-B: DNA324412, XM_029132,
gen.XM_029132
Figure 1314A-B: DNA324413, XM_029104,
gen.XM_029104
Figure 1315: DNA324414, XM_084120,
gen.XM_084120
Figure 1316: DNA254620, NM_005787,
gen.NM_005787
Figure 1317: PRO49722
Figure 1318: DNA324415, NM_032331,
gen.NM_032331
Figure 1319: PRO81079
Figure 1320: DNA324416, XM_011074,
gen.XM_011074
Figure 1321: PRO81080
Figure 1322: DNA324417, XM_087295,
gen.XM_087295
Figure 1323: DNA324418, XM_087289,
gen.XM_087289
Figure 1324: PRO81082
Figure 1325: DNA324419, XM_105658,
gen.XM_105658
Figure 1326: PRO81083

Figure 1327: DNA89239, NM_000893,
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Figure 1328: PRO2906
Figure 1329: DNA324420, XM_113422,
gen.XM_113422
Figure 1330: DNA225592, NM_001622,
gen.NM_001622
Figure 1331: PRO36055
Figure 1332: DNA324421, XM_005180,
gen.XM_005180
Figure 1333: DNA324422, XM_087392,
gen.XM_087392
Figure 1334: PRO81086
Figure 1335A-B: DNA272605, NM_003722,
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Figure 1336: PRO60741
Figure 1337: DNA324423, XM_117311,
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Figure 1338: DNA324424, XM_116034,
gen.XM_116034
Figure 1339: PRO81088
Figure 1340A-B: DNA324425, XM_084110,
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Figure 1341: DNA324426, XM_038243,
gen.XM_038243
Figure 1342: PRO81090
Figure 1343: DNA324427, XM_087359,
gen.XM_087359
Figure 1344: DNA324428, XM_114328,
gen.XM_114328
Figure 1345: DNA324429, XM_098109,
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Figure 1346: PRO81093
Figure 1347: DNA324430, XM_087410,
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Figure 1348: DNA324431, NM_033316,
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Figure 1349: PRO81095
Figure 1350: DNA324432, XM_166017,
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Figure 1351: PRO81096
Figure 1352: DNA79129, NM_001647,
gen.NM_001647
Figure 1353: PRO2551
Figure 1354: DNA324433, NM_032288,
gen.NM_032288
Figure 1355: PRO81097
Figure 1356: DNA324434, XM_086228,
gen.XM_086228
Figure 1357: PRO81098
Figure 1358: DNA324435, XM_087278,
gen.XM_087278
Figure 1359: DNA324436, XM_018523,
gen.XM_018523
Figure 1360: DNA324437, XM_087297,
gen.XM_087297

WO 2004/030615

PCT/US2003/028547

Figure 1361: DNA324438, XM_002255,
gen.XM_002255
Figure 1362: PRO81102
Figure 1363: DNA324439, XM_053122,
gen.XM_053122
Figure 1364: DNA324440, XM_042695,
gen.XM_042695
Figure 1365: DNA324441, XM_011160,
gen.XM_011160
Figure 1366: DNA324442, NM_007100,
gen.NM_007100
Figure 1367: PRO81106
Figure 1368: DNA139747, NM_002477,
gen.NM_002477
Figure 1369: PRO9785
Figure 1370: DNA253804, NM_032219,
gen.NM_032219
Figure 1371: PRO49209
Figure 1372: DNA324443, NM_138385,
gen.NM_138385
Figure 1373: PRO81107
Figure 1374: DNA324444, NM_006342,
gen.NM_006342
Figure 1375: PRO81108
Figure 1376A-C: DNA324445, NM_133330,
gen.NM_133330
Figure 1377: PRO81109
Figure 1378A-C: DNA324446, NM_014919,
gen.NM_014919
Figure 1379: PRO81110
Figure 1380A-C: DNA324447, NM_133332,
gen.NM_133332
Figure 1381: PRO81111
Figure 1382: DNA324448, NM_005663,
gen.NM_005663
Figure 1383: PRO81112
Figure 1384A-B: DNA324449, XM_098248,
gen.XM_098248
Figure 1385: PRO81113
Figure 1386: DNA270615, NM_002938,
gen.NM_002938
Figure 1387: PRO58986
Figure 1388A-B: DNA324450, NM_014190,
gen.NM_014190
Figure 1389: PRO81114
Figure 1390A-B: DNA324451, NM_014189,
gen.NM_014189
Figure 1391: PRO81115
Figure 1392: DNA324452, XM_035572,
gen.XM_035572
Figure 1393: PRO81116
Figure 1394A-B: DNA324453, NM_014556,
gen.NM_014556
Figure 1395: PRO81117
Figure 1396: DNA324454, NM_001313,
gen.NM_001313

Figure 1397: PRO60542
Figure 1398A-B: DNA324455, XM_052626,
gen.XM_052626
Figure 1399: PRO81118
Figure 1400: DNA324456, NM_016930,
gen.NM_016930
Figure 1401: PRO81119
Figure 1402: DNA324457, XM_035824,
gen.XM_035824
Figure 1403: PRO81120
Figure 1404: DNA324458, NM_033296,
gen.NM_033296
Figure 1405: PRO81121
Figure 1406: DNA324459, NM_138699,
gen.NM_138699
Figure 1407: PRO81122
Figure 1408: DNA324460, XM_116285,
gen.XM_116285
Figure 1409: PRO81123
Figure 1410: DNA324461, XM_041221,
gen.XM_041221
Figure 1411: PRO81124
Figure 1412: DNA324462, XM_117351,
gen.XM_117351
Figure 1413: DNA324463, XM_039165,
gen.XM_039165
Figure 1414: DNA324464, NM_025205,
gen.NM_025205
Figure 1415: PRO81127
Figure 1416: DNA324465, XM_039173,
gen.XM_039173
Figure 1417: DNA324466, XM_039176,
gen.XM_039176
Figure 1418: DNA324467, XM_087583,
gen.XM_087583
Figure 1419: DNA324468, NM_017491,
gen.NM_017491
Figure 1420: PRO12077
Figure 1421: DNA324469, NM_005112,
gen.NM_005112
Figure 1422: PRO81131
Figure 1423: DNA324470, XM_011129,
gen.XM_011129
Figure 1424A-B: DNA324471, XM_052530,
gen.XM_052530
Figure 1425: DNA324472, NM_000661,
gen.NM_000661
Figure 1426: PRO81134
Figure 1427A-B: DNA324473, NM_002913,
gen.NM_002913
Figure 1428: PRO81135
Figure 1429A-B: DNA324474, XM_047477,
gen.XM_047477
Figure 1430: DNA324475, NM_004181,
gen.NM_004181
Figure 1431: PRO81137

WO 2004/030615

PCT/US2003/028547

Figure 1432: DNA324476, XM_003435,
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Figure 1433: DNA324478, XM_010941,
gen.XM_010941
Figure 1434: DNA324479, XM_059593,
gen.XM_059593
Figure 1435: DNA324480, NM_001553,
gen.NM_001553
Figure 1436: PRO81141
Figure 1437: DNA257511, NM_032313,
gen.NM_032313
Figure 1438: PRO52083
Figure 1439: DNA324481, XM_071623,
gen.XM_071623
Figure 1440A-B: DNA324482, XM_036002,
gen.XM_036002
Figure 1441: DNA324483, XM_058927,
gen.XM_058927
Figure 1442: DNA324484, XM_059628,
gen.XM_059628
Figure 1443: DNA324485, XM_046057,
gen.XM_046057
Figure 1444: PRO81146
Figure 1445: DNA324486, XM_031320,
gen.XM_031320
Figure 1446: DNA225919, NM_001134,
gen.NM_001134
Figure 1447: PRO36382
Figure 1448A-B: DNA324487, XM_003511,
gen.XM_003511
Figure 1449: DNA324488, NM_006835,
gen.NM_006835
Figure 1450: PRO4605
Figure 1451: DNA324489, XM_003305,
gen.XM_003305
Figure 1452: DNA324490, XM_113425,
gen.XM_113425
Figure 1453: DNA324491, XM_001389,
gen.XM_001389
Figure 1454: PRO81148
Figure 1455: DNA324492, XM_087527,
gen.XM_087527
Figure 1456: DNA324493, XM_035986,
gen.XM_035986
Figure 1457A-B: DNA324494, NM_014933,
gen.NM_014933
Figure 1458: PRO81150
Figure 1459: DNA290585, NM_000582,
gen.NM_000582
Figure 1460: PRO70536
Figure 1461: DNA324495, XM_055551,
gen.XM_055551
Figure 1462: PRO81151
Figure 1463: DNA324496, XM_087498,
gen.XM_087498
Figure 1464: DNA324497, XM_096203,

gen.XM_096203
Figure 1465: DNA324498, XM_084158,
gen.XM_084158
Figure 1466: DNA324499, XM_034710,
gen.XM_034710
Figure 1467: PRO81156
Figure 1468: DNA324500, XM_034713,
gen.XM_034713
Figure 1469: DNA324501, XM_059633,
gen.XM_059633
Figure 1470: DNA324502, XM_114426,
gen.XM_114426
Figure 1471: DNA324503, XM_056957,
gen.XM_056957
Figure 1472: DNA324504, XM_088472,
gen.XM_088472
Figure 1473: DNA324505, XM_114424,
gen.XM_114424
Figure 1474A-B: DNA324506, XM_042301,
gen.XM_042301
Figure 1475: PRO81163
Figure 1476: DNA324507, XM_017925,
gen.XM_017925
Figure 1477: DNA324508, XM_052336,
gen.XM_052336
Figure 1478: DNA324509, NM_002106,
gen.NM_002106
Figure 1479: PRO10297
Figure 1480: DNA324510, XM_085068,
gen.XM_085068
Figure 1481: PRO81166
Figure 1482: DNA324511, XM_165473,
gen.XM_165473
Figure 1483: DNA324512, XM_087514,
gen.XM_087514
Figure 1484: DNA324513, XM_116247,
gen.XM_116247
Figure 1485: DNA324514, NM_002358,
gen.NM_002358
Figure 1486: PRO81169
Figure 1487: DNA324515, XM_050200,
gen.XM_050200
Figure 1488: PRO81170
Figure 1489: DNA225584, NM_001154,
gen.NM_001154
Figure 1490: PRO36047
Figure 1491: DNA324516, NM_024900,
gen.NM_024900
Figure 1492: PRO81171
Figure 1493: DNA324517, XM_040752,
gen.XM_040752
Figure 1494: DNA324518, NM_002413,
gen.NM_002413
Figure 1495: PRO60956
Figure 1496: DNA324519, XM_114401,
gen.XM_114401

WO 2004/030615

PCT/US2003/028547

Figure 1497: DNA324520, XM_068164,
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Figure 1498: PRO81174
Figure 1499: DNA324521, XM_060067,
gen.XM_060067
Figure 1500: DNA324522, XM_003555,
gen.XM_003555
Figure 1501: PRO81176
Figure 1502: DNA324523, XM_034321,
gen.XM_034321
Figure 1503: PRO81177
Figure 1504: DNA324524, NM_006439,
gen.NM_006439
Figure 1505: PRO81178
Figure 1506: DNA324525, NM_001006,
gen.NM_001006
Figure 1507: PRO81179
Figure 1508: DNA227575, NM_005141,
gen.NM_005141
Figure 1509: PRO38038
Figure 1510: DNA324526, XM_114368,
gen.XM_114368
Figure 1511A-B: DNA225920, NM_000508,
gen.NM_000508
Figure 1512: PRO36383
Figure 1513: DNA324527, NM_021871,
gen.NM_021871
Figure 1514: PRO81181
Figure 1515: DNA225921, NM_000509,
gen.NM_000509
Figure 1516: PRO36384
Figure 1517: DNA324528, NM_021870,
gen.NM_021870
Figure 1518: PRO81182
Figure 1519: DNA324529, XM_059623,
gen.XM_059623
Figure 1520: DNA324530, XM_106246,
gen.XM_106246
Figure 1521: PRO81184
Figure 1522: DNA324531, NM_002129,
gen.NM_002129
Figure 1523: PRO81185
Figure 1524: DNA324532, XM_040321,
gen.XM_040321
Figure 1525: DNA324533, XM_015563,
gen.XM_015563
Figure 1526: DNA324534, NM_024748,
gen.NM_024748
Figure 1527: PRO81188
Figure 1528: DNA324535, XM_165470,
gen.XM_165470
Figure 1529: PRO81189
Figure 1530A-E: DNA324536, XM_003477,
gen.XM_003477
Figure 1531: DNA324537, XM_165465,
gen.XM_165465

Figure 1532: DNA324538, XM_116204,
gen.XM_116204
Figure 1533: DNA324539, XM_116205,
gen.XM_116205
Figure 1534: DNA324540, XM_098405,
gen.XM_098405
Figure 1535: DNA324541, XM_052313,
gen.XM_052313
Figure 1536: PRO81195
Figure 1537: DNA324542, XM_087659,
gen.XM_087659
Figure 1538: PRO81196
Figure 1539: DNA324543, XM_029096,
gen.XM_029096
Figure 1540: DNA324544, XM_003825,
gen.XM_003825
Figure 1541: DNA324545, XM_057994,
gen.XM_057994
Figure 1542: PRO81199
Figure 1543: DNA324546, XM_087686,
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Figure 1544: DNA324547, XM_017641,
gen.XM_017641
Figure 1545: DNA324548, NM_030782,
gen.NM_030782
Figure 1546: PRO81202
Figure 1547: DNA324549, XM_084168,
gen.XM_084168
Figure 1548: DNA324550, XM_057492,
gen.XM_057492
Figure 1549: DNA324551, XM_087597,
gen.XM_087597
Figure 1550: DNA324552, XM_087601,
gen.XM_087601
Figure 1551: DNA324554, XM_087599,
gen.XM_087599
Figure 1552: DNA324555, XM_114435,
gen.XM_114435
Figure 1553: DNA324556, XM_087600,
gen.XM_087600
Figure 1554: DNA324557, XM_016170,
gen.XM_016170
Figure 1555: DNA324558, XM_114434,
gen.XM_114434
Figure 1556: DNA324559, XM_113452,
gen.XM_113452
Figure 1557: DNA324560, XM_071580,
gen.XM_071580
Figure 1558: PRO81213
Figure 1559: DNA324561, XM_087713,
gen.XM_087713
Figure 1560: PRO81214
Figure 1561: DNA324562, XM_094440,
gen.XM_094440
Figure 1562: DNA324563, XM_106739,
gen.XM_106739

WO 2004/030615

PCT/US2003/028547

Figure 1563: PRO81216
Figure 1564: DNA324564, XM_087614, gen.XM_087614
Figure 1565: DNA324565, XM_004009, gen.XM_004009
Figure 1566: PRO81219
Figure 1567: DNA324566, XM_114437, gen.XM_114437
Figure 1568: DNA324567, XM_043771, gen.XM_043771
Figure 1569: PRO81221
Figure 1570: DNA324568, NM_000997, gen.NM_000997
Figure 1571: PRO11077
Figure 1572: DNA324569, XM_003869, gen.XM_003869
Figure 1573: DNA227173, NM_001465, gen.NM_001465
Figure 1574: PRO37636
Figure 1575: DNA324570, NM_018034, gen.NM_018034
Figure 1576: PRO81223
Figure 1577: DNA324571, NM_032637, gen.NM_032637
Figure 1578: PRO81224
Figure 1579: DNA324572, NM_005983, gen.NM_005983
Figure 1580: PRO81225
Figure 1581A-B: DNA324573, XM_003896, gen.XM_003896
Figure 1582: DNA287282, NM_002130, gen.NM_002130
Figure 1583: PRO69554
Figure 1584: DNA324574, XM_114442, gen.XM_114442
Figure 1585: PRO81227
Figure 1586: DNA324575, XM_114439, gen.XM_114439
Figure 1587: DNA324576, XM_114440, gen.XM_114440
Figure 1588A-B: DNA324577, XM_032902, gen.XM_032902
Figure 1589: PRO81230
Figure 1590: DNA324578, XM_032895, gen.XM_032895
Figure 1591: DNA324579, XM_084179, gen.XM_084179
Figure 1592: DNA324580, XM_041712, gen.XM_041712
Figure 1593: DNA324581, XM_116439, gen.XM_116439
Figure 1594: PRO81234
Figure 1595: DNA324582, XM_087611, gen.XM_087611
Figure 1596: DNA324583, XM_059653, gen.XM_059653

Figure 1597: DNA324584, XM_087610, gen.XM_087610
Figure 1598: DNA288259, NM_031966, gen.NM_031966
Figure 1599: PRO4676
Figure 1600: DNA324585, XM_042025, gen.XM_042025
Figure 1601: PRO81238
Figure 1602: DNA324586, NM_005713, gen.NM_005713
Figure 1603: PRO81239
Figure 1604: DNA324587, XM_059709, gen.XM_059709
Figure 1605: PRO81240
Figure 1606: DNA324588, XM_116447, gen.XM_116447
Figure 1607: PRO81241
Figure 1608: DNA324589, XM_037260, gen.XM_037260
Figure 1609: DNA324590, XM_098351, gen.XM_098351
Figure 1610: DNA324591, XM_098354, gen.XM_098354
Figure 1611: DNA324592, XM_098352, gen.XM_098352
Figure 1612: DNA324593, XM_166037, gen.XM_166037
Figure 1613: PRO81246
Figure 1614: DNA324594, XM_041694, gen.XM_041694
Figure 1615: DNA324595, XM_165488, gen.XM_165488
Figure 1616: PRO81248
Figure 1617: DNA324596, XM_059669, gen.XM_059669
Figure 1618: PRO81249
Figure 1619: DNA324597, XM_027964, gen.XM_027964
Figure 1620: PRO81250
Figure 1621: DNA324598, XM_088020, gen.XM_088020
Figure 1622: DNA324599, XM_117387, gen.XM_117387
Figure 1623: DNA324600, XM_114469, gen.XM_114469
Figure 1624: DNA324601, NM_001207, gen.NM_001207
Figure 1625: PRO22771
Figure 1626A-B: DNA324602, XM_032553, gen.XM_032553
Figure 1627: DNA254147, NM_000521, gen.NM_000521
Figure 1628: PRO49262
Figure 1629: DNA324603, NM_031482, gen.NM_031482
Figure 1630: PRO81254

WO 2004/030615

PCT/US2003/028547

Figure 1631: DNA324604, XM_087790,
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Figure 1632: DNA324605, NM_001025,
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Figure 1633: PRO10685
Figure 1634: DNA324606, XM_098362,
gen.XM_098362
Figure 1635: PRO81256
Figure 1636: DNA324607, NM_003401,
gen.NM_003401
Figure 1637: PRO70327
Figure 1638: DNA290231, NM_022550,
gen.NM_022550
Figure 1639: PRO70327
Figure 1640: DNA324608, XM_017857,
gen.XM_017857
Figure 1641: DNA324609, XM_117398,
gen.XM_117398
Figure 1642A-B: DNA257253, NM_032280,
gen.NM_032280
Figure 1643: PRO51851
Figure 1644: DNA324610, XM_003771,
gen.XM_003771
Figure 1645: PRO81259
Figure 1646A-B: DNA269816, NM_002397,
gen.NM_002397
Figure 1647: PRO58219
Figure 1648: DNA324611, XM_116427,
gen.XM_116427
Figure 1649: PRO81260
Figure 1650: DNA324612, NM_004772,
gen.NM_004772
Figure 1651: PRO81261
Figure 1652: DNA324613, XM_016674,
gen.XM_016674
Figure 1653: PRO81262
Figure 1654: DNA324614, XM_113463,
gen.XM_113463
Figure 1655: DNA324615, XM_034744,
gen.XM_034744
Figure 1656: DNA324616, XM_087745,
gen.XM_087745
Figure 1657: PRO81264
Figure 1658: DNA324617, XM_018473,
gen.XM_018473
Figure 1659: PRO81265
Figure 1660: DNA324618, XM_087635,
gen.XM_087635
Figure 1661: PRO81266
Figure 1662: DNA324619, XM_087637,
gen.XM_087637
Figure 1663: DNA324620, XM_166027,
gen.XM_166027
Figure 1664: DNA324621, NM_014035,
gen.NM_014035
Figure 1665: PRO1285

Figure 1666: DNA324622, XM_003830,
gen.XM_003830
Figure 1667: PRO81269
Figure 1668: DNA324623, XM_037002,
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Figure 1669: DNA324624, XM_166026,
gen.XM_166026
Figure 1670: DNA324625, XM_041059,
gen.XM_041059
Figure 1671: DNA83020, NM_000358,
gen.NM_000358
Figure 1672: PRO2561
Figure 1673: DNA324626, NM_003687,
gen.NM_003687
Figure 1674: PRO81272
Figure 1675: DNA324627, XM_034862,
gen.XM_034862
Figure 1676: PRO34544
Figure 1677: DNA103380, NM_003374,
gen.NM_003374
Figure 1678: PRO4710
Figure 1679: DNA324628, XM_017474,
gen.XM_017474
Figure 1680: PRO63082
Figure 1681A-B: DNA324629, NM_014829,
gen.NM_014829
Figure 1682: PRO81273
Figure 1683A-B: DNA324630, XM_114482,
gen.XM_114482
Figure 1684: PRO81274
Figure 1685: DNA324631, NM_004893,
gen.NM_004893
Figure 1686: PRO81275
Figure 1687: DNA269809, NM_006805,
gen.NM_006805
Figure 1688: PRO58213
Figure 1689: DNA226872, NM_001964,
gen.NM_001964
Figure 1690: PRO37335
Figure 1691: DNA324632, XM_116307,
gen.XM_116307
Figure 1692: PRO81276
Figure 1693: DNA324633, NM_004134,
gen.NM_004134
Figure 1694: PRO81277
Figure 1695: DNA324634, XM_038221,
gen.XM_038221
Figure 1696: PRO81278
Figure 1697: DNA271931, NM_005754,
gen.NM_005754
Figure 1698: PRO60207
Figure 1699: DNA324635, XM_003841,
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Figure 1700: DNA324636, XM_032759,
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Figure 1701: DNA324637, XM_017591,

WO 2004/030615

PCT/US2003/028547

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Figure 1702: DNA324638, NM_006058,
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Figure 1703: PRO81280
Figure 1704: DNA324639, NM_002084,
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Figure 1705: PRO81281
Figure 1706: DNA324640, NM_018047,
gen.NM_018047
Figure 1707: PRO81282
Figure 1708: DNA324641, NM_005617,
gen.NM_005617
Figure 1709: PRO10849
Figure 1710: DNA324642, XM_003937,
gen.XM_003937
Figure 1711: DNA324643, XM_087621,
gen.XM_087621
Figure 1712A-B: DNA324644, XM_003789,
gen.XM_003789
Figure 1713: DNA324645, XM_087652,
gen.XM_087652
Figure 1714: DNA324646, XM_068853,
gen.XM_068853
Figure 1715: PRO81286
Figure 1716: DNA324647, XM_116465,
gen.XM_116465
Figure 1717: PRO81287
Figure 1718: DNA302020, NM_005573,
gen.NM_005573
Figure 1719: PRO70993
Figure 1720: DNA324648, XM_113467,
gen.XM_113467
Figure 1721: DNA271626, NM_014773,
gen.NM_014773
Figure 1722: PRO59913
Figure 1723A-B: DNA324649, XM_056315,
gen.XM_056315
Figure 1724: DNA324650, NM_024668,
gen.NM_024668
Figure 1725: PRO81289
Figure 1726: DNA324651, NM_080670,
gen.NM_080670
Figure 1727: PRO81290
Figure 1728A-B: DNA324652, NM_002588,
gen.NM_002588
Figure 1729: PRO81291
Figure 1730A-B: DNA324653, NM_003735,
gen.NM_003735
Figure 1731: PRO81292
Figure 1732A-B: DNA150679, NM_003736,
gen.NM_003736
Figure 1733: PRO12416
Figure 1734A-B: DNA324654, NM_018912,
gen.NM_018912
Figure 1735: PRO36058
Figure 1736A-B: DNA324655, NM_018913,

gen.NM_018913
Figure 1737: PRO81293
Figure 1738A-B: DNA324656, NM_018914,
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Figure 1739: PRO81294
Figure 1740A-B: DNA324657, NM_018915,
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Figure 1741: PRO36020
Figure 1742A-B: DNA324658, NM_018916,
gen.NM_018916
Figure 1743: PRO81295
Figure 1744A-B: DNA324659, NM_018917,
gen.NM_018917
Figure 1745: PRO81296
Figure 1746A-B: DNA324660, NM_018918,
gen.NM_018918
Figure 1747: PRO81297
Figure 1748A-B: DNA324661, NM_018919,
gen.NM_018919
Figure 1749: PRO81298
Figure 1750A-B: DNA324662, NM_018920,
gen.NM_018920
Figure 1751: PRO81299
Figure 1752A-B: DNA324663, NM_018921,
gen.NM_018921
Figure 1753: PRO81300
Figure 1754A-B: DNA324664, NM_018922,
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Figure 1755: PRO81301
Figure 1756A-B: DNA324665, NM_018923,
gen.NM_018923
Figure 1757: PRO81302
Figure 1758A-B: DNA324666, NM_018924,
gen.NM_018924
Figure 1759: PRO81303
Figure 1760A-B: DNA324667, NM_018925,
gen.NM_018925
Figure 1761: PRO81304
Figure 1762A-B: DNA324668, NM_018926,
gen.NM_018926
Figure 1763: PRO81305
Figure 1764A-B: DNA324669, NM_018927,
gen.NM_018927
Figure 1765: PRO37091
Figure 1766A-B: DNA324670, NM_018928,
gen.NM_018928
Figure 1767: PRO81306
Figure 1768A-B: DNA324671, NM_018929,
gen.NM_018929
Figure 1769: PRO81307
Figure 1770A-B: DNA324672, NM_032088,
gen.NM_032088
Figure 1771: PRO81308
Figure 1772A-B: DNA324673, NM_032092,
gen.NM_032092
Figure 1773: PRO81309

WO 2004/030615

PCT/US2003/028547

Figure 1774: DNA324674, NM_032403,
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Figure 1776: DNA324675, NM_032402,
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Figure 1777: PRO81311
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Figure 1779: DNA324677, NM_002109,
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Figure 1780: PRO4908
Figure 1781: DNA324678, XM_084180,
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Figure 1782: PRO81313
Figure 1783: DNA324679, XM_039975,
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Figure 1784: PRO81314
Figure 1785: DNA324680, NM_033551,
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Figure 1786: PRO81315
Figure 1787: DNA324681, NM_004821,
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Figure 1788: PRO81316
Figure 1789: DNA324682, XM_068395,
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Figure 1790: PRO81317
Figure 1791: DNA226418, NM_004060,
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Figure 1792: PRO36881
Figure 1793A-B: DNA324683, XM_056963,
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Figure 1794: PRO81318
Figure 1795: DNA324684, NM_004219,
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Figure 1796: PRO81319
Figure 1797: DNA324685, XM_094243,
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Figure 1798A-B: DNA324686, XM_047964,
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Figure 1799: DNA324687, XM_016345,
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Figure 1800: DNA324688, NM_002887,
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Figure 1801: PRO81323
Figure 1802: DNA324689, XM_166029,
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Figure 1803: DNA324690, NM_002520,
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Figure 1804: PRO58993
Figure 1805: DNA324691, XM_043340,
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Figure 1806: PRO81325
Figure 1807: DNA324692, XM_116340,
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Figure 1808A-B: DNA324693, XM_043388,
gen.XM_043388

Figure 1809: PRO81327
Figure 1810: DNA324694, XM_116856,
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Figure 1811: DNA324695, XM_003716,
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Figure 1812: DNA227320, NM_003714,
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Figure 1813: PRO37783
Figure 1814: DNA324696, NM_032361,
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Figure 1815: PRO81330
Figure 1816: DNA324697, XM_087773,
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Figure 1817: DNA324698, XM_114457,
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Figure 1818: DNA324699, XM_165483,
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Figure 1819: DNA324700, XM_114453,
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Figure 1820: DNA324701, XM_165484,
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Figure 1821: DNA324702, XM_030771,
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Figure 1822: PRO19615
Figure 1823: DNA324703, XM_030777,
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Figure 1824: DNA324704, XM_030782,
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Figure 1825: PRO81336
Figure 1826: DNA324705, NM_030567,
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Figure 1827: PRO81337
Figure 1828: DNA225909, NM_000505,
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Figure 1829: PRO36372
Figure 1830: DNA274206, NM_006816,
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Figure 1831: PRO62135
Figure 1832: DNA324706, NM_031300,
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Figure 1833: PRO81338
Figure 1834: DNA324707, NM_013237,
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Figure 1835: PRO81339
Figure 1836: DNA324708, NM_002011,
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Figure 1837: PRO81340
Figure 1838: DNA324709, NM_022963,
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Figure 1839: PRO81341
Figure 1840: DNA324710, XM_038946,
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Figure 1842: DNA324712, XM_166028,
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WO 2004/030615

PCT/US2003/028547

Figure 1843: DNA324713, NM_015043,
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Figure 1847: PRO1927
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Figure 1849: PRO81347
Figure 1850: DNA270675, NM_005520,
gen.NM_005520
Figure 1851: PRO59040
Figure 1852: DNA324717, NM_006098,
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Figure 1853: PRO25849
Figure 1854: DNA269593, NM_005110,
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Figure 1855: PRO58006
Figure 1856: DNA324718, XM_116365,
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Figure 1857: DNA324719, XM_116511,
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Figure 1858: DNA324720, XM_087823,
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Figure 1859A-C: DNA324721, XM_053955,
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Figure 1860: DNA324722, XM_113476,
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Figure 1861: DNA324723, XM_116514,
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Figure 1862: DNA324724, XM_094741,
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Figure 1863: DNA324725, NM_025168,
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Figure 1864: PRO81354
Figure 1865A-B: DNA324726, XM_165740,
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Figure 1866: DNA272171, NM_002388,
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Figure 1867: PRO60438
Figure 1868: DNA324727, XM_167169,
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Figure 1869: PRO81355
Figure 1870: DNA324728, NM_014452,
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Figure 1871: PRO868
Figure 1872: DNA324729, XM_166349,
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Figure 1873: PRO81356
Figure 1874: DNA304680, NM_007355,
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Figure 1875: PRO71106
Figure 1876: DNA324730, XM_165772,
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Figure 1879: DNA324733, XM_166469,
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Figure 1881: PRO81359
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Figure 1884: DNA324737, XM_166362,
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Figure 1885: PRO81362
Figure 1886: DNA227204, NM_015388,
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Figure 1887: PRO37667
Figure 1888: DNA324738, XM_166425,
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Figure 1889: PRO81363
Figure 1890: DNA324739, NM_057161,
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Figure 1891: PRO81364
Figure 1892: DNA270613, NM_006245,
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Figure 1893: PRO58984
Figure 1894: DNA324740, NM_006586,
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Figure 1895: PRO81365
Figure 1896: DNA324741, XM_166402,
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Figure 1897: PRO81366
Figure 1898: DNA324742, NM_001760,
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Figure 1899: PRO81367
Figure 1900: DNA287246, NM_004053,
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Figure 1901: PRO69521
Figure 1902: DNA324743, NM_017601,
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Figure 1903: PRO81368
Figure 1904: DNA275630, NM_006708,
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Figure 1905: PRO63253
Figure 1906: DNA324744, NM_014341,
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Figure 1907: PRO81369
Figure 1908: DNA304460, NM_016059,
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Figure 1909: PRO4984
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Figure 1911: PRO81370
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WO 2004/030615

PCT/US2003/028547

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Figure 1913: PRO71142
Figure 1914: DNA324746, XM_166417,
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Figure 1915: PRO81371
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Figure 1917: PRO81372
Figure 1918A-B: DNA324748, NM_004117,
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Figure 1919: PRO36841
Figure 1920: DNA324749, XM_166419,
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Figure 1921: DNA324750, XM_165794,
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Figure 1922: DNA324751, NM_007104,
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Figure 1923: PRO10360
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Figure 1927: PRO50582
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Figure 1931: DNA324756, XM_166459,
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Figure 1934: DNA324758, XM_058039,
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Figure 1935: PRO81380
Figure 1936: DNA324759, XM_087990,
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Figure 1938: DNA324761, XM_166360,
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Figure 1942: DNA227442, NM_001350,
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Figure 1943: PRO37905
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Figure 1950: PRO4884
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Figure 1952: DNA287227, NM_004159,
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Figure 1953: PRO69506
Figure 1954: DNA324770, XM_165717,
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Figure 1955: DNA324771, XM_166480,
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Figure 1956: DNA324772, XM_165801,
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Figure 1957A-B: DNA324773, NM_000592,
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Figure 1958: PRO36316
Figure 1959: DNA324774, NM_001710,
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Figure 1960: PRO36305
Figure 1961: DNA227607, NM_005346,
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Figure 1962: PRO38070
Figure 1963: DNA304668, NM_005345,
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Figure 1964: PRO71095
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Figure 1966: PRO81394
Figure 1967A-B: DNA272263, NM_006295,
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Figure 1968: PRO70138
Figure 1969: DNA287319, NM_001288,
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Figure 1970: PRO69584
Figure 1971: DNA324776, NM_001320,
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Figure 1972: PRO63052
Figure 1973A-B: DNA324777, NM_004639,
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Figure 1974: PRO81395
Figure 1975A-B: DNA324778, NM_080703,
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Figure 1976: PRO81396
Figure 1977A-B: DNA324779, NM_080702,
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Figure 1978: PRO81397
Figure 1979A-B: DNA324780, NM_004638,
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Figure 1980: PRO81398
Figure 1981A-B: DNA324781, NM_080686,
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WO 2004/030615

PCT/US2003/028547

Figure 1982: PRO81399
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Figure 1991: PRO81401
Figure 1992: DNA324786, XM_166381,
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Figure 1993: PRO81402
Figure 1994: DNA324787, XM_168104,
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Figure 1995: DNA324788, XM_166401,
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Figure 1996: PRO81404
Figure 1997: DNA271040, NM_001517,
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Figure 1998: PRO59365
Figure 1999A-B: DNA324789, XM_165738,
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Figure 2000: DNA324790, XM_087939,
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Figure 2001: PRO81406
Figure 2002: DNA324791, XM_166353,
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Figure 2003: PRO1112
Figure 2004A-B: DNA324792, XM_166376,
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Figure 2005: PRO81407
Figure 2006A-B: DNA324793, XM_165799,
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Figure 2007: DNA290264, NM_025263,
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Figure 2008: PRO70393
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Figure 2012: PRO81410
Figure 2013: DNA324796, XM_165758,
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Figure 2014: PRO81411
Figure 2015: DNA324797, XM_166406,
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Figure 2016: DNA324798, XM_165809,
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Figure 2017: DNA324799, NM_018950,

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Figure 2020: PRO81415
Figure 2021: DNA324801, XM_166336,
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Figure 2022: PRO81416
Figure 2023: DNA324802, XM_167128,
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Figure 2024: PRO23797
Figure 2025: DNA324803, XM_167161,
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Figure 2026: PRO81417
Figure 2027: DNA324804, NM_013375,
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Figure 2028: PRO81418
Figure 2029: DNA324805, NM_007047,
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Figure 2030: PRO81419
Figure 2031: DNA324806, XM_167179,
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Figure 2032: DNA290785, NM_003107,
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Figure 2033: PRO70544
Figure 2034: DNA150772, NM_003472,
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Figure 2035: PRO12797
Figure 2036A-B: DNA324807, XM_165728,
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Figure 2037: DNA324808, XM_165749,
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Figure 2038: PRO81421
Figure 2039A-B: DNA324809, NM_004973,
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Figure 2040: PRO81422
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Figure 2042: DNA324811, XM_166446,
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Figure 2043: PRO81424
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Figure 2045: DNA324813, XM_037875,
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Figure 2046: PRO81426
Figure 2047: DNA324814, XM_167225,
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Figure 2048: PRO81427
Figure 2049: DNA324815, XM_166357,
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Figure 2051: PRO81429
Figure 2052: DNA324817, NM_001500,
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WO 2004/030615

PCT/US2003/028547

Figure 2053: PRO81430
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Figure 2059: DNA324822, XM_011117,
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Figure 2061: PRO81435
Figure 2062: DNA324824, XM_059776,
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Figure 2063: PRO81436
Figure 2064: DNA324825, XM_055641,
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Figure 2065: DNA324826, XM_004151,
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Figure 2066: DNA324827, NM_133645,
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Figure 2067: PRO81439
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Figure 2069: DNA324829, XM_029228,
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Figure 2070: DNA103471, NM_006670,
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Figure 2071: PRO4798
Figure 2072: DNA324830, XM_068963,
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Figure 2073: PRO81441
Figure 2074: DNA324831, XM_040623,
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Figure 2075: DNA324832, NM_020320,
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Figure 2076: PRO81443
Figure 2077: DNA324833, NM_014107,
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Figure 2078: PRO81444
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Figure 2080: DNA324835, XM_017517,
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Figure 2081: DNA324836, NM_032929,
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Figure 2084: PRO81447
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Figure 2086: PRO81448

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Figure 2088: PRO81449
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Figure 2090: DNA324841, XM_087853,
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Figure 2092: DNA324843, XM_166303,
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Figure 2093: PRO81453
Figure 2094: DNA324844, XM_167027,
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Figure 2095: PRO81454
Figure 2096: DNA324845, XM_167037,
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Figure 2097: PRO81455
Figure 2098: DNA324846, XM_018182,
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Figure 2099: DNA227924, NM_000165,
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Figure 2100: PRO38387
Figure 2101: DNA324847, XM_166310,
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Figure 2102: PRO81457
Figure 2103: DNA324848, XM_168054,
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Figure 2104: DNA271418, NM_003287,
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Figure 2105: PRO59717
Figure 2106: DNA324849, XM_114492,
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Figure 2107: DNA324850, XM_037056,
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Figure 2108: DNA324851, XM_098468,
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Figure 2109: PRO19933
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Figure 2111: DNA324853, NM_001016,
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Figure 2112: PRO81462
Figure 2113: DNA324854, XM_004297,
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Figure 2114: DNA324855, XM_004256,
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Figure 2115: PRO81464
Figure 2116: DNA324856, NM_014320,
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Figure 2117: PRO81465
Figure 2118: DNA324857, XM_059741,
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Figure 2119: DNA324858, XM_017831,
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Figure 2120: PRO81467

WO 2004/030615

PCT/US2003/028547

Figure 2121: DNA324859, XM_049899,
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Figure 2124A-B: DNA324862, XM_087836,
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Figure 2125: PRO81471
Figure 2126: DNA324863, NM_005389,
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Figure 2127: PRO66279
Figure 2128A-C: DNA324864, XM_029746,
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Figure 2129: PRO66282
Figure 2130: DNA324865, XM_004383,
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Figure 2131: DNA324866, XM_059745,
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Figure 2132: DNA324867, XM_033912,
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Figure 2133: PRO81474
Figure 2134: DNA324868, XM_033910,
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Figure 2135: DNA324870, NM_003181,
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Figure 2136: PRO81476
Figure 2137: DNA324871, NM_002793,
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Figure 2138: PRO81477
Figure 2139: DNA324872, XM_044866,
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Figure 2140: DNA324873, XM_116524,
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Figure 2141: DNA324874, XM_059773,
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Figure 2142: DNA324875, XM_084998,
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Figure 2143: PRO81481
Figure 2144: DNA324876, XM_058266,
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Figure 2147: DNA324879, XM_166049,
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Figure 2151: PRO23797
Figure 2152: DNA324882, XM_071937,
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Figure 2158: PRO81491
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Figure 2164: PRO81495
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Figure 2166: PRO81496
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Figure 2168: DNA324892, XM_166541,
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Figure 2169: PRO81498
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Figure 2171: PRO81499
Figure 2172: DNA324894, NM_016003,
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Figure 2173: PRO81500
Figure 2174: DNA225631, NM_001101,
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Figure 2175: PRO36094
Figure 2176: DNA274326, NM_003088,
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Figure 2177: PRO62244
Figure 2178: DNA324895, NM_006303,
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Figure 2179: PRO81501
Figure 2180: DNA324896, NM_014413,
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Figure 2181: PRO60579
Figure 2182: DNA247595, NM_006908,
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Figure 2183: PRO45014
Figure 2184: DNA324897, NM_006854,
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Figure 2185: PRO12468
Figure 2186: DNA324898, NM_024067,
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Figure 2187: PRO81502
Figure 2188: DNA324899, NM_002947,
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Figure 2189: PRO81503

WO 2004/030615

PCT/US2003/028547

Figure 2190: DNA324900, XM_166531,
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Figure 2194: PRO23362
Figure 2195: DNA324902, XM_088264,
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Figure 2196: PRO81506
Figure 2197: DNA324903, XM_165841,
gen.XM_165841
Figure 2198: DNA324904, XM_166521,
gen.XM_166521
Figure 2199: PRO81508
Figure 2200: DNA324905, XM_166506,
gen.XM_166506
Figure 2201: PRO81509
Figure 2202: DNA324906, XM_166505,
gen.XM_166505
Figure 2203: DNA324907, XM_166514,
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Figure 2204: DNA324908, XM_166515,
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Figure 2205: DNA324909, XM_166512,
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Figure 2206: DNA227929, NM_019059,
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Figure 2207: PRO38392
Figure 2208A-B: DNA324910, NM_018947,
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Figure 2209: PRO81514
Figure 2210: DNA324911, NM_002137,
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Figure 2211: PRO81515
Figure 2212: DNA324912, NM_031243,
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Figure 2213: PRO6373
Figure 2214: DNA324913, NM_007276,
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Figure 2215: PRO81516
Figure 2216: DNA324914, NM_016587,
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Figure 2217: PRO81517
Figure 2218: DNA324915, XM_040853,
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Figure 2219: DNA324916, XM_166509,
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Figure 2220: DNA324917, XM_166513,
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Figure 2221: PRO81520
Figure 2222: DNA324918, XM_166504,
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Figure 2223: PRO81521
Figure 2224: DNA324919, XM_166494,

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Figure 2225: DNA324920, XM_107825,
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Figure 2226A-B: DNA324921, NM_022748,
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Figure 2227: PRO81523
Figure 2228: DNA324922, NM_000598,
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Figure 2229: PRO119
Figure 2230A-B: DNA324923, XM_166594,
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Figure 2231: PRO81524
Figure 2232A-B: DNA275334, NM_030900,
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Figure 2233: PRO63009
Figure 2234: DNA324924, NM_031443,
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Figure 2235: PRO81525
Figure 2236: DNA324925, NM_012412,
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Figure 2237: PRO61812
Figure 2238: DNA324926, NM_021130,
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Figure 2239: PRO7427
Figure 2240A-B: DNA324927, XM_165877,
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Figure 2241: PRO81526
Figure 2242: DNA227268, NM_019082,
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Figure 2243: PRO37731
Figure 2244: DNA324928, XM_015258,
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Figure 2245: DNA324929, XM_165870,
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Figure 2246: DNA273865, NM_006230,
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Figure 2247: PRO61824
Figure 2248A-B: DNA324930, XM_165882,
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Figure 2249: DNA324931, XM_165867,
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Figure 2250: PRO61688
Figure 2251: DNA324932, NM_014063,
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Figure 2252: PRO81529
Figure 2253: DNA324933, XM_165872,
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Figure 2254: DNA304707, NM_002787,
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Figure 2255: PRO71133
Figure 2256: DNA324934, XM_016733,
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Figure 2257: PRO81531
Figure 2258: DNA324935, XM_165876,
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Figure 2259A-B: DNA324936, NM_014800,

WO 2004/030615

PCT/US2003/028547

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Figure 2264A-B: DNA324938, XM_167339,
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Figure 2265: DNA287189, NM_002047,
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Figure 2266: PRO69475
Figure 2267: DNA324939, XM_170195,
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Figure 2268: PRO81536
Figure 2269: DNA324940, XM_168378,
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Figure 2270: PRO81537
Figure 2271: DNA324941, XM_168354,
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Figure 2272: PRO81538
Figure 2273: DNA324942, XM_167494,
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Figure 2274: DNA103588, NM_001762,
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Figure 2275: PRO4912
Figure 2276: DNA324943, XM_037741,
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Figure 2277: PRO81540
Figure 2278: DNA324944, XM_050265,
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Figure 2279: PRO81541
Figure 2280: DNA324945, XM_017483,
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Figure 2281A-B: DNA324946, XM_018359,
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Figure 2282: DNA324947, XM_059876,
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Figure 2283: PRO81544
Figure 2284: DNA324948, NM_032951,
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Figure 2285: PRO81545
Figure 2286: DNA324949, NM_032953,
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Figure 2287: PRO81546
Figure 2288: DNA324950, NM_022170,
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Figure 2289: PRO81547
Figure 2290: DNA324951, NM_031992,
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Figure 2291: PRO81548
Figure 2292: DNA324952, XM_004901,
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Figure 2294: PRO81550

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Figure 2297: DNA324955, XM_088239,
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Figure 2298: PRO81552
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Figure 2302: DNA324959, XM_168454,
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Figure 2303: PRO81556
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Figure 2308: DNA304710, NM_001540,
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Figure 2309: PRO71136
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Figure 2312A-B: DNA324964, XM_167502,
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Figure 2313: DNA324965, XM_017442,
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Figure 2314: PRO81561
Figure 2315: DNA324966, XM_168450,
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Figure 2316: DNA324967, XM_168435,
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Figure 2317: DNA324968, XM_168464,
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Figure 2318: DNA324969, XM_170427,
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Figure 2319A-B: DNA324971, NM_015068,
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Figure 2320: PRO81566
Figure 2321A-B: DNA324972, XM_167476,
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Figure 2322: DNA324973, XM_168181,
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Figure 2323: DNA324974, XM_168251,
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Figure 2324: PRO81569
Figure 2325: DNA324975, XM_167477,
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Figure 2326: DNA324976, NM_005837,
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Figure 2327: PRO81571

WO 2004/030615

PCT/US2003/028547

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Figure 2334: PRO81574
Figure 2335: DNA324981, NM_024070,
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Figure 2336: PRO81575
Figure 2337: DNA324982, XM_084241,
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Figure 2338: DNA324983, NM_006833,
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Figure 2339: PRO22897
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Figure 2347: PRO81580
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Figure 2353A-B: DNA324990, XM_166485,
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Figure 2356: PRO81585
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Figure 2358: PRO81586
Figure 2359: DNA324993, XM_168586,
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Figure 2362: PRO2604
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Figure 2366: PRO41882
Figure 2367: DNA324996, NM_003378,
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Figure 2368: PRO81589
Figure 2369: DNA324997, NM_001084,
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Figure 2370: PRO58437
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Figure 2372: PRO59074
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Figure 2377: PRO81591
Figure 2378: DNA325001, NM_002803,
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Figure 2379: PRO81592
Figure 2380: DNA325002, XM_168572,
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Figure 2382: PRO81594
Figure 2383: DNA325004, XM_033876,
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Figure 2384: PRO81595
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Figure 2387: DNA325007, XM_072430,
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Figure 2388: PRO81598
Figure 2389: DNA325008, XM_050430,
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Figure 2390: PRO81599
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Figure 2392: PRO81600
Figure 2393: DNA226560, NM_006136,
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Figure 2394: PRO37023
Figure 2395: DNA325010, XM_012284,
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Figure 2396: DNA325011, NM_005000,
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Figure 2397: PRO59380
Figure 2398: DNA325012, NM_001662,
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WO 2004/030615

PCT/US2003/028547

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Figure 2405: PRO81605
Figure 2406: DNA325017, XM_117481,
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Figure 2407A-C: DNA325018, XM_045856,
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Figure 2408: PRO81607
Figure 2409A-B: DNA325019, XM_088105,
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Figure 2410: PRO81608
Figure 2411: DNA325020, XM_011548,
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Figure 2412: PRO81609
Figure 2413: DNA325021, XM_045952,
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Figure 2414: DNA325022, XM_046001,
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Figure 2415: PRO81611
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Figure 2419: PRO81614
Figure 2420: DNA325026, XM_088122,
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Figure 2421: PRO81615
Figure 2422: DNA325027, XM_088119,
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Figure 2423: DNA325028, NM_001628,
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Figure 2424: PRO81617
Figure 2425: DNA325029, NM_020299,
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Figure 2426: PRO81618
Figure 2427: DNA325030, NM_024033,
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Figure 2428: PRO81619
Figure 2429: DNA325031, XM_114555,
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Figure 2431: PRO81621
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Figure 2436: PRO71111
Figure 2437: DNA325036, NM_018238,
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Figure 2438: PRO81625
Figure 2439: DNA325037, XM_035107,
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Figure 2440: DNA325038, NM_003461,
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Figure 2442: DNA325039, NM_004911,
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Figure 2443: PRO2733
Figure 2444A-B: DNA325040, XM_114578,
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Figure 2445: PRO81627
Figure 2446: DNA325041, XM_088135,
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Figure 2447: DNA325042, XM_098654,
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Figure 2448: PRO81629
Figure 2449: DNA325043, NM_023942,
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Figure 2450: PRO81630
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Figure 2452: PRO81631
Figure 2453: DNA325045, XM_084238,
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Figure 2454A-B: DNA325046, XM_032216,
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Figure 2455A-B: DNA325047, XM_032121,
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Figure 2456: DNA325048, NM_031434,
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Figure 2457: PRO1555
Figure 2458: DNA226337, NM_005692,
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Figure 2459: PRO36800
Figure 2460: DNA325049, NM_005614,
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Figure 2461: PRO37938
Figure 2462A-B: DNA325050, NM_053043,
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Figure 2463: PRO81634
Figure 2464: DNA325051, NM_022458,
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Figure 2465: PRO81635
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Figure 2467: DNA325053, NM_017760,
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WO 2004/030615

PCT/US2003/028547

Figure 2468: PRO81637
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Figure 2472: DNA325057, XM_117452,
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Figure 2473: DNA325058, XM_070203,
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Figure 2474: PRO81641
Figure 2475: DNA325059, XM_095371,
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Figure 2476: DNA325060, NM_004084,
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Figure 2477: PRO2570
Figure 2478: DNA325061, NM_005217,
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Figure 2479: PRO9980
Figure 2480: DNA325062, XM_070188,
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Figure 2481: PRO81643
Figure 2482: DNA325063, XM_035680,
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Figure 2483: DNA325064, XM_035662,
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Figure 2484: PRO3344
Figure 2485: DNA325065, XM_005305,
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Figure 2487: DNA325066, XM_050293,
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Figure 2488A-B: DNA325067, XM_027679,
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Figure 2489: PRO81647
Figure 2490A-B: DNA325068, XM_027651,
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Figure 2491: DNA274178, NM_005775,
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Figure 2492: PRO62108
Figure 2493: DNA325069, XM_113557,
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Figure 2494: PRO81649
Figure 2495: DNA83022, NM_001199,
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Figure 2496: PRO2042
Figure 2497: DNA325070, NM_006128,
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Figure 2498: PRO81650
Figure 2499: DNA325071, NM_006131,
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Figure 2500: PRO81651
Figure 2501: DNA325072, NM_006132,
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Figure 2502: PRO81652

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Figure 2504: PRO81653
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Figure 2507: PRO36134
Figure 2508: DNA325075, NM_024567,
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Figure 2509: PRO81654
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Figure 2511: PRO81655
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Figure 2513: PRO37730
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Figure 2518: PRO81658
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Figure 2520: PRO81659
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Figure 2522: PRO81660
Figure 2523: DNA325082, XM_114618,
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Figure 2524: PRO81661
Figure 2525: DNA325083, XM_050215,
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Figure 2527: DNA325085, NM_018310,
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Figure 2531: DNA325088, XM_059933,
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Figure 2532: PRO1108
Figure 2533: DNA325089, XM_011629,
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Figure 2534: DNA325090, NM_000930,
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Figure 2535: PRO4
Figure 2536: DNA325091, NM_000931,
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Figure 2537: PRO81668

WO 2004/030615

PCT/US2003/028547

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Figure 2541: DNA325094, NM_025070,
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Figure 2542: PRO81671
Figure 2543A-B: DNA325095, XM_030268,
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Figure 2544: DNA325096, XM_030274,
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Figure 2545: PRO81673
Figure 2546: DNA151010, NM_003350,
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Figure 2547: PRO12838
Figure 2548: DNA325097, XM_113540,
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Figure 2549: PRO81674
Figure 2550: DNA325098, NM_006330,
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Figure 2551: PRO59230
Figure 2552: DNA325099, NM_001023,
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Figure 2553: PRO58263
Figure 2554: DNA325100, XM_095667,
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Figure 2555: PRO81675
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Figure 2562: DNA325107, XM_011769,
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Figure 2563: DNA325108, XM_044627,
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Figure 2564: DNA325109, XM_098761,
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Figure 2566: PRO36959
Figure 2567: DNA325110, NM_014294,
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Figure 2569: DNA325111, NM_000971,
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Figure 2573: PRO81687
Figure 2574: DNA325114, XM_088323,
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Figure 2575: DNA325115, NM_001444,
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Figure 2576: PRO81689
Figure 2577: DNA325116, XM_013127,
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Figure 2578: PRO81690
Figure 2579: DNA325117, XM_165514,
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Figure 2580: PRO81691
Figure 2581: DNA325118, XM_017816,
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Figure 2584: DNA325121, NM_024613,
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Figure 2585: PRO81695
Figure 2586: DNA325122, XM_011642,
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Figure 2587: PRO81696
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Figure 2589: PRO11265
Figure 2590: DNA325124, NM_003406,
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Figure 2591: PRO71091
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Figure 2594: PRO7445
Figure 2595: DNA325126, XM_018287,
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Figure 2596: DNA325127, NM_001568,
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Figure 2597: PRO81699
Figure 2598: DNA325128, NM_003756,
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Figure 2599: PRO81700
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Figure 2603: PRO81701
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WO 2004/030615

PCT/US2003/028547

Figure 2606: DNA325132, NM_005005,
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Figure 2614: DNA325138, NM_016647,
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Figure 2615: PRO23201
Figure 2616: DNA325139, NM_052963,
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Figure 2617: PRO81708
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Figure 2619: DNA325141, XM_058968,
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Figure 2620: DNA325143, NM_023078,
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Figure 2621: PRO81711
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Figure 2623: DNA325145, XM_049226,
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Figure 2624: PRO81714
Figure 2625: DNA325146, XM_114613,
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Figure 2626: DNA325147, XM_035368,
gen.XM_035368
Figure 2627: DNA325148, XM_113532,
gen.XM_113532
Figure 2628: DNA325149, XM_088321,
gen.XM_088321
Figure 2629: DNA325150, XM_035373,
gen.XM_035373
Figure 2630: PRO81719
Figure 2631: DNA325151, XM_035370,
gen.XM_035370
Figure 2632: PRO81720
Figure 2633: DNA325152, NM_000973,
gen.NM_000973
Figure 2634: PRO22907
Figure 2635: DNA325153, NM_033301,
gen.NM_033301
Figure 2636: PRO22907
Figure 2637: DNA325154, XM_049421,
gen.XM_049421
Figure 2638: DNA325155, XM_034640,
gen.XM_034640

Figure 2639: PRO81722
Figure 2640: DNA325156, XM_088550,
gen.XM_088550
Figure 2641: DNA325157, XM_088552,
gen.XM_088552
Figure 2642: DNA325158, XM_088553,
gen.XM_088553
Figure 2643: PRO81725
Figure 2644: DNA325159, XM_059979,
gen.XM_059979
Figure 2645: DNA325160, XM_167558,
gen.XM_167558
Figure 2646: DNA325161, XM_039654,
gen.XM_039654
Figure 2647: DNA325162, XM_060006,
gen.XM_060006
Figure 2648: PRO81729
Figure 2649: DNA325163, NM_001122,
gen.NM_001122
Figure 2650: PRO81730
Figure 2651: DNA325164, NM_001010,
gen.NM_001010
Figure 2652: PRO10824
Figure 2653: DNA325165, NM_058195,
gen.NM_058195
Figure 2654: PRO81731
Figure 2655: DNA325166, NM_000077,
gen.NM_000077
Figure 2656: PRO36693
Figure 2657: DNA325167, NM_058196,
gen.NM_058196
Figure 2658: PRO81732
Figure 2659: DNA325168, XM_017931,
gen.XM_017931
Figure 2660: DNA271847, NM_001539,
gen.NM_001539
Figure 2661: PRO60127
Figure 2662: DNA270991, NM_004323,
gen.NM_004323
Figure 2663: PRO59321
Figure 2664: DNA325169, NM_016410,
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Figure 2665: PRO81734
Figure 2666: DNA325170, XM_005543,
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Figure 2667: PRO38028
Figure 2668: DNA325171, NM_001842,
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Figure 2669: PRO21481
Figure 2670: DNA226345, NM_005866,
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Figure 2671: PRO36808
Figure 2672: DNA325172, XM_088563,
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Figure 2673: DNA325173, XM_059998,
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WO 2004/030615

PCT/US2003/028547

Figure 2674: PRO59579
Figure 2675: DNA325174, NM_013442,
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Figure 2677: DNA325175, XM_114661,
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Figure 2678: PRO81736
Figure 2679: DNA325176, XM_048479,
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Figure 2680: DNA290319, NM_003289,
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Figure 2681: PRO70595
Figure 2682A-C: DNA325177, NM_006289,
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Figure 2683: PRO81738
Figure 2684: DNA325178, XM_048518,
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Figure 2685: PRO81739
Figure 2686: DNA325179, XM_048539,
gen.XM_048539
Figure 2687: PRO81740
Figure 2688: DNA325180, XM_114662,
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Figure 2689: DNA325181, NM_001833,
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Figure 2690: PRO81742
Figure 2691: DNA227491, NM_007096,
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Figure 2692: PRO37954
Figure 2693: DNA254771, NM_012203,
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Figure 2694: PRO49869
Figure 2695: DNA89242, NM_000700,
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Figure 2696: PRO2907
Figure 2697: DNA325182, XM_041020,
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Figure 2698: PRO81743
Figure 2699: DNA325183, XM_114686,
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Figure 2700: DNA325184, XM_088637,
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Figure 2701: DNA287216, NM_021154,
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Figure 2702: PRO69496
Figure 2703: DNA288247, NM_058179,
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Figure 2704: PRO70011
Figure 2705: DNA325185, XM_071178,
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Figure 2706: PRO81746
Figure 2707: DNA325186, XM_005490,
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Figure 2708: DNA325187, NM_031263,
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Figure 2709: PRO81748

Figure 2710: DNA325188, XM_018006,
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Figure 2711: DNA325189, XM_017996,
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Figure 2712: DNA325190, XM_016113,
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Figure 2713: PRO81751
Figure 2714: DNA272655, NM_001827,
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Figure 2715: PRO60781
Figure 2716A-B: DNA325191, NM_002161,
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Figure 2717: PRO81752
Figure 2718A-B: DNA325192, NM_013417,
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Figure 2719: PRO81753
Figure 2720A-B: DNA325193, XM_046863,
gen.XM_046863
Figure 2721: PRO81754
Figure 2722: DNA325194, XM_046836,
gen.XM_046836
Figure 2723: DNA275322, NM_003837,
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Figure 2724: PRO63000
Figure 2725A-B: DNA325195, XM_098943,
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Figure 2726: DNA325196, XM_016308,
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Figure 2727: DNA325197, XM_005525,
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Figure 2728: DNA325198, NM_003389,
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Figure 2729: PRO81759
Figure 2730: DNA325199, NM_033219,
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Figure 2731: PRO81760
Figure 2732: DNA325200, NM_006401,
gen.NM_006401
Figure 2733: PRO81761
Figure 2734: DNA272213, NM_002486,
gen.NM_002486
Figure 2735: PRO60475
Figure 2736: DNA325201, NM_001333,
gen.NM_001333
Figure 2737: PRO81762
Figure 2738: DNA325202, XM_116818,
gen.XM_116818
Figure 2739: PRO81763
Figure 2740: DNA254543, NM_006808,
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Figure 2741: PRO49648
Figure 2742: DNA325203, XM_070873,
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Figure 2743: PRO81764
Figure 2744: DNA325204, XM_042788,
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WO 2004/030615

PCT/US2003/028547

Figure 2745: PRO81765
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Figure 2747: PRO51901
Figure 2748: DNA325205, XM_088569,
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Figure 2749: PRO81766
Figure 2750: DNA325206, XM_088571,
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Figure 2751: DNA271722, NM_004697,
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Figure 2752: PRO60006
Figure 2753: DNA325207, NM_017443,
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Figure 2754: PRO81768
Figure 2755A-C: DNA325208, XM_005348,
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Figure 2756: DNA325209, XM_114646,
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Figure 2757: DNA325210, XM_038391,
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Figure 2758: PRO81771
Figure 2759A-B: DNA325211, XM_045296,
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Figure 2760: DNA325212, XM_005365,
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Figure 2761: DNA289530, NM_004435,
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Figure 2762: PRO70290
Figure 2763: DNA287271, NM_032799,
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Figure 2764: PRO69542
Figure 2765: DNA325213, XM_026987,
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Figure 2766: DNA325214, XM_026985,
gen.XM_026985
Figure 2767: DNA225630, NM_016174,
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Figure 2768: PRO36093
Figure 2769: DNA325215, XM_026968,
gen.XM_026968
Figure 2770: PRO81775
Figure 2771: DNA325216, XM_026951,
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Figure 2772: DNA325217, NM_025072,
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Figure 2773: PRO33818
Figure 2774: DNA325218, XM_033424,
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Figure 2775: DNA325219, NM_004957,
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Figure 2776: PRO81778
Figure 2777: DNA325220, XM_033457,
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Figure 2778A-B: DNA325221, XM_033460,
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Figure 2779: PRO81780
Figure 2780: DNA325222, NM_000976,
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Figure 2781: PRO62236
Figure 2782: DNA218841, NM_012098,
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Figure 2783: PRO34473
Figure 2784A-B: DNA325223, XM_052725,
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Figure 2785: PRO81781
Figure 2786: DNA325224, XM_011752,
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Figure 2787: DNA325225, XM_026944,
gen.XM_026944
Figure 2788: PRO81783
Figure 2789: DNA325226, XM_116806,
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Figure 2790A-B: DNA325227, NM_005347,
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Figure 2791: PRO81785
Figure 2792: DNA325228, NM_005833,
gen.NM_005833
Figure 2793: PRO81786
Figure 2794: DNA325229, NM_007209,
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Figure 2795: PRO61897
Figure 2796: DNA88350, NM_000177,
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Figure 2797: PRO2758
Figure 2798A-B: DNA325230, XM_011749,
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Figure 2799: DNA325231, XM_114679,
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Figure 2800: DNA325232, XM_087041,
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Figure 2801: DNA325233, XM_114678,
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Figure 2802: DNA325234, XM_114677,
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Figure 2803: DNA325235, XM_087038,
gen.XM_087038
Figure 2804: DNA325236, XM_059637,
gen.XM_059637
Figure 2805: PRO81792
Figure 2806: DNA325237, NM_000368,
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Figure 2807: PRO60115
Figure 2808: DNA325238, XM_033385,
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Figure 2809A-B: DNA325239, XM_033380,
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Figure 2810: PRO81794
Figure 2811: DNA325240, XM_033362,
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Figure 2812: PRO81795
Figure 2813: DNA325241, XM_059986,

WO 2004/030615

PCT/US2003/028547

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Figure 2814: PRO81796
Figure 2815A-B: DNA325242, XM_033361,
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Figure 2816: PRO81797
Figure 2817A-B: DNA325243, XM_033360,
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Figure 2818: DNA325244, XM_033359,
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Figure 2819A-B: DNA325245, XM_033355,
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Figure 2820: DNA325246, NM_014285,
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Figure 2821: PRO81800
Figure 2822: DNA325247, NM_054012,
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Figure 2823: PRO81801
Figure 2824: DNA325248, XM_035103,
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Figure 2825: DNA325249, XM_035109,
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Figure 2826: DNA325250, NM_000972,
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Figure 2827: PRO81804
Figure 2828: DNA325251, NM_033161,
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Figure 2829: PRO81805
Figure 2830: DNA325252, NM_000787,
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Figure 2831: PRO81806
Figure 2832A-B: DNA325253, XM_011778,
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Figure 2833: DNA325254, XM_088426,
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Figure 2834: DNA325255, NM_002003,
gen.NM_002003
Figure 2835: PRO1910
Figure 2836: DNA325256, NM_058199,
gen.NM_058199
Figure 2837: PRO81809
Figure 2838: DNA325257, XM_059945,
gen.XM_059945
Figure 2839: DNA325258, XM_088422,
gen.XM_088422
Figure 2840: PRO81811
Figure 2841: DNA325259, XM_029168,
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Figure 2842: PRO81812
Figure 2843: DNA325260, XM_098913,
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Figure 2844: PRO81813
Figure 2845: DNA325261, XM_114669,
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Figure 2846: DNA325262, XM_113564,
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Figure 2847A-B: DNA325263, XM_088459,

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Figure 2848: PRO81815
Figure 2849: DNA325264, XM_054752,
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Figure 2850: PRO81816
Figure 2851: DNA325265, XM_084270,
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Figure 2852: DNA325266, XM_054763,
gen.XM_054763
Figure 2853: PRO81817
Figure 2854: DNA325267, XM_114655,
gen.XM_114655
Figure 2855: DNA325268, XM_038030,
gen.XM_038030
Figure 2856: PRO59351
Figure 2857: DNA325269, XM_072526,
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Figure 2858: PRO81819
Figure 2859: DNA325270, XM_059961,
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Figure 2860: DNA325271, NM_032928,
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Figure 2861: PRO81821
Figure 2862: DNA325272, NM_014172,
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Figure 2863: PRO81822
Figure 2864: DNA325273, XM_038049,
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Figure 2865: PRO62069
Figure 2866: DNA325274, XM_038063,
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Figure 2867: PRO81823
Figure 2868: DNA325275, NM_000954,
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Figure 2869: PRO81824
Figure 2870: DNA325276, XM_088461,
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Figure 2871: DNA325277, XM_059966,
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Figure 2872: PRO81826
Figure 2873: DNA325278, XM_114649,
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Figure 2874: DNA325279, XM_117519,
gen.XM_117519
Figure 2875: DNA325280, XM_053206,
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Figure 2876: DNA325281, XM_040272,
gen.XM_040272
Figure 2877: PRO58939
Figure 2878: DNA325282, XM_005724,
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Figure 2879: DNA325283, XM_040267,
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Figure 2880: PRO81831
Figure 2881: DNA325284, XM_048859,
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WO 2004/030615

PCT/US2003/028547

Figure 2882: PRO62617
Figure 2883: DNA325285, NM_003739, gen.NM_003739
Figure 2884: PRO81832
Figure 2885: DNA325286, XM_060976, gen.XM_060976
Figure 2886: PRO81833
Figure 2887: DNA325287, XM_167626, gen.XM_167626
Figure 2888: PRO81834
Figure 2889: DNA325288, XM_165555, gen.XM_165555
Figure 2890: PRO81835
Figure 2891: DNA325289, NM_001494, gen.NM_001494
Figure 2892: PRO81836
Figure 2893: DNA325290, NM_032905, gen.NM_032905
Figure 2894: PRO81837
Figure 2895: DNA325291, NM_005174, gen.NM_005174
Figure 2896: PRO81838
Figure 2897: DNA325292, XM_165557, gen.XM_165557
Figure 2898: DNA325293, XM_167374, gen.XM_167374
Figure 2899: DNA273759, NM_006023, gen.NM_006023
Figure 2900: PRO61721
Figure 2901: DNA325294, XM_167411, gen.XM_167411
Figure 2902: DNA325295, NM_031453, gen.NM_031453
Figure 2903: PRO81841
Figure 2904: DNA325296, XM_167414, gen.XM_167414
Figure 2905: PRO12851
Figure 2906: DNA325297, XM_166717, gen.XM_166717
Figure 2907: PRO81842
Figure 2908: DNA325298, XM_005100, gen.XM_005100
Figure 2909: DNA325299, XM_038536, gen.XM_038536
Figure 2910A-B: DNA325300, XM_084420, gen.XM_084420
Figure 2911: DNA325301, XM_084429, gen.XM_084429
Figure 2912: PRO81846
Figure 2913A-C: DNA325302, XM_165551, gen.XM_165551
Figure 2914: DNA325303, XM_059720, gen.XM_059720
Figure 2915: PRO81848
Figure 2916A-B: DNA325304, NM_019619, gen.NM_019619

Figure 2917: PRO81849
Figure 2918: DNA325305, XM_166665, gen.XM_166665
Figure 2919A-B: DNA325306, NM_002211, gen.NM_002211
Figure 2920: PRO81851
Figure 2921A-B: DNA325307, XM_165567, gen.XM_165567
Figure 2922: DNA325308, XM_166157, gen.XM_166157
Figure 2923: DNA325309, NM_032023, gen.NM_032023
Figure 2924: PRO52537
Figure 2925: DNA325310, XM_165560, gen.XM_165560
Figure 2926: DNA325311, XM_165563, gen.XM_165563
Figure 2927: DNA325312, XM_113615, gen.XM_113615
Figure 2928: PRO81855
Figure 2929: DNA325313, XM_165890, gen.XM_165890
Figure 2930: DNA325314, XM_061126, gen.XM_061126
Figure 2931: DNA325315, XM_061125, gen.XM_061125
Figure 2932: PRO81858
Figure 2933: DNA325316, XM_054474, gen.XM_054474
Figure 2934: DNA325317, XM_165888, gen.XM_165888
Figure 2935: DNA325318, XM_054475, gen.XM_054475
Figure 2936: PRO81861
Figure 2937: DNA325319, XM_015652, gen.XM_015652
Figure 2938: PRO81862
Figure 2939: DNA325320, XM_036593, gen.XM_036593
Figure 2940: PRO81863
Figure 2941: DNA325321, XM_165891, gen.XM_165891
Figure 2942: DNA325322, XM_084450, gen.XM_084450
Figure 2943: PRO81865
Figure 2944: DNA325323, XM_084385, gen.XM_084385
Figure 2945: DNA325324, NM_021226, gen.NM_021226
Figure 2946: PRO81867
Figure 2947: DNA193957, NM_003055, gen.NM_003055
Figure 2948: PRO23364
Figure 2949: DNA325325, NM_032997, gen.NM_032997
Figure 2950: PRO81868

WO 2004/030615

PCT/US2003/028547

Figure 2951: DNA287642, NM_018464,
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Figure 2952: PRO9902
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Figure 2954: PRO81869
Figure 2955: DNA325327, NM_012207,
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Figure 2956: PRO81870
Figure 2957: DNA325328, NM_024045,
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Figure 2958: PRO81871
Figure 2959: DNA325329, NM_004728,
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Figure 2960: PRO81872
Figure 2961: DNA88562, NM_002727,
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Figure 2962: PRO2842
Figure 2963: DNA325330, XM_167395,
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Figure 2964: DNA227172, NM_021129,
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Figure 2965: PRO37635
Figure 2966A-B: DNA325331, XM_166125,
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Figure 2967: PRO81874
Figure 2968: DNA325332, XM_044354,
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Figure 2969: PRO81875
Figure 2970: DNA325333, XM_032520,
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Figure 2971: DNA325334, NM_019058,
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Figure 2972: PRO81877
Figure 2973: DNA325335, XM_045140,
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Figure 2974: PRO2875
Figure 2975: DNA325336, XM_116863,
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Figure 2976: DNA325337, XM_032476,
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Figure 2977: DNA325338, XM_114894,
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Figure 2978: DNA325339, NM_033022,
gen.NM_033022
Figure 2979: PRO81881
Figure 2980: DNA325340, NM_001026,
gen.NM_001026
Figure 2981: PRO11139
Figure 2982: DNA103421, NM_003375,
gen.NM_003375
Figure 2983: PRO4749
Figure 2984A-B: DNA325341, XM_166093,
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Figure 2985: PRO81882
Figure 2986: DNA304459, NM_005729,

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Figure 2987: PRO37073
Figure 2988: DNA325342, XM_166629,
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Figure 2989: PRO81883
Figure 2990: DNA103506, NM_001157,
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Figure 2991: PRO4833
Figure 2992: DNA325343, XM_016093,
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Figure 2993: PRO81884
Figure 2994: DNA325344, XM_084467,
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Figure 2995: PRO81885
Figure 2996: DNA304488, NM_032333,
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Figure 2997: PRO71057
Figure 2998: DNA325345, XM_043589,
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Figure 2999: DNA325346, XM_043605,
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Figure 3000: DNA325347, XM_087480,
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Figure 3001: PRO81887
Figure 3002: DNA325348, NM_002921,
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Figure 3003: PRO81888
Figure 3004: DNA226217, NM_005271,
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Figure 3005: PRO36680
Figure 3006: DNA325349, XM_089551,
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Figure 3007: PRO81889
Figure 3008: DNA287237, NM_001613,
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Figure 3009: PRO39648
Figure 3010: DNA325350, XM_084477,
gen.XM_084477
Figure 3011: PRO69523
Figure 3012: DNA325351, XM_084480,
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Figure 3013A-B: DNA325352, NM_013451,
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Figure 3014: PRO12813
Figure 3015: DNA325353, XM_018167,
gen.XM_018167
Figure 3016: DNA325354, XM_084372,
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Figure 3017: DNA325355, NM_020992,
gen.NM_020992
Figure 3018: PRO81893
Figure 3019: DNA325356, XM_089514,
gen.XM_089514
Figure 3020A-B: DNA325357, XM_058343,
gen.XM_058343
Figure 3021: PRO81895

WO 2004/030615

PCT/US2003/028547

Figure 3022: DNA325358, XM_058602,
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Figure 3023: PRO81896
Figure 3024A-B: DNA325359, NM_015179,
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Figure 3025: PRO81897
Figure 3026: DNA325360, XM_083842,
gen.XM_083842
Figure 3027: PRO69473
Figure 3028: DNA325361, XM_084413,
gen.XM_084413
Figure 3029: DNA325362, NM_022362,
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Figure 3030: PRO81899
Figure 3031: DNA325363, NM_032112,
gen.NM_032112
Figure 3032: PRO81900
Figure 3033: DNA325364, NM_021830,
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Figure 3034: PRO81901
Figure 3035A-B: DNA325365, XM_046743,
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Figure 3036: PRO81902
Figure 3037: DNA325366, NM_013274,
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Figure 3038: PRO81903
Figure 3039: DNA325367, NM_022039,
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Figure 3040: PRO81904
Figure 3041A-B: DNA325368, XM_031866,
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Figure 3042A-B: DNA325369, NM_015062,
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Figure 3043: PRO81905
Figure 3044A-B: DNA325370, XM_031890,
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Figure 3045A-B: DNA325371, NM_004193,
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Figure 3046: PRO81907
Figure 3047: DNA325372, NM_024040,
gen.NM_024040
Figure 3048: PRO81908
Figure 3049: DNA325373, XM_031949,
gen.XM_031949
Figure 3050: PRO4900
Figure 3051A-B: DNA144601, NM_016169,
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Figure 3052: PRO34073
Figure 3053: DNA325374, XM_005698,
gen.XM_005698
Figure 3054: PRO81909
Figure 3055: DNA325375, NM_006523,
gen.NM_006523
Figure 3056: PRO59043
Figure 3057: DNA325376, XM_018279,
gen.XM_018279

Figure 3058A-B: DNA325377, XM_005938,
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Figure 3059A-B: DNA325378, XM_031992,
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Figure 3060: PRO81912
Figure 3061: DNA325379, NM_032747,
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Figure 3062: PRO81913
Figure 3063: DNA325380, NM_005004,
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Figure 3064: PRO81914
Figure 3065: DNA325381, XM_030447,
gen.XM_030447
Figure 3066: DNA273521, NM_002079,
gen.NM_002079
Figure 3067: PRO61502
Figure 3068A-B: DNA325382, NM_032211,
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Figure 3069: PRO81916
Figure 3070: DNA325383, NM_031484,
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Figure 3071: PRO81917
Figure 3072: DNA325384, XM_084632,
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Figure 3073: DNA325385, XM_084359,
gen.XM_084359
Figure 3074A-D: DNA325386, XM_045667,
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Figure 3075: DNA325387, XM_109162,
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Figure 3076: DNA227509, NM_000274,
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Figure 3077: PRO37972
Figure 3078: DNA325388, XM_058361,
gen.XM_058361
Figure 3079: PRO81922
Figure 3080: DNA325389, XM_084505,
gen.XM_084505
Figure 3081: PRO81923
Figure 3082A-B: DNA325390, XM_049795,
gen.XM_049795
Figure 3083: PRO81924
Figure 3084: DNA325391, XM_058406,
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Figure 3085: PRO81925
Figure 3086: DNA325392, XM_055573,
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Figure 3087: PRO60991
Figure 3088: DNA325393, XM_005969,
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Figure 3089: DNA325394, NM_007190,
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Figure 3090: PRO81926
Figure 3091: DNA325395, NM_000982,
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Figure 3092: PRO81927

WO 2004/030615

PCT/US2003/028547

Figure 3093: DNA269952, NM_004725,
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Figure 3094: PRO58348
Figure 3095: DNA325396, NM_024942,
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Figure 3096: PRO81928
Figure 3097: DNA325397, NM_016567,
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Figure 3098: PRO81929
Figure 3099: DNA325398, NM_004092,
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Figure 3100: PRO81930
Figure 3101: DNA269431, NM_006659,
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Figure 3102: PRO57854
Figure 3103: DNA325399, XM_005675,
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Figure 3104: DNA325400, XM_114862,
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Figure 3105: PRO81932
Figure 3106: DNA325401, XM_088009,
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Figure 3107: DNA325402, NM_016526,
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Figure 3108: PRO81934
Figure 3109: DNA255696, NM_021932,
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Figure 3110: PRO50756
Figure 3111: DNA325403, XM_043220,
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Figure 3112: PRO81935
Figure 3113: DNA255078, NM_006435,
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Figure 3114: PRO50165
Figure 3115: DNA325404, NM_002339,
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Figure 3116: PRO81936
Figure 3117: DNA325405, XM_028192,
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Figure 3118: PRO81937
Figure 3119: DNA325406, XM_096544,
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Figure 3120: DNA325407, NM_000612,
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Figure 3121: PRO124
Figure 3122: DNA325408, XM_084742,
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Figure 3123: PRO81939
Figure 3124: DNA325409, XM_084739,
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Figure 3125: DNA325410, XM_058505,
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Figure 3126: PRO81941
Figure 3127: DNA325411, XM_006139,
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Figure 3128: PRO81942

Figure 3129: DNA325412, XM_044932,
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Figure 3130: PRO81943
Figure 3131A-B: DNA325413, XM_044957,
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Figure 3132: PRO81944
Figure 3133: DNA325414, NM_001909,
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Figure 3134: PRO292
Figure 3135: DNA325415, XM_006475,
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Figure 3136: DNA325416, XM_006483,
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Figure 3137: DNA325417, NM_001751,
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Figure 3138: PRO69635
Figure 3139: DNA325418, XM_114981,
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Figure 3140: PRO81945
Figure 3141: DNA325419, XM_083852,
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Figure 3142: DNA325420, NM_000559,
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Figure 3143: PRO81946
Figure 3144: DNA325421, NM_000184,
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Figure 3145: PRO81947
Figure 3146: DNA325422, NM_005330,
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Figure 3147: PRO81948
Figure 3148: DNA325423, XM_015243,
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Figure 3149: DNA325424, NM_015324,
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Figure 3150: PRO81950
Figure 3151: DNA325425, XM_006424,
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Figure 3152: DNA325426, XM_113238,
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Figure 3153A-C: DNA325427, XM_052786,
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Figure 3154: PRO81953
Figure 3155: DNA325428, NM_000990,
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Figure 3156: PRO25985
Figure 3157A-B: DNA325429, XM_045750,
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Figure 3158: PRO81954
Figure 3159: DNA325430, XM_058414,
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Figure 3160: PRO81955
Figure 3161A-B: DNA325431, XM_049197,
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Figure 3162: PRO81956
Figure 3163A-B: DNA325432, NM_001418,
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WO 2004/030615

PCT/US2003/028547

Figure 3164: PRO81957
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Figure 3167: DNA325434, XM_006212,
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Figure 3168: PRO81959
Figure 3169: DNA325435, XM_084527,
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Figure 3170: DNA325436, XM_016139,
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Figure 3171: DNA325437, NM_001017,
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Figure 3172: PRO11262
Figure 3173: DNA325438, NM_014267,
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Figure 3174: PRO81962
Figure 3175: DNA97285, NM_005566,
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Figure 3176: PRO3632
Figure 3177: DNA325439, XM_115081,
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Figure 3179: PRO81964
Figure 3180: DNA325441, XM_084514,
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Figure 3181: PRO81965
Figure 3182: DNA325442, XM_084516,
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Figure 3183: DNA325443, XM_084515,
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Figure 3184: DNA325444, XM_084517,
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Figure 3185: DNA325445, XM_034431,
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Figure 3186: PRO11691
Figure 3187: DNA325446, XM_030326,
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Figure 3188: DNA325447, NM_057174,
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Figure 3189: PRO81970
Figure 3190: DNA325448, NM_004813,
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Figure 3191: PRO81971
Figure 3192: DNA325449, XM_167437,
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Figure 3194: DNA325451, XM_004330,
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Figure 3196: DNA325453, XM_006297,
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Figure 3197: DNA325454, NM_003646,

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Figure 3198: PRO81977
Figure 3199: DNA325455, NM_004551,
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Figure 3200: PRO81978
Figure 3201: DNA325456, XM_006170,
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Figure 3202: DNA325457, XM_037173,
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Figure 3203: PRO81980
Figure 3204: DNA150974, NM_005693,
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Figure 3205: PRO12224
Figure 3206: DNA226080, NM_001610,
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Figure 3207: PRO36543
Figure 3208: DNA270134, NM_000107,
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Figure 3209: PRO58523
Figure 3210: DNA325458, NM_016223,
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Figure 3211: PRO81981
Figure 3212: DNA325459, XM_037147,
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Figure 3213: PRO81982
Figure 3214: DNA325460, XM_015705,
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Figure 3215: DNA272728, NM_003146,
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Figure 3216: PRO60847
Figure 3217: DNA325461, XM_165611,
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Figure 3218: DNA287417, NM_024098,
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Figure 3219: PRO69674
Figure 3220: DNA227088, NM_014502,
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Figure 3221: PRO37551
Figure 3222: DNA325462, XM_165610,
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Figure 3223A-B: DNA325463, XM_165612,
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Figure 3224: DNA325464, XM_166234,
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Figure 3225: DNA325465, NM_015533,
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Figure 3226: PRO81988
Figure 3227: DNA325466, XM_166232,
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Figure 3228A-B: DNA325467, XM_167748,
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Figure 3229: PRO81990
Figure 3230: DNA325468, NM_004739,
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Figure 3231: PRO81991
Figure 3232: DNA325469, NM_014610,

WO 2004/030615

PCT/US2003/028547

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Figure 3236: DNA287254, NM_024099,
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Figure 3237: PRO69528
Figure 3238: DNA325471, NM_015853,
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Figure 3239: PRO81994
Figure 3240: DNA325472, NM_032667,
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Figure 3241: PRO81995
Figure 3242: DNA325473, NM_006362,
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Figure 3243: PRO81996
Figure 3244: DNA325474, XM_167716,
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Figure 3245: DNA75863, NM_002411,
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Figure 3246: PRO2018
Figure 3247: DNA325475, XM_087710,
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Figure 3248: DNA325476, XM_167726,
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Figure 3249: DNA325477, NM_004265,
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Figure 3250: PRO12878
Figure 3251A-B: DNA325478, NM_013402,
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Figure 3252: PRO81999
Figure 3253: DNA325479, NM_004111,
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Figure 3254: PRO69568
Figure 3255: DNA325480, XM_048286,
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Figure 3256: DNA325481, NM_004322,
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Figure 3257: PRO20117
Figure 3258: DNA325482, NM_032989,
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Figure 3259: PRO20117
Figure 3260: DNA325483, XM_011988,
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Figure 3261: DNA325484, NM_031472,
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Figure 3262: PRO82002
Figure 3263: DNA325485, XM_037808,
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Figure 3264: DNA325486, NM_004074,
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Figure 3265: PRO82004
Figure 3266: DNA325487, NM_017670,
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Figure 3267: PRO82005

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Figure 3269: DNA325489, XM_045642,
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Figure 3271: DNA325491, XM_045613,
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Figure 3272: PRO59721
Figure 3273A-B: DNA325492, XM_045612,
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Figure 3274: PRO82009
Figure 3275: DNA325493, XM_113224,
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Figure 3276: DNA325494, XM_045499,
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Figure 3277: PRO82011
Figure 3278: DNA325495, XM_045525,
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Figure 3279: DNA325496, NM_013265,
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Figure 3280: PRO82013
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Figure 3282: PRO60008
Figure 3283: DNA325498, XM_053787,
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Figure 3284: DNA269803, NM_001667,
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Figure 3285: PRO58207
Figure 3286: DNA325499, XM_115031,
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Figure 3287: DNA325500, XM_084702,
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Figure 3288: DNA325501, XM_053796,
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Figure 3289: DNA325502, NM_002689,
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Figure 3290: PRO82018
Figure 3291A-D: DNA325503, XM_167804,
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Figure 3292: PRO82019
Figure 3293: DNA325504, XM_166235,
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Figure 3294: DNA325505, XM_166236,
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Figure 3295: DNA270721, NM_006842,
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Figure 3296: PRO59084
Figure 3297: DNA189687, NM_000852,
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Figure 3298: PRO25845
Figure 3299: DNA325506, NM_007103,
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Figure 3301: DNA325507, NM_005851,

WO 2004/030615

PCT/US2003/028547

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Figure 3303A-B: DNA325508, XM_165598,
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Figure 3306: DNA325510, NM_006053,
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Figure 3307: PRO24831
Figure 3308: DNA325511, XM_166196,
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Figure 3309: PRO82024
Figure 3310: DNA325512, XM_165600,
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Figure 3311A-B: DNA325513, NM_053056,
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Figure 3312: PRO4870
Figure 3313: DNA103474, NM_003824,
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Figure 3314: PRO4801
Figure 3315: DNA325514, XM_096486,
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Figure 3316A-B: DNA325515, NM_003626,
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Figure 3317: PRO82027
Figure 3318A-B: DNA325516, XM_167853,
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Figure 3319: PRO82028
Figure 3320: DNA325517, NM_014042,
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Figure 3321: PRO82029
Figure 3322A-B: DNA325518, NM_001567,
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Figure 3323: PRO61238
Figure 3324: DNA325519, XM_167433,
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Figure 3325: DNA325520, XM_165616,
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Figure 3326: DNA325521, NM_032871,
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Figure 3327: PRO57307
Figure 3328: DNA325522, XM_165631,
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Figure 3329: DNA254186, NM_014752,
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Figure 3330: PRO49298
Figure 3331: DNA325523, NM_001005,
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Figure 3332: PRO82032
Figure 3333: DNA88176, NM_001235,
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Figure 3334: PRO2685
Figure 3335A-B: DNA325524, XM_165627,
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Figure 3336: DNA325525, XM_166253,

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Figure 3337: DNA325526, NM_001293,
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Figure 3338: PRO82034
Figure 3339: DNA325527, XM_042852,
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Figure 3340: PRO82035
Figure 3341: DNA325528, XM_165628,
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Figure 3342A-B: DNA325529, NM_080491,
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Figure 3343: PRO82037
Figure 3344A-B: DNA325530, NM_012296,
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Figure 3345: PRO60311
Figure 3346: DNA325531, NM_032379,
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Figure 3347: PRO82038
Figure 3348: DNA325532, NM_007173,
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Figure 3349: DNA325533, XM_166239,
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Figure 3350: DNA325534, XM_084610,
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Figure 3351: PRO82040
Figure 3352: DNA325535, XM_058450,
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Figure 3353: DNA325536, XM_084601,
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Figure 3354: PRO82042
Figure 3355A-B: DNA325537, XM_006464,
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Figure 3356: PRO82043
Figure 3357: DNA325538, XM_084570,
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Figure 3358: DNA325539, XM_051435,
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Figure 3359: DNA325540, NM_001467,
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Figure 3360: PRO82045
Figure 3361: DNA325541, NM_001028,
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Figure 3362: PRO82046
Figure 3363: DNA325542, XM_113230,
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Figure 3364: DNA325543, XM_115062,
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Figure 3365: DNA325544, XM_115063,
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Figure 3366: DNA325545, XM_113229,
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Figure 3367A-B: DNA325546, XM_051489,
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Figure 3368: PRO82050
Figure 3369: DNA325547, NM_022003,
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WO 2004/030615

PCT/US2003/028547

Figure 3370: PRO82051
Figure 3371: DNA325548, XM_006432, gen.XM_006432
Figure 3372: PRO82052
Figure 3373: DNA325549, XM_051716, gen.XM_051716
Figure 3374: DNA325550, NM_025164, gen.NM_025164
Figure 3375: PRO82054
Figure 3376: DNA225752, NM_000039, gen.NM_000039
Figure 3377: PRO36215
Figure 3378: DNA325551, XM_052113, gen.XM_052113
Figure 3379: PRO82055
Figure 3380: DNA271324, NM_006169, gen.NM_006169
Figure 3381: PRO59629
Figure 3382: DNA325552, XM_084658, gen.XM_084658
Figure 3383: PRO82056
Figure 3384: DNA325553, NM_000795, gen.NM_000795
Figure 3385: PRO12448
Figure 3386: DNA325554, NM_017868, gen.NM_017868
Figure 3387: PRO82057
Figure 3388: DNA325555, XM_084654, gen.XM_084654
Figure 3389: PRO82058
Figure 3390: DNA272413, NM_003002, gen.NM_003002
Figure 3391: PRO60666
Figure 3392: DNA271843, NM_004398, gen.NM_004398
Figure 3393: PRO60123
Figure 3394: DNA325556, XM_017369, gen.XM_017369
Figure 3395: DNA325557, NM_032299, gen.NM_032299
Figure 3396: PRO82060
Figure 3397: DNA325558, XM_055369, gen.XM_055369
Figure 3398: DNA325559, XM_051430, gen.XM_051430
Figure 3399: DNA325560, XM_006467, gen.XM_006467
Figure 3400: DNA325561, XM_113226, gen.XM_113226
Figure 3401: DNA325562, XM_165592, gen.XM_165592
Figure 3402: PRO82064
Figure 3403: DNA325563, XM_166181, gen.XM_166181
Figure 3404: DNA325564, XM_052862, gen.XM_052862

Figure 3405: PRO82066
Figure 3406: DNA325565, XM_166177, gen.XM_166177
Figure 3407: DNA325566, XM_165571, gen.XM_165571
Figure 3408: PRO82068
Figure 3409: DNA325567, XM_166174, gen.XM_166174
Figure 3410: PRO82069
Figure 3411: DNA325568, NM_001274, gen.NM_001274
Figure 3412: PRO12187
Figure 3413: DNA325569, XM_165586, gen.XM_165586
Figure 3414: DNA325570, XM_165584, gen.XM_165584
Figure 3415: DNA257965, NM_032873, gen.NM_032873
Figure 3416: PRO52492
Figure 3417: DNA325571, XM_167780, gen.XM_167780
Figure 3418: DNA325572, XM_166743, gen.XM_166743
Figure 3419: PRO82072
Figure 3420: DNA325573, NM_012101, gen.NM_012101
Figure 3421: PRO82073
Figure 3422: DNA325574, NM_058193, gen.NM_058193
Figure 3423: PRO82074
Figure 3424: DNA325575, XM_084522, gen.XM_084522
Figure 3425: PRO82075
Figure 3426: DNA325576, XM_091786, gen.XM_091786
Figure 3427: DNA325577, XM_165390, gen.XM_165390
Figure 3428: DNA325578, XM_084525, gen.XM_084525
Figure 3429A-B: DNA325579, XM_010494, gen.XM_010494
Figure 3430A-B: DNA325580, NM_015064, gen.NM_015064
Figure 3431: PRO82078
Figure 3432: DNA325581, NM_030775, gen.NM_030775
Figure 3433: PRO71031
Figure 3434: DNA297398, NM_032642, gen.NM_032642
Figure 3435: PRO71031
Figure 3436: DNA325582, XM_017080, gen.XM_017080
Figure 3437: DNA325583, XM_113739, gen.XM_113739
Figure 3438: PRO82080
Figure 3439: DNA325584, NM_002014,

WO 2004/030615

PCT/US2003/028547

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Figure 3441: DNA325585, XM_096661,
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Figure 3443: PRO82082
Figure 3444: DNA325587, NM_021953,
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Figure 3445: PRO82083
Figure 3446: DNA325588, NM_031465,
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Figure 3447: PRO82084
Figure 3448: DNA325589, NM_005002,
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Figure 3449: PRO82085
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Figure 3453: PRO2660
Figure 3454: DNA325592, XM_058574,
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Figure 3455: DNA325593, NM_007273,
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Figure 3456: PRO36970
Figure 3457A-B: DNA325594, XM_032588,
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Figure 3458: DNA325595, NM_001975,
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Figure 3459: PRO38010
Figure 3460: DNA325596, NM_000365,
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Figure 3461: PRO69549
Figure 3462: DNA325597, XM_032614,
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Figure 3463: DNA325598, NM_002075,
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Figure 3464: PRO82091
Figure 3465: DNA325599, XM_165910,
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Figure 3466: DNA151827, NM_005439,
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Figure 3467: PRO12902
Figure 3468A-B: DNA254624, NM_001273,
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Figure 3469: PRO49726
Figure 3470: DNA325600, NM_015438,
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Figure 3471: PRO82093
Figure 3472: DNA325601, XM_033263,
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Figure 3473: DNA225632, NM_002046,
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Figure 3474: PRO36095
Figure 3475A-B: DNA325602, XM_006958,
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Figure 3476: DNA83180, NM_002342,
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Figure 3477: PRO2622
Figure 3478: DNA103514, NM_001038,
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Figure 3479: PRO4841
Figure 3480: DNA188396, NM_001065,
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Figure 3481: PRO21924
Figure 3482A-C: DNA325603, XM_006947,
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Figure 3483A-B: DNA325604, XM_006936,
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Figure 3484: PRO82097
Figure 3485A-B: DNA325605, XM_006925,
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Figure 3486: DNA325606, XM_096630,
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Figure 3487: PRO82099
Figure 3488: DNA325607, XM_084901,
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Figure 3489: DNA226028, NM_002355,
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Figure 3490: PRO36491
Figure 3491: DNA325608, XM_031807,
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Figure 3492: PRO82101
Figure 3493A-B: DNA325609, XM_049663,
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Figure 3494: DNA325610, XM_012159,
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Figure 3495: DNA325611, XM_084922,
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Figure 3496: DNA325612, NM_031289,
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Figure 3497: PRO82104
Figure 3498: DNA226771, NM_003979,
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Figure 3499: PRO37234
Figure 3500: DNA325613, XM_084918,
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Figure 3501: DNA325614, NM_007178,
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Figure 3502: PRO82106
Figure 3503: DNA325615, XM_041100,
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Figure 3504A-B: DNA325616, XM_058567,
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Figure 3505: PRO82107
Figure 3506A-B: DNA325617, XM_166605,
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Figure 3507: DNA325618, XM_029805,
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WO 2004/030615

PCT/US2003/028547

Figure 3508: PRO82109
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Figure 3511: DNA256072, NM_001644,
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Figure 3512: PRO51121
Figure 3513: DNA325620, NM_018686,
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Figure 3514: PRO82111
Figure 3515: DNA325621, XM_084770,
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Figure 3516: PRO82112
Figure 3517: DNA325622, NM_018048,
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Figure 3518: PRO82113
Figure 3519: DNA325623, XM_113730,
gen.XM_113730
Figure 3520: DNA150978, NM_007244,
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Figure 3521: PRO11601
Figure 3522: DNA325624, NM_006250,
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Figure 3523: PRO82115
Figure 3524: DNA79313, NM_005042,
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Figure 3525: PRO2555
Figure 3526: DNA150997, NM_004982,
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Figure 3527: PRO12573
Figure 3528: DNA325625, XM_050074,
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Figure 3529: DNA325626, NM_024854,
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Figure 3530: PRO82117
Figure 3531: DNA325627, XM_084807,
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Figure 3532: DNA325628, XM_165906,
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Figure 3533A-B: DNA325629, XM_038659,
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Figure 3534: PRO82120
Figure 3535: DNA325630, XM_006694,
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Figure 3536: DNA325631, XM_006748,
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Figure 3537: PRO82122
Figure 3538: DNA325632, XM_016640,
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Figure 3539: DNA325633, XM_096146,
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Figure 3540A-B: DNA325634, XM_084841,
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Figure 3541: PRO82125
Figure 3542: DNA325635, XM_090218,
gen.XM_090218

Figure 3543: DNA325636, XM_012272,
gen.XM_012272
Figure 3544: PRO82127
Figure 3545A-B: DNA325637, XM_056481,
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Figure 3546: DNA325638, NM_006262,
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Figure 3547: PRO82129
Figure 3548: DNA325639, NM_018113,
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Figure 3549: PRO82130
Figure 3550: DNA271344, NM_001659,
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Figure 3551: PRO59647
Figure 3552: DNA325640, NM_017822,
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Figure 3553: PRO82131
Figure 3554A-E: DNA325641, XM_028760,
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Figure 3555: DNA272379, NM_002733,
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Figure 3556: PRO60634
Figure 3557: DNA325642, XM_084866,
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Figure 3558: PRO82133
Figure 3559: DNA325643, XM_006826,
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Figure 3560: DNA325644, XM_113719,
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Figure 3561: DNA325645, XM_028662,
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Figure 3562: DNA325646, XM_035497,
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Figure 3563: PRO82137
Figure 3564: DNA325647, XM_035490,
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Figure 3565: PRO82138
Figure 3566: DNA325648, NM_013277,
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Figure 3567: PRO82139
Figure 3568: DNA325649, NM_003076,
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Figure 3569: PRO82140
Figure 3570: DNA325650, XM_115117,
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Figure 3571: DNA325651, XM_035485,
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Figure 3572A-B: DNA325652, NM_016357,
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Figure 3573: PRO82143
Figure 3574: DNA325653, NM_005171,
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Figure 3575: PRO60924
Figure 3576: DNA325654, NM_014033,
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Figure 3577: PRO4348

WO 2004/030615

PCT/US2003/028547

Figure 3578: DNA325655, XM_096620,
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Figure 3581: DNA325658, XM_049148,
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Figure 3582: DNA325659, XM_084885,
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Figure 3583: DNA325660, XM_084884,
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Figure 3584: DNA325661, XM_113726,
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Figure 3585: DNA325662, XM_015476,
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Figure 3586: DNA325663, XM_049141,
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Figure 3587: PRO82152
Figure 3588: DNA227191, NM_021934,
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Figure 3589: PRO37654
Figure 3590: DNA325664, XM_083868,
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Figure 3591: DNA270458, NM_002273,
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Figure 3592: PRO58837
Figure 3593: DNA227092, NM_000224,
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Figure 3594: PRO37555
Figure 3595: DNA325665, XM_029728,
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Figure 3596: DNA325666, XM_015468,
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Figure 3597: PRO82155
Figure 3598: DNA325667, XM_012162,
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Figure 3599: DNA325668, XM_084789,
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Figure 3601: PRO3449
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Figure 3603: PRO82158
Figure 3604: DNA325670, NM_015665,
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Figure 3605: PRO82159
Figure 3606: DNA325671, NM_014311,
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Figure 3607: PRO82160
Figure 3608: DNA325672, XM_096606,
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Figure 3609: PRO82161
Figure 3610: DNA325673, NM_018457,
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Figure 3612: DNA325674, NM_031157,
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Figure 3613: PRO82163
Figure 3614: DNA325675, NM_004178,
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Figure 3615: PRO82164
Figure 3616: DNA325676, NM_134323,
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Figure 3617: PRO82165
Figure 3618: DNA325677, NM_134324,
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Figure 3619: PRO82166
Figure 3620: DNA290294, NM_005016,
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Figure 3621: PRO70453
Figure 3622: DNA325678, NM_031989,
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Figure 3623: PRO82167
Figure 3624: DNA325679, XM_028643,
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Figure 3625: PRO82168
Figure 3626: DNA325680, XM_006710,
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Figure 3627: PRO82169
Figure 3628: DNA227094, NM_005594,
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Figure 3629: PRO37557
Figure 3630: DNA325681, XM_084824,
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Figure 3631: DNA304783, NM_014255,
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Figure 3632: PRO4426
Figure 3633: DNA325682, XM_165903,
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Figure 3634: DNA325683, XM_115140,
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Figure 3635: DNA325684, XM_113712,
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Figure 3636: DNA325685, NM_006601,
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Figure 3637: PRO82174
Figure 3638: DNA325686, XM_012182,
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Figure 3639: PRO82175
Figure 3640: DNA325687, XM_048943,
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Figure 3641: DNA325688, XM_053164,
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Figure 3642: DNA325689, XM_048991,
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Figure 3643: DNA325690, NM_024068,
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Figure 3644: PRO82179
Figure 3645A-B: DNA325691, XM_056346,
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WO 2004/030615

PCT/US2003/028547

Figure 3646: DNA325692, NM_021019,
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Figure 3649: PRO82182
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Figure 3651: PRO82183
Figure 3652: DNA325695, XM_049048,
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Figure 3653: PRO82184
Figure 3654: DNA325696, NM_021104,
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Figure 3655: PRO11213
Figure 3656: DNA325697, NM_001029,
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Figure 3657: PRO10838
Figure 3658: DNA325698, XM_001482,
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Figure 3659: DNA325699, XM_049150,
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Figure 3660: DNA325700, NM_006928,
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Figure 3661: PRO2846
Figure 3662: DNA325701, XM_056353,
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Figure 3663: DNA325702, NM_001780,
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Figure 3664: PRO283
Figure 3665: DNA325703, NM_031479,
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Figure 3666: PRO21773
Figure 3667A-: DNA137231, NM_005269,
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Figure 3668: PRO9112
Figure 3669: DNA325704, NM_004990,
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Figure 3670: PRO82188
Figure 3671: DNA325705, XM_058528,
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Figure 3673: PRO82190
Figure 3674: DNA325707, XM_048603,
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Figure 3675: PRO82191
Figure 3676: DNA325708, NM_133483,
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Figure 3677: PRO82192
Figure 3678: DNA79101, NM_006812,
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Figure 3679: PRO2549
Figure 3680: DNA325709, XM_096566,
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Figure 3682: PRO4666
Figure 3683: DNA325711, NM_000075,
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Figure 3684: PRO4873
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Figure 3686: PRO82194
Figure 3687: DNA325713, NM_000785,
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Figure 3688: PRO58440
Figure 3689: DNA325714, NM_005371,
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Figure 3690: PRO82195
Figure 3691: DNA325715, NM_023032,
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Figure 3692: PRO82196
Figure 3693: DNA325716, NM_023033,
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Figure 3695: DNA325717, NM_005726,
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Figure 3696: PRO82198
Figure 3697: DNA325718, NM_006576,
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Figure 3698: PRO82199
Figure 3699A-B: DNA325719, XM_096038,
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Figure 3703: PRO82202
Figure 3704: DNA325722, XM_004098,
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Figure 3705: DNA325723, XM_084912,
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Figure 3706: PRO82204
Figure 3707: DNA325724, XM_040221,
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Figure 3708: DNA325725, XM_016605,
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Figure 3709: PRO82206
Figure 3710: DNA325726, XM_017508,
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Figure 3711: PRO82207
Figure 3712: DNA325727, NM_032338,
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Figure 3713: PRO82208
Figure 3714A-B: DNA325728, XM_052460,
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Figure 3715: DNA325729, XM_083866,
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Figure 3716: PRO82210
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WO 2004/030615

PCT/US2003/028547

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Figure 3721: PRO37937
Figure 3722: DNA325731, XM_053952,
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Figure 3723: PRO82212
Figure 3724: DNA227171, NM_014515,
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Figure 3725: PRO37634
Figure 3726: DNA325732, XM_046041,
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Figure 3727: DNA271492, NM_006530,
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Figure 3728: PRO59785
Figure 3729: DNA226014, NM_000239,
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Figure 3730: PRO36477
Figure 3731: DNA325733, XM_084645,
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Figure 3732A-B: DNA325734, XM_039395,
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Figure 3733: PRO82213
Figure 3734: DNA325736, XM_040644,
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Figure 3735: PRO82214
Figure 3736A-B: DNA325737, XM_006578,
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Figure 3737: DNA325738, XM_038308,
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Figure 3738: PRO82215
Figure 3739: DNA325739, XM_096597,
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Figure 3740: DNA325740, NM_001920,
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Figure 3741: PRO2841
Figure 3742: DNA325741, NM_133503,
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Figure 3743: PRO2841
Figure 3744: DNA325742, NM_133504,
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Figure 3745: PRO82218
Figure 3746: DNA325743, NM_133505,
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Figure 3747: PRO82219
Figure 3748: DNA325744, NM_133507,
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Figure 3749: PRO82220
Figure 3750: DNA325745, NM_133506,
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Figure 3751: PRO82221
Figure 3752: DNA325746, NM_002345,
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Figure 3753: PRO9987
Figure 3754: DNA325747, XM_167518,
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Figure 3755: DNA325748, XM_052542,
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Figure 3756: PRO82223
Figure 3757: DNA325749, NM_003877,
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Figure 3758: PRO12839
Figure 3759: DNA325750, XM_012219,
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Figure 3760: PRO69473
Figure 3761: DNA325751, XM_012145,
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Figure 3762: PRO82224
Figure 3763: DNA274361, NM_000895,
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Figure 3764: PRO62273
Figure 3765: DNA325752, XM_006887,
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Figure 3766: DNA325753, XM_006589,
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Figure 3767: DNA325754, XM_090458,
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Figure 3768: PRO82227
Figure 3769: DNA325755, XM_052641,
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Figure 3770: PRO82228
Figure 3771A-B: DNA325756, XM_049211,
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Figure 3772: DNA325757, XM_049201,
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Figure 3773: DNA325758, XM_058556,
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Figure 3774: DNA325759, XM_083864,
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Figure 3775: DNA325760, XM_062437,
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Figure 3776: PRO82232
Figure 3777: DNA254777, NM_014325,
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Figure 3778: PRO49875
Figure 3779: DNA325761, XM_090413,
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Figure 3780: PRO82233
Figure 3781: DNA325762, NM_000970,
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Figure 3782: PRO82234
Figure 3783: DNA325763, XM_084800,
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Figure 3784: PRO82235
Figure 3785: DNA325764, NM_006817,
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Figure 3786: PRO70694
Figure 3787A-C: DNA325765, XM_083892,
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WO 2004/030615

PCT/US2003/028547

Figure 3788A-B: DNA325766, XM_084941,
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Figure 3791: PRO82238
Figure 3792A-B: DNA325768, NM_014776,
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Figure 3793: PRO82239
Figure 3794: DNA325769, NM_032904,
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Figure 3795: PRO82240
Figure 3796A-B: DNA325770, XM_007003,
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Figure 3797: DNA325771, XM_007002,
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Figure 3798: DNA325772, XM_056996,
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Figure 3799: PRO82243
Figure 3800: DNA325773, XM_084946,
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Figure 3801: PRO82244
Figure 3802: DNA325775, XM_027102,
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Figure 3803: PRO82245
Figure 3804: DNA325776, XM_084948,
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Figure 3805: DNA325777, NM_007062,
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Figure 3806: PRO82247
Figure 3807: DNA325778, NM_006825,
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Figure 3808: PRO82248
Figure 3809: DNA325779, XM_115197,
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Figure 3810: DNA325780, NM_017901,
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Figure 3812: DNA325781, NM_032814,
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Figure 3813: PRO82252
Figure 3814: DNA325782, XM_084889,
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Figure 3815: PRO82253
Figure 3816: DNA325783, NM_002567,
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Figure 3817: PRO59001
Figure 3818: DNA325784, XM_084808,
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Figure 3819: DNA325785, XM_096572,
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Figure 3820: PRO82255
Figure 3821: DNA325786, XM_045010,
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Figure 3822: PRO82256
Figure 3823: DNA270677, NM_014868,

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Figure 3824: PRO59042
Figure 3825: DNA325787, XM_052893,
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Figure 3826A-B: DNA325788, XM_045802,
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Figure 3827: DNA302016, NM_001002,
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Figure 3828: PRO70989
Figure 3829: DNA325789, NM_053275,
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Figure 3830: PRO70989
Figure 3831: DNA325790, NM_006253,
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Figure 3832: PRO82259
Figure 3833: DNA325791, XM_045187,
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Figure 3834: DNA325792, XM_045963,
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Figure 3835: DNA325793, XM_006595,
gen.XM_006595
Figure 3836: DNA325794, XM_012124,
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Figure 3837: DNA325795, NM_002813,
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Figure 3838: PRO82263
Figure 3839: DNA325796, NM_019887,
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Figure 3840: PRO69471
Figure 3841A-B: DNA325797, XM_038791,
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Figure 3842: PRO82264
Figure 3843: DNA325798, NM_016638,
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Figure 3844: PRO82265
Figure 3845: DNA325799, XM_116913,
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Figure 3846: PRO82266
Figure 3847: DNA325800, NM_006815,
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Figure 3848: PRO4793
Figure 3849: DNA325801, XM_006566,
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Figure 3850: PRO82267
Figure 3851: DNA325802, NM_032656,
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Figure 3852: PRO82268
Figure 3853: DNA325803, XM_055013,
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Figure 3854: PRO82269
Figure 3855: DNA325804, XM_113737,
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Figure 3856A-C: DNA325805, XM_045602,
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Figure 3857: DNA325806, XM_087955,
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WO 2004/030615

PCT/US2003/028547

Figure 3858: PRO82272
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Figure 3860: PRO82273
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Figure 3862: DNA325809, XM_113702,
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Figure 3863: PRO82275
Figure 3864A-B: DNA270015, NM_003453,
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Figure 3865: PRO58410
Figure 3866: DNA226853, NM_004004,
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Figure 3867: PRO37316
Figure 3868: DNA325810, XM_167911,
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Figure 3869: DNA325811, XM_167918,
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Figure 3870: DNA325812, XM_084982,
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Figure 3871: PRO82278
Figure 3872: DNA325813, NM_024026,
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Figure 3873: PRO82279
Figure 3874: DNA325814, XM_012638,
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Figure 3875: PRO82280
Figure 3876: DNA325815, XM_167439,
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Figure 3877: DNA325816, XM_167906,
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Figure 3878A-B: DNA325817, NM_014778,
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Figure 3879: PRO82283
Figure 3880: DNA325818, XM_169414,
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Figure 3881A-B: DNA325819, NM_006646,
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Figure 3882: PRO82285
Figure 3883: DNA325820, XM_167892,
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Figure 3884: DNA325821, NM_015932,
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Figure 3885: PRO82287
Figure 3886: DNA325822, XM_166273,
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Figure 3887: DNA304669, NM_002128,
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Figure 3888: PRO71096
Figure 3889: DNA325823, NM_014887,
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Figure 3890: PRO82289
Figure 3891: DNA325824, NM_002915,
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Figure 3892: PRO82290

Figure 3893: DNA325825, XM_085017,
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Figure 3894: PRO82291
Figure 3895: DNA325826, XM_017432,
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Figure 3896A-B: DNA270254, NM_002015,
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Figure 3897: PRO58642
Figure 3898: DNA325827, NM_005830,
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Figure 3899: PRO58092
Figure 3900: DNA281436, NM_003295,
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Figure 3901: PRO66275
Figure 3902: DNA325828, XM_038371,
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Figure 3903A-B: DNA325829, XM_165636,
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Figure 3904: DNA325830, XM_166266,
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Figure 3905: PRO82295
Figure 3906: DNA325831, NM_014166,
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Figure 3907: PRO82296
Figure 3908: DNA325832, NM_021999,
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Figure 3909: PRO1869
Figure 3910: DNA325833, NM_030925,
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Figure 3911: PRO82297
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Figure 3913: PRO61999
Figure 3914: DNA325834, NM_032565,
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Figure 3915: PRO11982
Figure 3916: DNA325835, XM_085044,
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Figure 3917: DNA325836, XM_165639,
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Figure 3918: DNA325837, XM_018399,
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Figure 3919: PRO82300
Figure 3920: DNA325838, XM_058977,
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Figure 3921: DNA325839, XM_015840,
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Figure 3922: PRO82302
Figure 3923: DNA325840, XM_007199,
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Figure 3924: DNA325841, XM_016351,
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Figure 3925: DNA325842, XM_041209,
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Figure 3926: DNA325843, XM_058611,
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WO 2004/030615

PCT/US2003/028547

Figure 3927: PRO82305
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Figure 3929: PRO82306
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Figure 3932: DNA325848, XM_015842,
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Figure 3933: DNA325849, XM_084997,
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Figure 3934: PRO82311
Figure 3935: DNA325850, NM_024089,
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Figure 3936: PRO82312
Figure 3937A-B: DNA325851, XM_049904,
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Figure 3939: PRO82314
Figure 3940: DNA325853, NM_023011,
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Figure 3941: PRO82315
Figure 3942: DNA325854, NM_080687,
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Figure 3943: PRO82316
Figure 3944: DNA325855, XM_041484,
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Figure 3945: PRO82317
Figure 3946A-B: DNA325856, XM_113752,
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Figure 3947: PRO82318
Figure 3948: DNA325857, XM_115215,
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Figure 3952: PRO10404
Figure 3953: DNA325861, XM_017914,
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Figure 3954: PRO82321
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Figure 3956: PRO82322
Figure 3957: DNA325863, XM_007316,
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Figure 3958: DNA325864, XM_007315,
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Figure 3965: PRO82326
Figure 3966: DNA325868, XM_096772,
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Figure 3967: DNA325869, XM_007293,
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Figure 3968: DNA325870, XM_007288,
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Figure 3971: DNA325872, NM_017815,
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Figure 3972: PRO82330
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Figure 3974: PRO82331
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Figure 3984: DNA227321, NM_001344,
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Figure 3993: PRO36568
Figure 3994: DNA325884, XM_033595,
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WO 2004/030615

PCT/US2003/028547

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Figure 4002: PRO82344
Figure 4003: DNA325889, NM_017807,
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Figure 4004: PRO82345
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Figure 4008: DNA325892, XM_041235,
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Figure 4009: PRO82348
Figure 4010: DNA325893, NM_002028,
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Figure 4011: PRO82349
Figure 4012: DNA325894, NM_002083,
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Figure 4013: PRO82350
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Figure 4015: PRO82351
Figure 4016A-B: DNA325896, NM_001530,
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Figure 4017: PRO82352
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Figure 4023: PRO82356
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Figure 4027: DNA325903, XM_007324,
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Figure 4028: PRO82358
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Figure 4030: PRO82359

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Figure 4038: PRO82365
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Figure 4047: PRO82369
Figure 4048: DNA325916, NM_006432,
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Figure 4049: PRO2066
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Figure 4051: PRO82370
Figure 4052: DNA325918, NM_002632,
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Figure 4053: PRO82371
Figure 4054: DNA325919, XM_085162,
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Figure 4055: DNA325920, NM_012111,
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Figure 4057: DNA325921, NM_024824,
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Figure 4058: PRO82374
Figure 4059: DNA269498, NM_002802,
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Figure 4060: PRO57917
Figure 4061: DNA325922, XM_058677,
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Figure 4062: PRO82375
Figure 4063: DNA325923, NM_006888,
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Figure 4064: PRO4904
Figure 4065: DNA325924, NM_001275,

WO 2004/030615

PCT/US2003/028547

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Figure 4073: DNA325930, XM.028358,
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Figure 4074: DNA325931, XM.028347,
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Figure 4075: DNA325932, XM.028322,
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Figure 4076: PRO82381
Figure 4077: DNA325933, XM.056317,
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Figure 4078: PRO82382
Figure 4079: DNA151893, NM.021966,
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Figure 4080: PRO12916
Figure 4081: DNA325934, XM.007272,
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Figure 4082: DNA325935, XM.090914,
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Figure 4083: PRO82383
Figure 4084: DNA325936, NM.022747,
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Figure 4085: PRO82384
Figure 4086: DNA325937, XM.041014,
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Figure 4087: PRO60575
Figure 4088: DNA325938, NM.003836,
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Figure 4089: PRO82385
Figure 4090A-B: DNA325939, XM.040952,
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Figure 4091: DNA325940, XM.058618,
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Figure 4092: DNA325941, NM.005348,
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Figure 4093: PRO82388
Figure 4094: DNA325942, XM.040942,
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Figure 4095: DNA226324, NM.014226,
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Figure 4096: PRO36787
Figure 4097A-B: DNA325943, XM.007254,
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Figure 4098A-B: DNA325944, NM.001969,
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Figure 4101: DNA325946, NM.005432,
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Figure 4102: PRO60070
Figure 4103A-B: DNA325947, XM.050278,
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Figure 4104: PRO82393
Figure 4105: DNA325948, XM.113759,
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Figure 4106: DNA325949, NM.006427,
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Figure 4107: PRO82395
Figure 4108: DNA325950, NM.021709,
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Figure 4109: PRO82396
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Figure 4111: PRO4836
Figure 4112: DNA325951, NM.017955,
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Figure 4113: PRO82397
Figure 4114: DNA325952, XM.088588,
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Figure 4115: DNA325953, XM.060012,
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Figure 4116: DNA325954, XM.034953,
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Figure 4117: PRO82400
Figure 4118: DNA325955, XM.058636,
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Figure 4119: DNA325956, XM.035014,
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Figure 4121: DNA325958, XM.088589,
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Figure 4122: DNA325959, XM.071801,
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Figure 4123: DNA325960, XM.018054,
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Figure 4124: DNA325961, XM.091108,
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Figure 4125A-B: DNA325962, XM.039225,
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Figure 4126: PRO82408
Figure 4127: DNA325963, XM.165921,
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Figure 4128: PRO82409
Figure 4129: DNA325964, XM.007751,
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Figure 4130: DNA325965, XM.085203,
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Figure 4131: PRO82411
Figure 4132: DNA325966, XM.085204,

WO 2004/030615

PCT/US2003/028547

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Figure 4136: DNA325970, NM_020149,
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Figure 4137: PRO82415
Figure 4138A-B: DNA325971, XM_031617,
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Figure 4139A-B: DNA325972, NM_001211,
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Figure 4140: PRO82417
Figure 4141A-B: DNA151831, NM_004573,
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Figure 4142: PRO12198
Figure 4143: DNA325973, NM_130468,
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Figure 4144: PRO82418
Figure 4145: DNA325974, XM_031554,
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Figure 4146: PRO82419
Figure 4147: DNA325975, XM_031515,
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Figure 4148: DNA325976, NM_024111,
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Figure 4149: PRO82421
Figure 4150: DNA325977, NM_032196,
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Figure 4151: PRO82422
Figure 4152: DNA325978, NM_016359,
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Figure 4153: PRO82423
Figure 4154: DNA325979, NM_018454,
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Figure 4155: PRO82424
Figure 4156A-B: DNA325980, XM_007545,
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Figure 4157: DNA325981, XM_091159,
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Figure 4158: PRO82425
Figure 4159: DNA325982, XM_031718,
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Figure 4160: DNA325983, XM_085307,
gen.XM_085307
Figure 4161: DNA227559, NM_000070,
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Figure 4162: PRO38022
Figure 4163A-B: DNA325984, XM_113823,
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Figure 4164: PRO82428
Figure 4165: DNA325985, XM_016713,
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Figure 4166: PRO82429

Figure 4167A-B: DNA325986, XM_007531,
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Figure 4168: DNA325987, NM_014444,
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Figure 4169: PRO82431
Figure 4170A-B: DNA227206, NM_005657,
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Figure 4171: PRO37669
Figure 4172: DNA325988, NM_020990,
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Figure 4173: PRO82432
Figure 4174: DNA325989, NM_005313,
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Figure 4175: PRO2732
Figure 4176: DNA325990, NM_005770,
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Figure 4177: PRO82433
Figure 4178: DNA325991, NM_004048,
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Figure 4179: PRO4379
Figure 4180: DNA325992, XM_032403,
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Figure 4181: PRO82434
Figure 4182: DNA219233, NM_014335,
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Figure 4183: PRO34557
Figure 4184A-C: DNA325993, XM_034890,
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Figure 4186: DNA325994, XM_058684,
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Figure 4187: DNA325995, NM_003104,
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Figure 4188: PRO82437
Figure 4189: DNA325996, XM_007651,
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Figure 4190: PRO82438
Figure 4191: DNA325997, XM_090991,
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Figure 4192: PRO82439
Figure 4193: DNA325998, NM_016304,
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Figure 4194: PRO82440
Figure 4195: DNA325999, NM_017610,
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Figure 4196: PRO82441
Figure 4197: DNA326000, NM_004701,
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Figure 4198: PRO82442
Figure 4199A-B: DNA326001, XM_012418,
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Figure 4200: DNA326002, XM_039702,
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Figure 4201: PRO82444
Figure 4202: DNA326003, XM_113266,
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WO 2004/030615

PCT/US2003/028547

Figure 4203: DNA326004, NM_001218,
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Figure 4205: DNA326005, NM_015920,
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Figure 4206: PRO82446
Figure 4207: DNA326006, XM_113268,
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Figure 4208: DNA255340, NM_017684,
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Figure 4209: PRO50409
Figure 4210: DNA326007, NM_002537,
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Figure 4211: DNA326008, XM_085283,
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Figure 4212: PRO82448
Figure 4213: DNA326009, XM_016985,
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Figure 4214: DNA234442, NM_014736,
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Figure 4215: PRO38852
Figure 4216: DNA326010, NM_022048,
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Figure 4217: PRO82450
Figure 4218: DNA326011, NM_000942,
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Figure 4219: PRO2720
Figure 4220: DNA326012, XM_050964,
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Figure 4221: DNA326013, XM_007623,
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Figure 4222A-B: DNA326014, NM_133375,
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Figure 4223: PRO82453
Figure 4224: DNA226646, NM_017882,
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Figure 4225: PRO37109
Figure 4226: DNA326015, NM_015322,
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Figure 4227: PRO82454
Figure 4228: DNA326016, NM_001003,
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Figure 4229: PRO82455
Figure 4230A-B: DNA326017, XM_051463,
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Figure 4231: PRO82456
Figure 4232: DNA326018, NM_018357,
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Figure 4233: PRO82457
Figure 4234: DNA326019, XM_063639,
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Figure 4235: PRO82458
Figure 4236: DNA326020, XM_085249,
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Figure 4237: DNA326021, XM_016076,
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Figure 4239: DNA326022, XM_015366,
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Figure 4240: PRO82461
Figure 4241: DNA326023, XM_096060,
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Figure 4243: PRO69595
Figure 4244: DNA326024, XM_037778,
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Figure 4245: DNA326025, XM_096842,
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Figure 4246: DNA326026, NM_022369,
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Figure 4247: PRO82465
Figure 4248: DNA326027, NM_032907,
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Figure 4249: PRO82466
Figure 4250: DNA326028, XM_058699,
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Figure 4251: DNA326029, XM_118637,
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Figure 4252: DNA326030, XM_053585,
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Figure 4253: PRO82469
Figure 4254: DNA326031, XM_085239,
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Figure 4255: PRO82470
Figure 4256: DNA326032, XM_034897,
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Figure 4257A-B: DNA326033, XM_057020,
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Figure 4258: PRO82472
Figure 4259: DNA326034, NM_000743,
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Figure 4260: PRO61219
Figure 4261: DNA326035, NM_002789,
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Figure 4262: PRO60499
Figure 4263: DNA326036, XM_091100,
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Figure 4264: PRO82473
Figure 4265: DNA255370, NM_012170,
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Figure 4266: PRO50438
Figure 4267: DNA273014, NM_000126,
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Figure 4268: PRO61085
Figure 4269: DNA326037, XM_044565,
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Figure 4270: DNA326038, NM_025234,
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Figure 4271: PRO82475
Figure 4272: DNA326039, XM_044569,
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WO 2004/030615

PCT/US2003/028547

Figure 4273: DNA326040, NM_005724,
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Figure 4276: PRO82477
Figure 4277: DNA326042, NM_007364,
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Figure 4279: DNA326044, NM_006791,
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Figure 4280: PRO82479
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Figure 4283: DNA326047, NM_001021,
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Figure 4284: PRO82482
Figure 4285: DNA326048, XM_031404,
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Figure 4288: PRO82485
Figure 4289: DNA326051, XM_085280,
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Figure 4291: PRO82487
Figure 4292: DNA326053, XM_031354,
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Figure 4293: DNA326054, NM_002168,
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Figure 4294: PRO82489
Figure 4295: DNA326055, XM_031292,
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Figure 4296: DNA326056, NM_022566,
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Figure 4297: PRO82491
Figure 4298A-B: DNA326057, XM_051860,
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Figure 4299: PRO82492
Figure 4300: DNA275144, NM_000137,
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Figure 4301: PRO62852
Figure 4302: DNA326058, NM_016645,
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Figure 4303: PRO82493
Figure 4304: DNA326059, XM_044523,
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Figure 4305: DNA150485, NM_006384,
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Figure 4306: PRO12774

Figure 4307A-B: DNA326060, XM_044533,
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Figure 4308: PRO82495
Figure 4309A-C: DNA326061, XM_054900,
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Figure 4310: DNA326062, NM_032162,
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Figure 4311A-B: DNA326063, XM_015835,
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Figure 4312: DNA326064, NM_018668,
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Figure 4313: PRO82499
Figure 4314: DNA326065, XM_085262,
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Figure 4315: DNA326066, NM_033544,
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Figure 4316: PRO82501
Figure 4317: DNA326067, XM_049372,
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Figure 4318: PRO82502
Figure 4319: DNA326068, XM_017971,
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Figure 4320: DNA275181, NM_003090,
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Figure 4321: PRO62882
Figure 4322: DNA326069, XM_012462,
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Figure 4323A-B: DNA326070, XM_085525,
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Figure 4324: PRO82505
Figure 4325: DNA326071, XM_165923,
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Figure 4326: DNA326072, XM_113836,
gen.XM_113836
Figure 4327: DNA326073, NM_017668,
gen.NM_017668
Figure 4328: PRO82508
Figure 4329: DNA326074, XM_027309,
gen.XM_027309
Figure 4330: PRO82509
Figure 4331: DNA326075, XM_018432,
gen.XM_018432
Figure 4332: PRO82510
Figure 4333: DNA326076, XM_115352,
gen.XM_115352
Figure 4334: DNA326077, XM_027365,
gen.XM_027365
Figure 4335: DNA326078, NM_016641,
gen.NM_016641
Figure 4336: PRO38464
Figure 4337: DNA326079, XM_058796,
gen.XM_058796
Figure 4338: DNA326080, XM_017984,
gen.XM_017984
Figure 4339: PRO82513
Figure 4340: DNA326081, NM_020677,

WO 2004/030615

PCT/US2003/028547

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Figure 4341: PRO82514
Figure 4342: DNA326082, XM_036680,
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Figure 4343: PRO37961
Figure 4344A-B: DNA326083, XM_048119,
gen.XM_048119
Figure 4345: PRO82515
Figure 4346: DNA326084, NM_024589,
gen.NM_024589
Figure 4347: PRO82516
Figure 4348: DNA326085, XM_050534,
gen.XM_050534
Figure 4349: PRO82517
Figure 4350: DNA326086, NM_024571,
gen.NM_024571
Figure 4351: PRO82518
Figure 4352: DNA326087, XM_027558,
gen.XM_027558
Figure 4353: DNA326088, XM_008126,
gen.XM_008126
Figure 4354: DNA326089, NM_000517,
gen.NM_000517
Figure 4355: PRO3629
Figure 4356: DNA326090, NM_000558,
gen.NM_000558
Figure 4357: PRO3629
Figure 4358: DNA326091, NM_018032,
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Figure 4359: PRO38311
Figure 4360: DNA273839, NM_006428,
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Figure 4361: PRO61799
Figure 4362A-B: DNA256844, NM_005632,
gen.NM_005632
Figure 4363: PRO51775
Figure 4364: DNA326092, XM_083939,
gen.XM_083939
Figure 4365: PRO82521
Figure 4366: DNA326093, NM_058192,
gen.NM_058192
Figure 4367: PRO82522
Figure 4368: DNA326094, XM_027412,
gen.XM_027412
Figure 4369: PRO82523
Figure 4370: DNA256886, NM_014587,
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Figure 4371: PRO51815
Figure 4372A-B: DNA326095, NM_001287,
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Figure 4373: PRO38480
Figure 4374: DNA254781, NM_016111,
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Figure 4375: PRO49879
Figure 4376: DNA326096, XM_034586,
gen.XM_034586

Figure 4377: PRO82524
Figure 4378: DNA326097, NM_023936,
gen.NM_023936
Figure 4379: PRO82525
Figure 4380: DNA326098, XM_034590,
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Figure 4381: PRO82526
Figure 4382: DNA326099, NM_002952,
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Figure 4383: PRO82527
Figure 4384: DNA326100, NM_006453,
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Figure 4385: PRO82528
Figure 4386: DNA326101, NM_014353,
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Figure 4387: PRO82529
Figure 4388: DNA326102, NM_032271,
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Figure 4389: PRO82530
Figure 4390: DNA326103, XM_028848,
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Figure 4391: PRO82531
Figure 4392: DNA326104, NM_006711,
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Figure 4393: PRO82532
Figure 4394: DNA326105, NM_080594,
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Figure 4395: PRO82533
Figure 4396: DNA326106, NM_024339,
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Figure 4397: PRO82534
Figure 4398: DNA326107, NM_016639,
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Figure 4399: PRO12683
Figure 4400: DNA326108, NM_021195,
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Figure 4401: PRO82535
Figure 4402: DNA326109, NM_004203,
gen.NM_004203
Figure 4403: PRO82536
Figure 4404: DNA326110, XM_058784,
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Figure 4405: PRO82537
Figure 4406: DNA326111, NM_024507,
gen.NM_024507
Figure 4407: PRO82538
Figure 4408: DNA326112, NM_006799,
gen.NM_006799
Figure 4409: PRO303
Figure 4410A-C: DNA326113, XM_036528,
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Figure 4411: DNA326114, NM_025108,
gen.NM_025108
Figure 4412: PRO82540
Figure 4413A-C: DNA326115, XM_165411,
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WO 2004/030615

PCT/US2003/028547

Figure 4414: DNA326116, NM_016292,
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Figure 4416: DNA326117, NM_002484,
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Figure 4417: PRO82543
Figure 4418: DNA326118, XM_113845,
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Figure 4419: PRO82544
Figure 4420: DNA326119, XM_113843,
gen.XM_113843
Figure 4421: DNA97293, NM_003366,
gen.NM_003366
Figure 4422: PRO3640
Figure 4423: DNA326120, NM_006110,
gen.NM_006110
Figure 4424: PRO82546
Figure 4425: DNA326121, XM_085445,
gen.XM_085445
Figure 4426: DNA326122, XM_113876,
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Figure 4427A-B: DNA326123, XM_055195,
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Figure 4428: PRO82548
Figure 4429: DNA326124, XM_113291,
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Figure 4430A-B: DNA326125, XM_007988,
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Figure 4431: DNA326126, XM_113874,
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Figure 4432: DNA326127, XM_102377,
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Figure 4433: PRO82551
Figure 4434: DNA326128, XM_086278,
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Figure 4435: DNA326129, XM_085452,
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Figure 4436: DNA326130, NM_018054,
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Figure 4437: PRO82554
Figure 4438A-B: DNA326131, XM_056260,
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Figure 4439: PRO82555
Figure 4440: DNA326132, NM_032626,
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Figure 4441: PRO82556
Figure 4442: DNA326133, NM_005030,
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Figure 4443: PRO82557
Figure 4444: DNA326134, NM_032486,
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Figure 4445: PRO82558
Figure 4446: DNA289522, NM_005003,
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Figure 4447: PRO70276
Figure 4448: DNA326135, XM_085340,

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Figure 4449: DNA326136, NM_003752,
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Figure 4450: PRO60325
Figure 4451: DNA326137, NM_012248,
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Figure 4452: PRO82560
Figure 4453A-B: DNA326138, XM_046035,
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Figure 4454: DNA326139, NM_024671,
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Figure 4455: PRO82562
Figure 4456: DNA326140, NM_033410,
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Figure 4457: PRO82563
Figure 4458: DNA326141, NM_024031,
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Figure 4459: PRO82564
Figure 4460A-B: DNA326142, XM_034375,
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Figure 4461: DNA326143, XM_012569,
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Figure 4462: DNA326144, XM_050194,
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Figure 4463: DNA326145, XM_008106,
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Figure 4464: PRO82567
Figure 4465: DNA326146, NM_004960,
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Figure 4466: PRO82568
Figure 4467: DNA326147, XM_113293,
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Figure 4468: DNA326148, NM_022744,
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Figure 4469: PRO82570
Figure 4470: DNA326149, NM_024048,
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Figure 4471: PRO82571
Figure 4472: DNA326150, XM_018088,
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Figure 4473: PRO82572
Figure 4474: DNA326151, XM_007963,
gen.XM_007963
Figure 4475: PRO82573
Figure 4476: DNA274002, NM_014321,
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Figure 4477: PRO61948
Figure 4478: DNA326152, XM_015700,
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Figure 4479: DNA326153, XM_051219,
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Figure 4480: DNA326154, XM_085393,
gen.XM_085393
Figure 4481: PRO82576
Figure 4482: DNA326155, XM_085395,
gen.XM_085395

WO 2004/030615

PCT/US2003/028547

Figure 4483: DNA326156, XM_091270, gen.XM_091270
Figure 4484: DNA326157, XM_165656, gen.XM_165656
Figure 4485: DNA326158, NM_032330, gen.NM_032330
Figure 4486: PRO82579
Figure 4487: DNA254532, NM_001043, gen.NM_001043
Figure 4488: PRO49639
Figure 4489: DNA326159, XM_165658, gen.XM_165658
Figure 4490: DNA326160, XM_166285, gen.XM_166285
Figure 4491: DNA326161, XM_166282, gen.XM_166282
Figure 4492: PRO82582
Figure 4493: DNA326162, XM_165657, gen.XM_165657
Figure 4494: PRO82583
Figure 4495: DNA326163, NM_032038, gen.NM_032038
Figure 4496: PRO82584
Figure 4497: DNA326164, XM_008065, gen.XM_008065
Figure 4498: DNA326165, NM_017458, gen.NM_017458
Figure 4499: PRO82585
Figure 4500: DNA326166, NM_005115, gen.NM_005115
Figure 4501: PRO82586
Figure 4502: DNA326167, NM_024516, gen.NM_024516
Figure 4503: PRO82587
Figure 4504: DNA326168, XM_113299, gen.XM_113299
Figure 4505: DNA326169, XM_055771, gen.XM_055771
Figure 4506: PRO82589
Figure 4507: DNA271171, NM_007317, gen.NM_007317
Figure 4508: PRO59491
Figure 4509: DNA326170, XM_008064, gen.XM_008064
Figure 4510: PRO82590
Figure 4511: DNA326171, NM_003123, gen.NM_003123
Figure 4512: PRO2355
Figure 4513: DNA326172, XM_085442, gen.XM_085442
Figure 4514: DNA326173, XM_055132, gen.XM_055132
Figure 4515: PRO82592
Figure 4516: DNA274180, NM_007074, gen.NM_007074
Figure 4517: PRO62110

Figure 4518: DNA326174, NM_002720, gen.NM_002720
Figure 4519: PRO42208
Figure 4520: DNA287355, NM_000034, gen.NM_000034
Figure 4521: PRO69617
Figure 4522: DNA326175, NM_031478, gen.NM_031478
Figure 4523: PRO82593
Figure 4524: DNA326176, XM_085434, gen.XM_085434
Figure 4525: PRO82594
Figure 4526: DNA326177, XM_058116, gen.XM_058116
Figure 4527: DNA326178, XM_165649, gen.XM_165649
Figure 4528: DNA326179, XM_165647, gen.XM_165647
Figure 4529: PRO82597
Figure 4530: DNA194805, NM_014685, gen.NM_014685
Figure 4531: PRO24075
Figure 4532: DNA326180, XM_166277, gen.XM_166277
Figure 4533: PRO82598
Figure 4534: DNA326181, XM_165645, gen.XM_165645
Figure 4535: DNA326182, NM_018110, gen.NM_018110
Figure 4536: PRO82599
Figure 4537: DNA326183, XM_165648, gen.XM_165648
Figure 4538: DNA326184, XM_167453, gen.XM_167453
Figure 4539: DNA326185, NM_022770, gen.NM_022770
Figure 4540: PRO82602
Figure 4541: DNA326186, XM_167456, gen.XM_167456
Figure 4542: PRO82603
Figure 4543: DNA326187, XM_058745, gen.XM_058745
Figure 4544: DNA326188, XM_091420, gen.XM_091420
Figure 4545: DNA326189, NM_004691, gen.NM_004691
Figure 4546: PRO82606
Figure 4547: DNA326190, NM_000196, gen.NM_000196
Figure 4548: PRO82607
Figure 4549A-B: DNA326191, NM_004360, gen.NM_004360
Figure 4550: PRO2672
Figure 4551: DNA326192, XM_039306, gen.XM_039306
Figure 4552: PRO82608

WO 2004/030615

PCT/US2003/028547

Figure 4553: DNA326193, NM_030579,
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Figure 4555: DNA326194, XM_012487,
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Figure 4557: PRO82611
Figure 4558: DNA326196, XM_085471,
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Figure 4559: PRO82612
Figure 4560: DNA326197, XM_113855,
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Figure 4561: DNA326198, XM_085475,
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Figure 4562: DNA326199, XM_028151,
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Figure 4563: PRO82615
Figure 4564: DNA275408, NM_001605,
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Figure 4565: PRO63068
Figure 4566: DNA326200, NM_007242,
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Figure 4567: PRO82616
Figure 4568: DNA189703, NM_005548,
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Figure 4569: PRO22637
Figure 4570: DNA326201, XM_113853,
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Figure 4571: DNA326202, NM_032140,
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Figure 4572: PRO82618
Figure 4573: DNA326203, NM_030819,
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Figure 4574: PRO82619
Figure 4575: DNA304704, NM_005796,
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Figure 4576: PRO71130
Figure 4577: DNA326204, XM_043047,
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Figure 4578: PRO49967
Figure 4579: DNA88261, NM_001907,
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Figure 4580: PRO2719
Figure 4581A-B: DNA326205, NM_005072,
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Figure 4582: PRO4814
Figure 4583: DNA326206, XM_165410,
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Figure 4584: DNA326207, NM_017803,
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Figure 4585: PRO82621
Figure 4586A-B: DNA326208, NM_004555,
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Figure 4587: PRO82622
Figure 4588A-B: DNA326209, NM_018124,

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Figure 4589: PRO82623
Figure 4590: DNA326210, XM_091399,
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Figure 4591: PRO82624
Figure 4592A-B: DNA326211, NM_014003,
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Figure 4593: PRO82625
Figure 4594: DNA326212, NM_017853,
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Figure 4595: PRO82626
Figure 4596: DNA326213, XM_042621,
gen.XM_042621
Figure 4597: DNA326214, XM_064091,
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Figure 4598: PRO82627
Figure 4599: DNA326215, XM_085981,
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Figure 4600A-B: DNA326216, XM_051778,
gen.XM_051778
Figure 4601: PRO82629
Figure 4602: DNA326217, NM_004483,
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Figure 4603: PRO82630
Figure 4604: DNA326218, NM_020188,
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Figure 4605: PRO82631
Figure 4606: DNA326219, XM_033922,
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Figure 4607: PRO82632
Figure 4608: DNA326220, XM_113840,
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Figure 4609: PRO82633
Figure 4610: DNA326221, NM_016095,
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Figure 4611: PRO82634
Figure 4612: DNA326222, NM_006067,
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Figure 4613: PRO50658
Figure 4614: DNA326223, NM_001861,
gen.NM_001861
Figure 4615: PRO82635
Figure 4616A-B: DNA326224, XM_085483,
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Figure 4617: DNA326225, NM_017566,
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Figure 4618: PRO82637
Figure 4619: DNA326226, XM_057150,
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Figure 4620: PRO82638
Figure 4621: DNA326227, XM_058739,
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Figure 4622: DNA326228, XM_085327,
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Figure 4623: PRO82640
Figure 4624: DNA326229, XM_047436,

WO 2004/030615

PCT/US2003/028547

gen.XM_047436
Figure 4625: PRO82641
Figure 4626: DNA227234, NM_002386,
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Figure 4627: PRO37697
Figure 4628: DNA326230, NM_014972,
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Figure 4629: PRO82642
Figure 4630: DNA326231, XM_071873,
gen.XM_071873
Figure 4631: PRO82643
Figure 4632: DNA326232, XM_047525,
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Figure 4633: DNA326233, NM_000977,
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Figure 4634: PRO82645
Figure 4635: DNA326234, NM_033251,
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Figure 4636: PRO82646
Figure 4637: DNA326235, XM_085408,
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Figure 4638: DNA326236, NM_004933,
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Figure 4639: PRO2198
Figure 4640: DNA326237, XM_113882,
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Figure 4641: DNA326238, XM_010938,
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Figure 4642: DNA326239, NM_006761,
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Figure 4643: PRO39530
Figure 4644A-B: DNA326240, XM_017096,
gen.XM_017096
Figure 4645: DNA326241, XM_033714,
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Figure 4646A-B: DNA326242, XM_033689,
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Figure 4647: DNA326243, NM_002615,
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Figure 4648: DNA326244, XM_056082,
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Figure 4649: PRO82654
Figure 4650: DNA326245, XM_008557,
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Figure 4651: DNA326246, XM_045183,
gen.XM_045183
Figure 4652: PRO82656
Figure 4653: DNA326247, XM_113901,
gen.XM_113901
Figure 4654: DNA326248, NM_080822,
gen.NM_080822
Figure 4655: PRO82658
Figure 4656A-B: DNA326249, XM_029438,
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Figure 4657: PRO82659
Figure 4658: DNA326250, XM_008509,

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Figure 4659: DNA326251, XM_085687,
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Figure 4660: PRO82661
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Figure 4662: PRO82662
Figure 4663: DNA326253, XM_053717,
gen.XM_053717
Figure 4664: PRO82663
Figure 4665: DNA326254, NM_005022,
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Figure 4666: PRO62780
Figure 4667A-B: DNA326255, XM_028398,
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Figure 4668: PRO82664
Figure 4669: DNA326256, NM_000018,
gen.NM_000018
Figure 4670: PRO66265
Figure 4671: DNA326257, XM_008334,
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Figure 4672: DNA326258, NM_024297,
gen.NM_024297
Figure 4673: PRO82665
Figure 4674: DNA326259, XM_113324,
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Figure 4675: DNA326260, XM_012676,
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Figure 4676: PRO82667
Figure 4677: DNA326261, XM_085691,
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Figure 4678: DNA326262, XM_028417,
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Figure 4679: PRO82669
Figure 4680A-B: DNA326263, XM_041964,
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Figure 4681: PRO82670
Figure 4682: DNA326264, NM_019013,
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Figure 4683: PRO82671
Figure 4684: DNA326265, XM_008538,
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Figure 4685: PRO82672
Figure 4686: DNA326266, XM_008441,
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Figure 4687: DNA97300, NM_001416,
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Figure 4688: PRO3647
Figure 4689: DNA326267, NM_004870,
gen.NM_004870
Figure 4690: PRO82674
Figure 4691: DNA326268, NM_006942,
gen.NM_006942
Figure 4692: PRO82675
Figure 4693: DNA326269, XM_008679,
gen.XM_008679

WO 2004/030615

PCT/US2003/028547

Figure 4694: DNA326270, XM_008231,
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Figure 4697: DNA326273, NM_001970,
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Figure 4698: PRO82678
Figure 4699: DNA297388, NM_004217,
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Figure 4700: PRO70812
Figure 4701: DNA326274, XM_165421,
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Figure 4702: PRO82679
Figure 4703: DNA326275, XM_113325,
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Figure 4704: DNA326276, XM_165422,
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Figure 4705: PRO49182
Figure 4706: DNA326277, XM_113931,
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Figure 4707: DNA326278, XM_036659,
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Figure 4708: DNA103401, NM_003876,
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Figure 4709: PRO4729
Figure 4710A-B: DNA326279, XM_042698,
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Figure 4711: PRO82683
Figure 4712A-B: DNA326280, XM_017234,
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Figure 4713: DNA326281, XM_165418,
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Figure 4714: DNA304715, NM_000987,
gen.NM_000987
Figure 4715: PRO71141
Figure 4716A-B: DNA326282, NM_004618,
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Figure 4717: PRO62981
Figure 4718: DNA326283, XM_085743,
gen.XM_085743
Figure 4719A-B: DNA254198, NM_002018,
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Figure 4720: PRO49310
Figure 4721A-B: DNA326284, XM_039910,
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Figure 4722: PRO82687
Figure 4723A-C: DNA326285, XM_113310,
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Figure 4724: DNA326286, XM_085613,
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Figure 4725: DNA326287, NM_006470,
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Figure 4726: PRO82689
Figure 4727: DNA326288, XM_051763,

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Figure 4728: DNA290292, NM_018955,
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Figure 4729: PRO70449
Figure 4730: DNA326289, XM_058900,
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Figure 4731: PRO82691
Figure 4732: DNA326290, XM_039921,
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Figure 4733: PRO82692
Figure 4734: DNA326291, XM_012549,
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Figure 4735: DNA326292, XM_085548,
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Figure 4736: PRO82694
Figure 4737: DNA326293, NM_018019,
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Figure 4738: PRO82695
Figure 4739: DNA326294, NM_138427,
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Figure 4740: PRO82696
Figure 4741: DNA326295, XM_085545,
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Figure 4742A-B: DNA227084, NM_004176,
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Figure 4743: PRO37547
Figure 4744: DNA326296, XM_012615,
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Figure 4745: DNA326297, XM_085722,
gen.XM_085722
Figure 4746: PRO82699
Figure 4747: DNA255414, NM_018242,
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Figure 4748: PRO50481
Figure 4749: DNA326298, XM_045044,
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Figure 4750: DNA326299, XM_008323,
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Figure 4751: DNA326300, XM_045535,
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Figure 4752A-B: DNA326301, XM_045551,
gen.XM_045551
Figure 4753: PRO82702
Figure 4754: DNA326302, XM_097204,
gen.XM_097204
Figure 4755: DNA326303, XM_058867,
gen.XM_058867
Figure 4756: PRO82704
Figure 4757: DNA326304, XM_085672,
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Figure 4760: DNA326306, XM_008486,
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Figure 4761: DNA326307, NM_015584,

WO 2004/030615

PCT/US2003/028547

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Figure 4764: PRO82708
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Figure 4766: PRO82709
Figure 4767: DNA326310, XM_031415,
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Figure 4768: DNA326311, XM_117066,
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Figure 4769: DNA326312, XM_031427,
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Figure 4772: PRO82713
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Figure 4774: PRO82714
Figure 4775: DNA326315, XM_056730,
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Figure 4776: PRO82715
Figure 4777: DNA326316, XM_008462,
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Figure 4779: PRO69684
Figure 4780: DNA326317, NM_015544,
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Figure 4783: PRO21887
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Figure 4787: PRO82719
Figure 4788: DNA326320, NM_133630,
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Figure 4789: PRO82720
Figure 4790: DNA326321, NM_133629,
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Figure 4792: DNA326322, NM_018096,
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Figure 4793: PRO37791
Figure 4794A-B: DNA326323, XM_039474,
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Figure 4795: PRO82722
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Figure 4797: PRO1204

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Figure 4804: PRO82725
Figure 4805: DNA270979, NM_002809,
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Figure 4806: PRO59309
Figure 4807: DNA326328, NM_000422,
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Figure 4808: PRO82726
Figure 4809: DNA326329, XM_008579,
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Figure 4812: DNA272889, NM_002275,
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Figure 4813: PRO60979
Figure 4814: DNA326331, NM_002274,
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Figure 4817: PRO82730
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Figure 4825: DNA326337, XM_036465,
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WO 2004/030615

PCT/US2003/028547

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Figure 4843: DNA270975, NM_000386,
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Figure 4846: PRO2769
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Figure 4853: PRO82746
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Figure 4855: PRO52010
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Figure 4858: PRO82748
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Figure 4863: DNA326355, XM_032813,
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Figure 4874: PRO82757
Figure 4875: DNA326362, NM_006373,
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Figure 4876: PRO82758
Figure 4877: DNA196642, NM_005440,
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Figure 4878: PRO25115
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Figure 4892: PRO38227
Figure 4893A-B: DNA326367, NM_020038,
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Figure 4895A-B: DNA326368, NM_020037,
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Figure 4896: PRO82764
Figure 4897: DNA326369, XM_037971,
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Figure 4901: PRO69682
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WO 2004/030615

PCT/US2003/028547

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Figure 4914: PRO82771
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Figure 4916A-B: DNA326378, XM_012651,
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Figure 4919: DNA287291, NM_021213,
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Figure 4954: PRO12806
Figure 4955: DNA326399, NM_024844,
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WO 2004/030615

PCT/US2003/028547

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Figure 4986: PRO7143
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Figure 4989: DNA326416, XM_045104,
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Figure 4993: PRO82805
Figure 4994A-B: DNA326419, XM_049934,
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Figure 4995: DNA326420, XM_049931,
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Figure 4996A-B: DNA326421, XM_045581,
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Figure 4997: PRO82807
Figure 4998: DNA326422, XM_113945,
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Figure 4999: DNA326423, XM_046481,
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Figure 5001: DNA326425, XM_097193,
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Figure 5002: DNA326426, NM_004309,
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Figure 5003: PRO61246
Figure 5004: DNA326427, XM_046472,
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Figure 5005: PRO82812
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Figure 5009: PRO82814
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Figure 5013: DNA326432, XM_113303,
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Figure 5015: PRO69513
Figure 5016: DNA326433, NM_022158,
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Figure 5017: PRO82818
Figure 5018: DNA326434, XM_038424,
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Figure 5019: DNA326435, XM_085735,
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Figure 5024: PRO61661
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Figure 5028: DNA326442, XM_113343,
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Figure 5030: DNA326443, XM_067325,
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Figure 5031: DNA326444, XM_012741,
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Figure 5032: DNA326445, NM_014214,
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Figure 5034A-B: DNA326446, XM_035640,
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Figure 5035: PRO82829
Figure 5036: DNA326447, XM_016382,
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WO 2004/030615

PCT/US2003/028547

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Figure 5046: DNA326452, XM_015755,
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Figure 5047: PRO82835
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Figure 5053: PRO60121
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Figure 5059: PRO82840
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Figure 5061: PRO82841
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Figure 5063: PRO82842
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Figure 5065: DNA326461, XM_167363,
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Figure 5066: DNA326462, XM_031944,
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Figure 5070: PRO61113
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Figure 5073: PRO60800

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Figure 5076: DNA326469, XM_011089,
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Figure 5078: DNA326470, XM_169540,
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Figure 5079: PRO82851
Figure 5080: DNA326471, XM_167008,
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Figure 5081: PRO82852
Figure 5082: DNA326472, XM_048471,
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Figure 5083A-B: DNA326473, XM_008812,
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Figure 5084A-B: DNA326474, XM_117096,
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Figure 5087: PRO82856
Figure 5088: DNA326476, XM_015241,
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Figure 5091: PRO82859
Figure 5092: DNA326479, XM_051586,
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Figure 5094: PRO1077
Figure 5095: DNA326481, XM_042018,
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Figure 5096: PRO2560
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Figure 5099: PRO82861
Figure 5100: DNA326484, NM_031990,
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Figure 5101: PRO82862
Figure 5102: DNA326485, NM_002819,
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Figure 5103: PRO62899
Figure 5104: DNA326486, NM_005224,
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WO 2004/030615

PCT/US2003/028547

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Figure 5116: PRO62039
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Figure 5118: PRO82871
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Figure 5121: PRO82872
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Figure 5123: PRO58046
Figure 5124: DNA326498, NM_138924,
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Figure 5125: PRO82873
Figure 5126: DNA326499, NM_001018,
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Figure 5127: PRO10485
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Figure 5129: PRO82874
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Figure 5131: DNA326502, XM_047584,
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Figure 5136: PRO82877
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Figure 5147: PRO51586
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Figure 5149: PRO82884
Figure 5150A-B: DNA326513, XM_046822,
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Figure 5152: DNA326514, NM_007165,
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Figure 5153: PRO82886
Figure 5154: DNA287636, NM_004152,
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Figure 5155: DNA326515, NM_012458,
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Figure 5156: PRO82887
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Figure 5158: PRO82888
Figure 5159: DNA326517, XM_030485,
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Figure 5160: DNA326518, XM_046934,
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Figure 5162: PRO62302
Figure 5163: DNA326520, XM_055686,
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Figure 5164: PRO37951
Figure 5165: DNA326521, XM_009222,
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Figure 5166: DNA326522, XM_052635,
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Figure 5167: PRO82892
Figure 5168: DNA326523, XM_052661,
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Figure 5169: DNA326524, NM_016263,
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Figure 5170: PRO82893
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Figure 5174: PRO82895
Figure 5175: DNA326527, XM_056421,
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Figure 5176A-B: DNA326528, XM_031917,
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WO 2004/030615

PCT/US2003/028547

Figure 5177: PRO82897
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Figure 5180: DNA326530, XM_016871,
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Figure 5181: DNA326531, NM_016539,
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Figure 5182: PRO82899
Figure 5183: DNA326532, XM_117122,
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Figure 5184: DNA326533, XM_031857,
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Figure 5185: PRO82901
Figure 5186: DNA326534, NM_024333,
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Figure 5187: PRO82902
Figure 5188: DNA326535, NM_003025,
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Figure 5189: PRO82903
Figure 5190: DNA326536, NM_025241,
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Figure 5191: PRO82904
Figure 5192: DNA326537, XM_035638,
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Figure 5193: PRO82905
Figure 5194A-B: DNA326538, XM_035636,
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Figure 5195: DNA326539, XM_012862,
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Figure 5196A-B: DNA326540, XM_035627,
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Figure 5197A-B: DNA326541, XM_035625,
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Figure 5199: DNA274761, NM_014649,
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Figure 5200: PRO62531
Figure 5201: DNA272421, NM_006012,
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Figure 5202: PRO60674
Figure 5203: DNA326542, NM_003685,
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Figure 5204: PRO82910
Figure 5205A-B: DNA326543, XM_009010,
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Figure 5206: DNA270315, NM_004240,
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Figure 5207: PRO58702
Figure 5208: DNA326544, NM_005490,
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Figure 5209: PRO201
Figure 5210: DNA326546, XM_044619,
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Figure 5211: PRO82912
Figure 5212: DNA326547, XM_012798,

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Figure 5213: DNA326548, XM_044608,
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Figure 5214: DNA326549, NM_003624,
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Figure 5215: PRO82915
Figure 5216: DNA326550, NM_016579,
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Figure 5217: PRO224
Figure 5218A-B: DNA326551, XM_048351,
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Figure 5219: DNA326552, XM_048364,
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Figure 5220: PRO82917
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Figure 5222: DNA326554, XM_097300,
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Figure 5223: DNA326555, XM_049282,
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Figure 5226: DNA326557, XM_045151,
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Figure 5227A-B: DNA326558, XM_050435,
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Figure 5228: PRO82923
Figure 5229: DNA326559, XM_113988,
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Figure 5235: PRO58991
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Figure 5245: PRO82930

WO 2004/030615

PCT/US2003/028547

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Figure 5251: PRO23794
Figure 5252: DNA326572, XM_032724,
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Figure 5253: PRO82934
Figure 5254A-B: DNA326573, NM_003072,
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Figure 5255: PRO82935
Figure 5256A-B: DNA326574, XM_009082,
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Figure 5257: DNA326575, XM_032774,
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Figure 5258: DNA218271, NM_000121,
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Figure 5259: PRO34323
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Figure 5292: DNA326592, XM_031345,
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WO 2004/030615

PCT/US2003/028547

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Figure 5338A-B: DNA326618, XM_009293,
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Figure 5348: PRO82979
Figure 5349: DNA326624, XM_114004,
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Figure 5353: PRO37712
Figure 5354: DNA326626, XM_018515,
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Figure 5355: DNA326627, NM_033415,
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Figure 5377: PRO4756
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WO 2004/030615

PCT/US2003/028547

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Figure 5389: DNA326648, NM_024321,
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Figure 5390: PRO82999
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Figure 5393: DNA326650, NM_032635,
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Figure 5394: PRO23845
Figure 5395: DNA326651, XM_115615,
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Figure 5398: DNA326653, XM_085986,
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Figure 5400: PRO83004
Figure 5401: DNA326655, NM_002812,
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Figure 5402: PRO83005
Figure 5403A-E: DNA326656, XM_029455,
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Figure 5404: DNA326657, XM_029450,
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Figure 5405: PRO83007
Figure 5406: DNA326658, XM_009149,
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Figure 5413: DNA326662, NM_017827,
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Figure 5414: PRO83010
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Figure 5417: DNA326664, NM_033363,
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Figure 5418: PRO83012
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Figure 5424: PRO83014
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Figure 5426: DNA272347, NM_001020,
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Figure 5427: PRO60603
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Figure 5431: PRO83016
Figure 5432: DNA326670, NM_016941,
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Figure 5433: PRO83017
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Figure 5436: DNA326671, NM_001436,
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Figure 5437: PRO83018
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Figure 5445: DNA326677, XM_047376,
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Figure 5446A-B: DNA326678, XM_047374,
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Figure 5447: DNA326679, XM_059052,
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Figure 5448: DNA273600, NM_004596,
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Figure 5449: PRO61575
Figure 5450: DNA326680, XM_030914,
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Figure 5451: DNA326681, NM_052848,
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Figure 5453: DNA326682, XM_008912,

WO 2004/030615

PCT/US2003/028547

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Figure 5458: DNA326685, NM_018035,
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Figure 5461: DNA326687, XM_085875,
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Figure 5462: DNA326688, XM_085876,
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Figure 5463: DNA326689, XM_058949,
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Figure 5464: PRO83035
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Figure 5469: PRO83038
Figure 5470: DNA326693, NM_004706,
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Figure 5473: PRO83040
Figure 5474: DNA326695, NM_022752,
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Figure 5475: PRO83041
Figure 5476: DNA151808, NM_006494,
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Figure 5477: PRO12892
Figure 5478: DNA326696, NM_001816,
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Figure 5479: PRO34151
Figure 5480: DNA326697, NM_000554,
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Figure 5485: DNA326701, XM_008860,
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Figure 5487: DNA326703, XM_085950,

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Figure 5490: PRO36963
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Figure 5493: PRO83050
Figure 5494: DNA103580, NM_001743,
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Figure 5495: PRO4904
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Figure 5498: PRO25881
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Figure 5503: PRO12800
Figure 5504: DNA270931, NM_012099,
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Figure 5505: PRO59264
Figure 5506A-B: DNA257531, NM_031417,
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Figure 5508: DNA326712, NM_001294,
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Figure 5510: DNA326713, XM_097274,
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Figure 5512: PRO2644
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Figure 5514: PRO51565
Figure 5515: DNA251057, NM_002856,
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Figure 5516: PRO47354
Figure 5517: DNA226011, NM_005581,
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Figure 5518: PRO36474
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WO 2004/030615

PCT/US2003/028547

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Figure 5530: DNA326721, XM_114025,
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Figure 5534: DNA326724, NM_025129,
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Figure 5537: DNA326726, XM_085934,
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Figure 5538: PRO83068
Figure 5539: DNA326727, NM_001536,
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Figure 5540: PRO83069
Figure 5541: DNA326728, XM_165432,
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Figure 5542: DNA274823, NM_001571,
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Figure 5543: PRO62582
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Figure 5545: PRO83071
Figure 5546: DNA326730, NM_015953,
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Figure 5547: PRO83072
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Figure 5549: DNA326732, XM_084026,
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Figure 5553: PRO83073
Figure 5554: DNA326734, NM_017916,
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Figure 5555: PRO83074
Figure 5556: DNA326735, NM_003598,

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Figure 5557: PRO83075
Figure 5558: DNA326736, NM_006666,
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Figure 5563: PRO71085
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Figure 5565: PRO38101
Figure 5566: DNA326739, NM_006184,
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Figure 5567: PRO83078
Figure 5568: DNA273066, NM_001190,
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Figure 5569: PRO61129
Figure 5570: DNA326740, XM_058987,
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Figure 5571: DNA326741, NM_000979,
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Figure 5572: PRO83080
Figure 5573: DNA326742, XM_085935,
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Figure 5576: DNA103239, NM_006801,
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Figure 5578: DNA326744, XM_046419,
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Figure 5581: PRO83083
Figure 5582: DNA326746, XM_056286,
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Figure 5583: PRO83084
Figure 5584: DNA326747, XM_058990,
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Figure 5585: PRO83085
Figure 5586: DNA326748, XM_091981,
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Figure 5587: PRO83086
Figure 5588: DNA326749, NM_032712,
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Figure 5589: PRO23238
Figure 5590: DNA83154, NM_001648,
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Figure 5591: PRO2109
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WO 2004/030615

PCT/US2003/028547

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Figure 5601: PRO83090
Figure 5602: DNA326755, XM_050236,
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Figure 5603: DNA326756, XM_050589,
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Figure 5604: PRO83092
Figure 5605: DNA326757, XM_117128,
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Figure 5606: PRO83093
Figure 5607: DNA326758, XM_059321,
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Figure 5616: PRO61349
Figure 5617: DNA326763, NM_013333,
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Figure 5619: DNA326764, NM_007279,
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Figure 5626: PRO60333
Figure 5627: DNA254548, NM_005762,
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Figure 5628: PRO49653

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Figure 5664: PRO83117

WO 2004/030615

PCT/US2003/028547

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Figure 5674: DNA326789, XM_045460,
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Figure 5711: PRO83139
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Figure 5726: PRO83146
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WO 2004/030615

PCT/US2003/028547

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Figure 5762: DNA326830, XM_009686,
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Figure 5763: DNA326831, NM_030877,
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Figure 5765: DNA326832, XM_028806,
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Figure 5777: PRO83167
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Figure 5780: PRO2065
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Figure 5782: PRO1720
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Figure 5803: PRO83177
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WO 2004/030615

PCT/US2003/028547

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Figure 5815: PRO57942
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Figure 5828: DNA326863, NM_080425,
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Figure 5830: DNA304670, NM_000516,
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Figure 5831: PRO71097
Figure 5832: DNA326864, NM_080426,
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Figure 5833: PRO83187
Figure 5834: DNA326865, XM_030699,
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Figure 5835: PRO83188
Figure 5836: DNA188229, NM_000114,
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Figure 5837: PRO21728
Figure 5838: DNA326866, NM_002792,
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Figure 5839: PRO83189
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Figure 5843: PRO83191
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Figure 5845: PRO4813
Figure 5846A-D: DNA326869, XM_037217,
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Figure 5848: PRO83193
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Figure 5856: PRO83197
Figure 5857: DNA326875, NM_022105,
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Figure 5858: PRO83198
Figure 5859: DNA326876, NM_080797,
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Figure 5860: PRO83199
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Figure 5870: PRO83204
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Figure 5872: PRO83205
Figure 5873: DNA269746, NM_012469,
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Figure 5874: PRO58155
Figure 5875: DNA326883, XM_114154,
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Figure 5877: DNA326885, XM_086759,

WO 2004/030615

PCT/US2003/028547

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Figure 5887: DNA326889, NM_005806,
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Figure 5894: DNA326891, NM_001757,
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Figure 5912: PRO83219

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Figure 5918: PRO83223
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Figure 5925: DNA326908, XM_097817,
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Figure 5937: DNA326916, NM_033070,
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Figure 5938: PRO83235
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Figure 5940: PRO50134
Figure 5941: DNA326917, NM_001696,
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Figure 5942: PRO83236
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Figure 5944: PRO83237
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Figure 5946: DNA326920, XM_033090,

WO 2004/030615

PCT/US2003/028547

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Figure 5953: DNA326924, XM_086809,
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Figure 5954: DNA326925, NM_006440,
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Figure 5955: PRO83244
Figure 5956: DNA226561, NM_000754,
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Figure 5957: PRO37024
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Figure 5968: DNA326932, XM_096156,
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Figure 5969A-B: DNA326933, XM_036937,
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Figure 5980: PRO83255

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Figure 5994: DNA103462, NM_000268,
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Figure 5997: PRO83263
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Figure 5999: DNA326947, NM_005877,
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Figure 6002: PRO83265
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Figure 6004: PRO49256
Figure 6005A-B: DNA151882, NM_014941,
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Figure 6006: PRO12134
Figure 6007: DNA326949, NM_006932,
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Figure 6010: PRO83267
Figure 6011: DNA270697, NM_004147,
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Figure 6012: PRO59061
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Figure 6014: DNA326952, XM_018539,
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Figure 6015: DNA326953, NM_014306,
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WO 2004/030615

PCT/US2003/028547

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Figure 6021: PRO12886
Figure 6022: DNA326956, XM_009947,
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Figure 6023: PRO12845
Figure 6024: DNA326957, XM_114209,
gen.XM_114209
Figure 6025A-B: DNA326958, NM_002473,
gen.NM_002473
Figure 6026: PRO83273
Figure 6027: DNA188740, NM_003753,
gen.NM_003753
Figure 6028: PRO22481
Figure 6029: DNA326959, NM_021126,
gen.NM_021126
Figure 6030: PRO70331
Figure 6031: DNA326960, XM_009967,
gen.XM_009967
Figure 6032: DNA326961, NM_013365,
gen.NM_013365
Figure 6033: PRO83274
Figure 6034: DNA290259, NM_018957,
gen.NM_018957
Figure 6035: PRO70383
Figure 6036: DNA326962, NM_020315,
gen.NM_020315
Figure 6037: PRO83275
Figure 6038: DNA304719, NM_002305,
gen.NM_002305
Figure 6039: PRO71145
Figure 6040: DNA326963, NM_007032,
gen.NM_007032
Figure 6041: PRO83276
Figure 6042: DNA326964, XM_009973,
gen.XM_009973
Figure 6043: DNA326965, XM_086830,
gen.XM_086830
Figure 6044: PRO83278
Figure 6045: DNA254240, NM_016091,
gen.NM_016091
Figure 6046: PRO49352
Figure 6047A-B: DNA326966, XM_039236,
gen.XM_039236
Figure 6048: PRO83279
Figure 6049: DNA326967, NM_006941,
gen.NM_006941
Figure 6050: PRO83280
Figure 6051: DNA326968, XM_039248,
gen.XM_039248

Figure 6052: DNA326969, NM_012323,
gen.NM_012323
Figure 6053: PRO83282
Figure 6054: DNA326970, NM_012264,
gen.NM_012264
Figure 6055: PRO12490
Figure 6056: DNA326971, NM_015373,
gen.NM_015373
Figure 6057: PRO83283
Figure 6058: DNA326972, NM_020243,
gen.NM_020243
Figure 6059: PRO23231
Figure 6060: DNA326973, XM_039339,
gen.XM_039339
Figure 6061: DNA326974, NM_000967,
gen.NM_000967
Figure 6062: PRO83285
Figure 6063: DNA326975, XM_010000,
gen.XM_010000
Figure 6064: DNA326976, XM_010002,
gen.XM_010002
Figure 6065: DNA326977, XM_039372,
gen.XM_039372
Figure 6066: DNA326978, XM_013010,
gen.XM_013010
Figure 6067: PRO83288
Figure 6068: DNA254165, NM_000026,
gen.NM_000026
Figure 6069: PRO49278
Figure 6070: DNA326979, NM_003932,
gen.NM_003932
Figure 6071: PRO4586
Figure 6072: DNA326980, NM_014248,
gen.NM_014248
Figure 6073: PRO83289
Figure 6074: DNA326981, XM_086844,
gen.XM_086844
Figure 6075: DNA219225, NM_002883,
gen.NM_002883
Figure 6076: PRO34531
Figure 6077: DNA326982, NM_003216,
gen.NM_003216
Figure 6078: PRO83291
Figure 6079: DNA270954, NM_001098,
gen.NM_001098
Figure 6080: PRO59285
Figure 6081: DNA326983, NM_001469,
gen.NM_001469
Figure 6082: PRO4872
Figure 6083: DNA326984, NM_005008,
gen.NM_005008
Figure 6084: PRO83292
Figure 6085A-B: DNA326985, NM_004599,
gen.NM_004599
Figure 6086: PRO83293
Figure 6087A-B: DNA326986, XM_010024,

WO 2004/030615

PCT/US2003/028547

gen.XM_010024
Figure 6088: DNA326987, XM_040066,
gen.XM_040066
Figure 6089: DNA326988, XM_013015,
gen.XM_013015
Figure 6090A-B: DNA326989, XM_084084,
gen.XM_084084
Figure 6091: DNA326990, XM_040095,
gen.XM_040095
Figure 6092: PRO83297
Figure 6093: DNA326991, XM_086875,
gen.XM_086875
Figure 6094: DNA326992, XM_010029,
gen.XM_010029
Figure 6095: DNA326993, NM_007311,
gen.NM_007311
Figure 6096: PRO83300
Figure 6097: DNA326994, NM_015140,
gen.NM_015140
Figure 6098: PRO83301
Figure 6099: DNA326995, XM_043614,
gen.XM_043614
Figure 6100: PRO83302
Figure 6101: DNA256070, NM_022141,
gen.NM_022141
Figure 6102: PRO51119
Figure 6103: DNA326996, XM_010040,
gen.XM_010040
Figure 6104: DNA237931, NM_005036,
gen.NM_005036
Figure 6105: PRO39030
Figure 6106A-B: DNA326997, XM_027143,
gen.XM_027143
Figure 6107: PRO83304
Figure 6108A-B: DNA326998, XM_010055,
gen.XM_010055
Figure 6109: DNA326999, NM_025204,
gen.NM_025204
Figure 6110: PRO83306
Figure 6111: DNA327000, XM_041248,
gen.XM_041248
Figure 6112: PRO83307
Figure 6113: DNA327001, XM_092966,
gen.XM_092966
Figure 6114: DNA327002, XM_037468,
gen.XM_037468
Figure 6115: PRO83309
Figure 6116: DNA327003, XM_037474,
gen.XM_037474
Figure 6117: PRO83310
Figure 6118: DNA327004, XM_013029,
gen.XM_013029
Figure 6119: DNA327005, XM_114724,
gen.XM_114724
Figure 6120: PRO83312
Figure 6121: DNA327006, XM_115924,

gen.XM_115924
Figure 6122: DNA327007, XM_113585,
gen.XM_113585
Figure 6123A-C: DNA327008, XM_035465,
gen.XM_035465
Figure 6124: DNA327009, NM_002414,
gen.NM_002414
Figure 6125: PRO2373
Figure 6126: DNA269793, NM_005333,
gen.NM_005333
Figure 6127: PRO58198
Figure 6128: DNA327010, XM_088747,
gen.XM_088747
Figure 6129: PRO83316
Figure 6130: DNA327011, XM_114720,
gen.XM_114720
Figure 6131: DNA327012, XM_115886,
gen.XM_115886
Figure 6132: DNA327013, XM_010272,
gen.XM_010272
Figure 6133: PRO83319
Figure 6134: DNA327014, NM_006746,
gen.NM_006746
Figure 6135: PRO83320
Figure 6136: DNA327015, XM_115890,
gen.XM_115890
Figure 6137: PRO83321
Figure 6138: DNA327016, NM_000284,
gen.NM_000284
Figure 6139: PRO59441
Figure 6140: DNA327017, NM_004595,
gen.NM_004595
Figure 6141: PRO61744
Figure 6142: DNA327018, XM_166078,
gen.XM_166078
Figure 6143: DNA327019, NM_001415,
gen.NM_001415
Figure 6144: PRO83323
Figure 6145: DNA327020, XM_013086,
gen.XM_013086
Figure 6146: DNA327021, XM_060030,
gen.XM_060030
Figure 6147: DNA227689, NM_002364,
gen.NM_002364
Figure 6148: PRO38152
Figure 6149: DNA274829, NM_003662,
gen.NM_003662
Figure 6150: PRO62588
Figure 6151: DNA327022, XM_088619,
gen.XM_088619
Figure 6152: DNA327023, XM_088622,
gen.XM_088622
Figure 6153A-B: DNA327024, XM_084288,
gen.XM_084288
Figure 6154: PRO59168
Figure 6155: DNA327025, XM_054221,

WO 2004/030615

PCT/US2003/028547

gen.XM_054221
Figure 6156: PRO83328
Figure 6157: DNA327026, XM_018019,
gen.XM_018019
Figure 6158: DNA327027, XM_088665,
gen.XM_088665
Figure 6159: DNA327028, NM_005300,
gen.NM_005300
Figure 6160: PRO37083
Figure 6161: DNA327029, XM_018241,
gen.XM_018241
Figure 6162: PRO83331
Figure 6163: DNA327030, NM_014138,
gen.NM_014138
Figure 6164: PRO83332
Figure 6165: DNA327031, NM_005676,
gen.NM_005676
Figure 6166: PRO83333
Figure 6167: DNA327032, NM_003334,
gen.NM_003334
Figure 6168: PRO83334
Figure 6169: DNA327033, XM_010378,
gen.XM_010378
Figure 6170: DNA327034, XM_033884,
gen.XM_033884
Figure 6171: PRO83335
Figure 6172: DNA327035, XM_033878,
gen.XM_033878
Figure 6173: DNA327036, XM_033862,
gen.XM_033862
Figure 6174: DNA327037, NM_004182,
gen.NM_004182
Figure 6175: PRO83337
Figure 6176: DNA327038, XM_047032,
gen.XM_047032
Figure 6177: DNA327039, XM_047024,
gen.XM_047024
Figure 6178: PRO83339
Figure 6179: DNA327040, NM_017883,
gen.NM_017883
Figure 6180: PRO83340
Figure 6181: DNA238039, NM_005710,
gen.NM_005710
Figure 6182: PRO39127
Figure 6183: DNA327041, XM_054098,
gen.XM_054098
Figure 6184: PRO83341
Figure 6185: DNA327042, NM_002668,
gen.NM_002668
Figure 6186: PRO34584
Figure 6187: DNA271580, NM_014008,
gen.NM_014008
Figure 6188: PRO59868
Figure 6189A-B: DNA327043, XM_032930,
gen.XM_032930
Figure 6190: DNA273992, NM_004493,

gen.NM_004493
Figure 6191: PRO61938
Figure 6192A-B: DNA327044, XM_050403,
gen.XM_050403
Figure 6193: PRO83343
Figure 6194: DNA327045, XM_029187,
gen.XM_029187
Figure 6195: PRO83344
Figure 6196: DNA327046, XM_013060,
gen.XM_013060
Figure 6197: DNA227943, NM_006787,
gen.NM_006787
Figure 6198: PRO38406
Figure 6199: DNA327047, NM_014481,
gen.NM_014481
Figure 6200: PRO83345
Figure 6201: DNA327048, XM_034935,
gen.XM_034935
Figure 6202: PRO83346
Figure 6203: DNA327049, XM_084287,
gen.XM_084287
Figure 6204: DNA327050, NM_007268,
gen.NM_007268
Figure 6205: PRO34043
Figure 6206: DNA327051, XM_015516,
gen.XM_015516
Figure 6207A-B: DNA327052, XM_013042,
gen.XM_013042
Figure 6208: PRO83349
Figure 6209: DNA327053, XM_088630,
gen.XM_088630
Figure 6210: DNA327054, NM_031206,
gen.NM_031206
Figure 6211: PRO83351
Figure 6212: DNA327055, XM_093050,
gen.XM_093050
Figure 6213: PRO83352
Figure 6214A-B: DNA225721, NM_018977,
gen.NM_018977
Figure 6215: PRO36184
Figure 6216: DNA327056, XM_010141,
gen.XM_010141
Figure 6217: PRO38021
Figure 6218: DNA327057, XM_088689,
gen.XM_088689
Figure 6219: PRO83353
Figure 6220: DNA327058, XM_088688,
gen.XM_088688
Figure 6221: PRO83354
Figure 6222: DNA327059, NM_018486,
gen.NM_018486
Figure 6223: PRO83355
Figure 6224: DNA327060, NM_001007,
gen.NM_001007
Figure 6225: PRO42022
Figure 6226: DNA327061, XM_093130,

WO 2004/030615

PCT/US2003/028547

gen.XM_093130
Figure 6227: DNA327062, XM_084296,
gen.XM_084296
Figure 6228: DNA327063, XM_093241,
gen.XM_093241
Figure 6229: DNA327064, XM_084283,
gen.XM_084283
Figure 6230: DNA273254, NM_000291,
gen.NM_000291
Figure 6231: PRO61271
Figure 6232: DNA327065, XM_018142,
gen.XM_018142
Figure 6233: DNA327066, XM_030373,
gen.XM_030373
Figure 6234: PRO83360
Figure 6235: DNA327067, XM_165533,
gen.XM_165533
Figure 6236: PRO83361
Figure 6237: DNA327068, XM_051476,
gen.XM_051476
Figure 6238: DNA327069, XM_051471,
gen.XM_051471
Figure 6239: DNA270496, NM_001325,
gen.NM_001325
Figure 6240: PRO58875
Figure 6241: DNA327070, XM_033147,
gen.XM_033147
Figure 6242: DNA327071, NM_004085,
gen.NM_004085
Figure 6243: PRO59022
Figure 6244: DNA327072, NM_021029,
gen.NM_021029
Figure 6245: PRO10723
Figure 6246: DNA327073, NM_012286,
gen.NM_012286
Figure 6247: PRO83365
Figure 6248: DNA327074, NM_024863,
gen.NM_024863
Figure 6249: PRO83366
Figure 6250: DNA327075, XM_043643,
gen.XM_043643
Figure 6251: DNA327076, NM_052936,
gen.NM_052936
Figure 6252: PRO83368
Figure 6253: DNA327077, XM_088710,
gen.XM_088710
Figure 6254: PRO83369
Figure 6255: DNA327078, XM_166081,
gen.XM_166081
Figure 6256: DNA327079, XM_096303,
gen.XM_096303
Figure 6257: DNA254785, NM_032227,
gen.NM_032227
Figure 6258: PRO49883
Figure 6259: DNA327080, XM_115923,
gen.XM_115923

Figure 6260: PRO83372
Figure 6261: DNA327081, XM_066900,
gen.XM_066900
Figure 6262: PRO83373
Figure 6263: DNA327082, XM_104983,
gen.XM_104983
Figure 6264: PRO83374
Figure 6265: DNA327083, XM_088736,
gen.XM_088736
Figure 6266: PRO83375
Figure 6267: DNA327084, XM_088738,
gen.XM_088738
Figure 6268: DNA327085, XM_088739,
gen.XM_088739
Figure 6269: DNA327086, XM_010117,
gen.XM_010117
Figure 6270A-B: DNA76504, NM_001560,
gen.NM_001560
Figure 6271: PRO2537
Figure 6272: DNA227181, NM_006667,
gen.NM_006667
Figure 6273: PRO37644
Figure 6274: DNA327087, XM_010362,
gen.XM_010362
Figure 6275: DNA327088, XM_016125,
gen.XM_016125
Figure 6276: DNA327089, NM_015129,
gen.NM_015129
Figure 6277: PRO83381
Figure 6278: DNA327090, NM_001000,
gen.NM_001000
Figure 6279: PRO10935
Figure 6280: DNA327091, XM_010436,
gen.XM_010436
Figure 6281: DNA327092, XM_115874,
gen.XM_115874
Figure 6282: DNA327093, XM_029461,
gen.XM_029461
Figure 6283: PRO83383
Figure 6284: DNA327094, XM_017930,
gen.XM_017930
Figure 6285: DNA227656, NM_004208,
gen.NM_004208
Figure 6286: PRO38119
Figure 6287: DNA273487, NM_004794,
gen.NM_004794
Figure 6288: PRO61470
Figure 6289: DNA327095, XM_088745,
gen.XM_088745
Figure 6290: PRO83385
Figure 6291: DNA327096, XM_114708,
gen.XM_114708
Figure 6292: PRO83386
Figure 6293: DNA327097, NM_016267,
gen.NM_016267
Figure 6294: PRO83387

WO 2004/030615

PCT/US2003/028547

Figure 6295A-B: DNA327098, XM_042963,
gen.XM_042963
Figure 6296: PRO83388
Figure 6297: DNA327099, XM_042968,
gen.XM_042968
Figure 6298: PRO83389
Figure 6299: DNA327100, XM_093219,
gen.XM_093219
Figure 6300: DNA327101, NM_016249,
gen.NM_016249
Figure 6301: PRO83391
Figure 6302: DNA327102, XM_098995,
gen.XM_098995
Figure 6303: PRO83392
Figure 6304: DNA327103, XM_041921,
gen.XM_041921
Figure 6305: PRO83393
Figure 6306: DNA327104, XM_048905,
gen.XM_048905
Figure 6307: PRO83394
Figure 6308: DNA327105, NM_005364,
gen.NM_005364
Figure 6309: PRO83395
Figure 6310: DNA327106, XM_010178,
gen.XM_010178
Figure 6311: DNA327107, XM_088592,
gen.XM_088592
Figure 6312: PRO25245
Figure 6313: DNA327108, XM_018108,
gen.XM_018108
Figure 6314: PRO83397
Figure 6315: DNA327109, XM_018109,
gen.XM_018109
Figure 6316: DNA327110, NM_005362,
gen.NM_005362
Figure 6317: PRO24021
Figure 6318: DNA254783, NM_001363,
gen.NM_001363
Figure 6319: PRO49881
Figure 6320: DNA327111, XM_049337,
gen.XM_049337
Figure 6321: DNA227917, NM_019848,
gen.NM_019848
Figure 6322: PRO38380
Figure 6323: DNA327112, NM_004699,
gen.NM_004699
Figure 6324: PRO83400
Figure 6325: DNA327113, XM_048420,
gen.XM_048420
Figure 6326: DNA327114, NM_006013,

gen.NM_006013
Figure 6327: PRO62466
Figure 6328: DNA327115, XM_048410,
gen.XM_048410
Figure 6329A-C: DNA327116, XM_048404,
gen.XM_048404
Figure 6330A-C: DNA327117, NM_004992,
gen.NM_004992
Figure 6331: PRO83403
Figure 6332: DNA227013, NM_001569,
gen.NM_001569
Figure 6333: PRO37476
Figure 6334A-B: DNA225800, NM_000425,
gen.NM_000425
Figure 6335: PRO36263
Figure 6336A-B: DNA327118, NM_024003,
gen.NM_024003
Figure 6337: PRO83404
Figure 6338: DNA225655, NM_006280,
gen.NM_006280
Figure 6339: PRO36118
Figure 6340: DNA276159, NM_004135,
gen.NM_004135
Figure 6341: PRO63299
Figure 6342A-B: DNA230792, NM_000033,
gen.NM_000033
Figure 6343: PRO38730
Figure 6344: DNA103558, NM_005745,
gen.NM_005745
Figure 6345: PRO4885
Figure 6346: DNA327119, XM_042155,
gen.XM_042155
Figure 6347: PRO83405
Figure 6348: DNA327120, XM_042153,
gen.XM_042153
Figure 6349: DNA327121, XM_117555,
gen.XM_117555
Figure 6350: DNA327122, XM_084311,
gen.XM_084311
Figure 6351: DNA327123, XM_033232,
gen.XM_033232
Figure 6352: DNA327124, XM_117539,
gen.XM_117539
Figure 6353: DNA327125, XM_027952,
gen.XM_027952
Figure 6354: DNA327126, XM_114692,
gen.XM_114692
Figure 6355A-B: DNA327127, XM_165530,
gen.XM_165530

WO 2004/030615

PCT/US2003/028547

DNA Index (to Figure number)

DNA0, 1188	DNA171408, 48
DNA103214, 218	DNA188229, 5836
DNA103217, 649	DNA188351, 4782
DNA103239, 5576	DNA188396, 3480
DNA103253, 188	DNA188732, 5882
DNA103320, 5272	DNA188740, 6027
DNA103380, 1677	DNA188748, 146
DNA103401, 4708	DNA189315, 167
DNA103421, 2982	DNA189687, 3297
DNA103436, 457	DNA189697, 998
DNA103462, 5994	DNA189703, 4568
DNA103471, 2070	DNA193882, 585
DNA103474, 3313	DNA193955, 2193
DNA103486, 5844	DNA193957, 2947
DNA103505, 1149	DNA194600, 428
DNA103506, 2990	DNA194701, 5747
DNA103509, 4110	DNA194740, 854
DNA103514, 3478	DNA194805, 4530
DNA103525, 5774	DNA194807, 5760
DNA103558, 6344	DNA194827, 977
DNA103580, 5494	DNA196344, 576
DNA103588, 2274	DNA196349, 124
DNA103593, 711	DNA196351, 3600
DNA129504, 4985	DNA196642, 4877
DNA131588, 2593	DNA210134, 367
DNA137231, 3667	DNA210180, 3962
DNA139747, 1368	DNA218271, 5258
DNA144601, 3051	DNA218841, 2782
DNA150457, 4936	DNA219225, 6075
DNA150485, 4305	DNA219233, 4182
DNA150548, 5703	DNA225584, 1489
DNA150562, 1153	DNA225592, 1330
DNA150679, 1732	DNA225630, 2767
DNA150725, 806	DNA225631, 2174
DNA150767, 5721	DNA225632, 3473
DNA150772, 2034	DNA225649, 4042
DNA150784, 5502	DNA225655, 6338
DNA150814, 4953	DNA225671, 2506
DNA150884, 1024	DNA225721, 6214
DNA150974, 3204	DNA225752, 3376
DNA150976, 1145	DNA225800, 6334
DNA150978, 3520	DNA225809, 356
DNA150997, 3526	DNA225865, 3976
DNA151010, 2546	DNA225909, 1828
DNA151017, 1066	DNA225910, 1128
DNA151148, 44	DNA225919, 1446
DNA151752, 6020	DNA225920, 1511
DNA151808, 5476	DNA225921, 1515
DNA151827, 3466	DNA225954, 5947
DNA151831, 4141	DNA226005, 553
DNA151882, 6005	DNA226011, 5517
DNA151893, 4079	DNA226014, 3729
DNA151898, 5896	DNA226028, 3489

WO 2004/030615

PCT/US2003/028547

DNA226080, 3206
DNA226105, 3992
DNA226125, 409
DNA226217, 3004
DNA226260, 271
DNA226262, 105
DNA226324, 4095
DNA226337, 2458
DNA226345, 2670
DNA226389, 4820
DNA226409, 5921
DNA226416, 2262
DNA226418, 1791
DNA226428, 741
DNA226496, 2565
DNA226547, 1108
DNA226560, 2393
DNA226561, 5956
DNA226617, 5935
DNA226619, 474
DNA226646, 4224
DNA226758, 5745
DNA226771, 3498
DNA226793, 436
DNA226853, 3866
DNA226872, 1689
DNA227013, 6332
DNA227055, 4939
DNA227071, 4889
DNA227084, 4742
DNA227088, 3220
DNA227092, 3593
DNA227094, 3628
DNA227165, 684
DNA227171, 3724
DNA227172, 2964
DNA227173, 1573
DNA227181, 6272
DNA227190, 814
DNA227191, 3588
DNA227204, 1886
DNA227206, 4170
DNA227213, 157
DNA227234, 4626
DNA227246, 550
DNA227249, 5352
DNA227267, 2512
DNA227268, 2242
DNA227280, 5232
DNA227307, 1165
DNA227320, 1812
DNA227321, 3984
DNA227348, 5681
DNA227442, 1942
DNA227472, 5771
DNA227474, 3720

DNA227491, 2691
DNA227504, 594
DNA227509, 3076
DNA227528, 803
DNA227529, 346
DNA227545, 698
DNA227559, 4161
DNA227575, 1508
DNA227577, 374
DNA227607, 1961
DNA227656, 6285
DNA227689, 6147
DNA227764, 4891
DNA227795, 792
DNA227821, 36
DNA227873, 4841
DNA227917, 6321
DNA227924, 2099
DNA227929, 2206
DNA227943, 6197
DNA230792, 6342
DNA234442, 4214
DNA237931, 6104
DNA238039, 6181
DNA247474, 578
DNA247595, 2182
DNA251057, 5515
DNA252367, 1081
DNA253804, 1370
DNA254141, 6003
DNA254147, 1627
DNA254165, 6068
DNA254186, 3329
DNA254198, 4719
DNA254204, 994
DNA254240, 6045
DNA254298, 499
DNA254346, 603
DNA254532, 4487
DNA254543, 2740
DNA254548, 5627
DNA254572, 5885
DNA254582, 1155
DNA254620, 1316
DNA254624, 3468
DNA254771, 2693
DNA254777, 3777
DNA254781, 4374
DNA254783, 6318
DNA254785, 6257
DNA254791, 4898
DNA254994, 5890
DNA255046, 5939
DNA255078, 3113
DNA255340, 4208
DNA255370, 4265

WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

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WO 2004/030615

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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DNA326377, 4915
DNA326378, 4916
DNA326379, 4917
DNA326380, 4921
DNA326381, 4923
DNA326382, 4924
DNA326383, 4926
DNA326384, 4927
DNA326385, 4929
DNA326386, 4931
DNA326387, 4933
DNA326388, 4935
DNA326389, 4938
DNA326390, 4941
DNA326391, 4942
DNA326392, 4943
DNA326393, 4944
DNA326394, 4945
DNA326395, 4946
DNA326396, 4948
DNA326397, 4950
DNA326398, 4951
DNA326399, 4955
DNA326400, 4957
DNA326401, 4958
DNA326402, 4960
DNA326403, 4962
DNA326404, 4965
DNA326405, 4967
DNA326406, 4969
DNA326407, 4971
DNA326408, 4973
DNA326409, 4977
DNA326410, 4978
DNA326411, 4980
DNA326412, 4982
DNA326413, 4984

WO 2004/030615

PCT/US2003/028547

DNA326414, 4987
DNA326415, 4988
DNA326416, 4989
DNA326417, 4991
DNA326418, 4992
DNA326419, 4994
DNA326420, 4995
DNA326421, 4996
DNA326422, 4998
DNA326423, 4999
DNA326424, 5000
DNA326425, 5001
DNA326426, 5002
DNA326427, 5004
DNA326428, 5006
DNA326429, 5008
DNA326430, 5010
DNA326431, 5011
DNA326432, 5013
DNA326433, 5016
DNA326434, 5018
DNA326435, 5019
DNA326436, 5020
DNA326437, 5021
DNA326438, 5022
DNA326439, 5025
DNA326440, 5026
DNA326441, 5027
DNA326442, 5028
DNA326443, 5030
DNA326444, 5031
DNA326445, 5032
DNA326446, 5034
DNA326447, 5036
DNA326448, 5037
DNA326449, 5042
DNA326450, 5043
DNA326451, 5045
DNA326452, 5046
DNA326453, 5048
DNA326454, 5049
DNA326455, 5054
DNA326456, 5055
DNA326457, 5058
DNA326458, 5060
DNA326459, 5062
DNA326460, 5064
DNA326461, 5065
DNA326462, 5066
DNA326463, 5067
DNA326464, 5069
DNA326465, 5071
DNA326466, 5072
DNA326467, 5074
DNA326468, 5075
DNA326469, 5076

DNA326470, 5078
DNA326471, 5080
DNA326472, 5082
DNA326473, 5083
DNA326474, 5084
DNA326475, 5086
DNA326476, 5088
DNA326477, 5089
DNA326478, 5090
DNA326479, 5092
DNA326480, 5093
DNA326481, 5095
DNA326482, 5097
DNA326483, 5098
DNA326484, 5100
DNA326485, 5102
DNA326486, 5104
DNA326487, 5106
DNA326488, 5108
DNA326489, 5109
DNA326490, 5110
DNA326491, 5112
DNA326492, 5113
DNA326493, 5114
DNA326494, 5117
DNA326495, 5119
DNA326496, 5120
DNA326497, 5122
DNA326498, 5124
DNA326499, 5126
DNA326500, 5128
DNA326501, 5130
DNA326502, 5131
DNA326503, 5132
DNA326504, 5134
DNA326505, 5135
DNA326506, 5137
DNA326507, 5138
DNA326508, 5140
DNA326509, 5141
DNA326510, 5143
DNA326511, 5145
DNA326512, 5148
DNA326513, 5150
DNA326514, 5152
DNA326515, 5155
DNA326516, 5157
DNA326517, 5159
DNA326518, 5160
DNA326519, 5161
DNA326520, 5163
DNA326521, 5165
DNA326522, 5166
DNA326523, 5168
DNA326524, 5169
DNA326525, 5171

WO 2004/030615

PCT/US2003/028547

DNA326526, 5173
DNA326527, 5175
DNA326528, 5176
DNA326529, 5178
DNA326530, 5180
DNA326531, 5181
DNA326532, 5183
DNA326533, 5184
DNA326534, 5186
DNA326535, 5188
DNA326536, 5190
DNA326537, 5192
DNA326538, 5194
DNA326539, 5195
DNA326540, 5196
DNA326541, 5197
DNA326542, 5203
DNA326543, 5205
DNA326544, 5208
DNA326546, 5210
DNA326547, 5212
DNA326548, 5213
DNA326549, 5214
DNA326550, 5216
DNA326551, 5218
DNA326552, 5219
DNA326553, 5221
DNA326554, 5222
DNA326555, 5223
DNA326556, 5225
DNA326557, 5226
DNA326558, 5227
DNA326559, 5229
DNA326560, 5230
DNA326561, 5236
DNA326562, 5237
DNA326563, 5239
DNA326564, 5240
DNA326565, 5241
DNA326566, 5243
DNA326567, 5244
DNA326568, 5246
DNA326569, 5247
DNA326570, 5248
DNA326571, 5250
DNA326572, 5252
DNA326573, 5254
DNA326574, 5256
DNA326575, 5257
DNA326576, 5260
DNA326577, 5261
DNA326578, 5262
DNA326579, 5264
DNA326580, 5266
DNA326581, 5267
DNA326582, 5269

DNA326583, 5270
DNA326584, 5274
DNA326585, 5276
DNA326586, 5281
DNA326587, 5283
DNA326588, 5285
DNA326589, 5286
DNA326590, 5288
DNA326591, 5290
DNA326592, 5292
DNA326593, 5294
DNA326594, 5295
DNA326595, 5297
DNA326596, 5300
DNA326597, 5302
DNA326598, 5303
DNA326599, 5305
DNA326600, 5307
DNA326601, 5308
DNA326602, 5310
DNA326603, 5311
DNA326604, 5314
DNA326605, 5316
DNA326606, 5317
DNA326607, 5319
DNA326608, 5321
DNA326609, 5323
DNA326610, 5325
DNA326611, 5326
DNA326612, 5330
DNA326613, 5331
DNA326614, 5332
DNA326615, 5334
DNA326616, 5336
DNA326617, 5337
DNA326618, 5338
DNA326619, 5339
DNA326620, 5341
DNA326621, 5343
DNA326622, 5345
DNA326623, 5347
DNA326624, 5349
DNA326625, 5350
DNA326626, 5354
DNA326627, 5355
DNA326628, 5357
DNA326629, 5358
DNA326630, 5360
DNA326631, 5362
DNA326632, 5364
DNA326633, 5366
DNA326634, 5367
DNA326635, 5369
DNA326636, 5370
DNA326637, 5371
DNA326638, 5372

WO 2004/030615

PCT/US2003/028547

DNA326639, 5374
DNA326640, 5376
DNA326641, 5378
DNA326642, 5379
DNA326643, 5380
DNA326644, 5382
DNA326645, 5383
DNA326646, 5384
DNA326647, 5385
DNA326648, 5389
DNA326649, 5391
DNA326650, 5393
DNA326651, 5395
DNA326652, 5396
DNA326653, 5398
DNA326654, 5399
DNA326655, 5401
DNA326656, 5403
DNA326657, 5404
DNA326658, 5406
DNA326659, 5408
DNA326660, 5409
DNA326661, 5411
DNA326662, 5413
DNA326663, 5415
DNA326664, 5417
DNA326665, 5419
DNA326666, 5423
DNA326667, 5425
DNA326668, 5428
DNA326669, 5430
DNA326670, 5432
DNA326671, 5436
DNA326672, 5438
DNA326673, 5439
DNA326674, 5440
DNA326675, 5443
DNA326676, 5444
DNA326677, 5445
DNA326678, 5446
DNA326679, 5447
DNA326680, 5450
DNA326681, 5451
DNA326682, 5453
DNA326683, 5454
DNA326684, 5456
DNA326685, 5458
DNA326686, 5460
DNA326687, 5461
DNA326688, 5462
DNA326689, 5463
DNA326690, 5465
DNA326691, 5466
DNA326692, 5468
DNA326693, 5470
DNA326694, 5472

DNA326695, 5474
DNA326696, 5478
DNA326697, 5480
DNA326698, 5482
DNA326699, 5483
DNA326700, 5484
DNA326701, 5485
DNA326702, 5486
DNA326703, 5487
DNA326704, 5488
DNA326705, 5489
DNA326706, 5491
DNA326707, 5492
DNA326708, 5496
DNA326709, 5497
DNA326710, 5499
DNA326711, 5501
DNA326712, 5508
DNA326713, 5510
DNA326714, 5519
DNA326715, 5521
DNA326716, 5522
DNA326717, 5525
DNA326718, 5527
DNA326719, 5528
DNA326720, 5529
DNA326721, 5530
DNA326722, 5531
DNA326723, 5532
DNA326724, 5534
DNA326725, 5536
DNA326726, 5537
DNA326727, 5539
DNA326728, 5541
DNA326729, 5544
DNA326730, 5546
DNA326731, 5548
DNA326732, 5549
DNA326733, 5552
DNA326734, 5554
DNA326735, 5556
DNA326736, 5558
DNA326737, 5560
DNA326738, 5564
DNA326739, 5566
DNA326740, 5570
DNA326741, 5571
DNA326742, 5573
DNA326743, 5574
DNA326744, 5578
DNA326745, 5580
DNA326746, 5582
DNA326747, 5584
DNA326748, 5586
DNA326749, 5588
DNA326750, 5592

WO 2004/030615

PCT/US2003/028547

DNA326751, 5595
DNA326752, 5597
DNA326753, 5598
DNA326754, 5600
DNA326755, 5602
DNA326756, 5603
DNA326757, 5605
DNA326758, 5607
DNA326759, 5608
DNA326760, 5610
DNA326761, 5612
DNA326762, 5613
DNA326763, 5617
DNA326764, 5619
DNA326765, 5621
DNA326766, 5623
DNA326767, 5629
DNA326768, 5631
DNA326769, 5633
DNA326770, 5635
DNA326771, 5636
DNA326772, 5642
DNA326773, 5644
DNA326774, 5646
DNA326775, 5647
DNA326776, 5648
DNA326777, 5650
DNA326778, 5652
DNA326779, 5656
DNA326780, 5658
DNA326781, 5660
DNA326782, 5661
DNA326783, 5663
DNA326784, 5665
DNA326785, 5667
DNA326786, 5670
DNA326787, 5671
DNA326788, 5673
DNA326789, 5674
DNA326790, 5675
DNA326791, 5678
DNA326792, 5683
DNA326793, 5687
DNA326794, 5688
DNA326795, 5689
DNA326796, 5691
DNA326797, 5693
DNA326798, 5695
DNA326799, 5696
DNA326800, 5698
DNA326801, 5700
DNA326802, 5701
DNA326803, 5705
DNA326804, 5706
DNA326805, 5708
DNA326806, 5710

DNA326807, 5712
DNA326808, 5713
DNA326809, 5715
DNA326810, 5717
DNA326811, 5719
DNA326812, 5723
DNA326813, 5725
DNA326814, 5727
DNA326815, 5728
DNA326816, 5729
DNA326817, 5731
DNA326818, 5733
DNA326819, 5736
DNA326820, 5740
DNA326821, 5742
DNA326822, 5744
DNA326823, 5749
DNA326824, 5750
DNA326825, 5752
DNA326826, 5754
DNA326827, 5756
DNA326828, 5757
DNA326829, 5759
DNA326830, 5762
DNA326831, 5763
DNA326832, 5765
DNA326833, 5766
DNA326834, 5768
DNA326835, 5769
DNA326836, 5773
DNA326837, 5776
DNA326838, 5778
DNA326839, 5779
DNA326840, 5781
DNA326841, 5783
DNA326842, 5787
DNA326843, 5793
DNA326844, 5794
DNA326845, 5795
DNA326846, 5796
DNA326847, 5798
DNA326848, 5800
DNA326849, 5802
DNA326850, 5804
DNA326851, 5806
DNA326852, 5808
DNA326853, 5809
DNA326854, 5811
DNA326855, 5813
DNA326856, 5816
DNA326857, 5818
DNA326858, 5819
DNA326859, 5821
DNA326860, 5823
DNA326861, 5824
DNA326862, 5826

WO 2004/030615

PCT/US2003/028547

DNA326863, 5828
DNA326864, 5832
DNA326865, 5834
DNA326866, 5838
DNA326867, 5840
DNA326868, 5842
DNA326869, 5846
DNA326870, 5847
DNA326871, 5849
DNA326872, 5851
DNA326873, 5853
DNA326874, 5855
DNA326875, 5857
DNA326876, 5859
DNA326877, 5861
DNA326878, 5863
DNA326879, 5865
DNA326880, 5867
DNA326881, 5869
DNA326882, 5871
DNA326883, 5875
DNA326884, 5876
DNA326885, 5877
DNA326886, 5878
DNA326887, 5879
DNA326888, 5883
DNA326889, 5887
DNA326890, 5889
DNA326891, 5894
DNA326892, 5898
DNA326893, 5900
DNA326894, 5902
DNA326895, 5903
DNA326896, 5905
DNA326897, 5907
DNA326898, 5908
DNA326899, 5910
DNA326900, 5911
DNA326901, 5913
DNA326902, 5914
DNA326903, 5915
DNA326904, 5917
DNA326905, 5919
DNA326906, 5923
DNA326907, 5924
DNA326908, 5925
DNA326909, 5926
DNA326910, 5927
DNA326911, 5928
DNA326912, 5929
DNA326913, 5930
DNA326914, 5931
DNA326915, 5933
DNA326916, 5937
DNA326917, 5941
DNA326918, 5943

DNA326919, 5945
DNA326920, 5946
DNA326921, 5949
DNA326922, 5950
DNA326923, 5951
DNA326924, 5953
DNA326925, 5954
DNA326926, 5958
DNA326927, 5960
DNA326928, 5961
DNA326929, 5963
DNA326930, 5964
DNA326931, 5967
DNA326932, 5968
DNA326933, 5969
DNA326934, 5971
DNA326935, 5975
DNA326936, 5977
DNA326937, 5979
DNA326938, 5981
DNA326939, 5983
DNA326940, 5985
DNA326941, 5986
DNA326942, 5987
DNA326943, 5991
DNA326944, 5993
DNA326945, 5996
DNA326946, 5998
DNA326947, 5999
DNA326948, 6001
DNA326949, 6007
DNA326950, 6009
DNA326951, 6013
DNA326952, 6014
DNA326953, 6015
DNA326954, 6017
DNA326955, 6019
DNA326956, 6022
DNA326957, 6024
DNA326958, 6025
DNA326959, 6029
DNA326960, 6031
DNA326961, 6032
DNA326962, 6036
DNA326963, 6040
DNA326964, 6042
DNA326965, 6043
DNA326966, 6047
DNA326967, 6049
DNA326968, 6051
DNA326969, 6052
DNA326970, 6054
DNA326971, 6056
DNA326972, 6058
DNA326973, 6060
DNA326974, 6061

WO 2004/030615

PCT/US2003/028547

DNA326975, 6063
DNA326976, 6064
DNA326977, 6065
DNA326978, 6066
DNA326979, 6070
DNA326980, 6072
DNA326981, 6074
DNA326982, 6077
DNA326983, 6081
DNA326984, 6083
DNA326985, 6085
DNA326986, 6087
DNA326987, 6088
DNA326988, 6089
DNA326989, 6090
DNA326990, 6091
DNA326991, 6093
DNA326992, 6094
DNA326993, 6095
DNA326994, 6097
DNA326995, 6099
DNA326996, 6103
DNA326997, 6106
DNA326998, 6108
DNA326999, 6109
DNA327000, 6111
DNA327001, 6113
DNA327002, 6114
DNA327003, 6116
DNA327004, 6118
DNA327005, 6119
DNA327006, 6121
DNA327007, 6122
DNA327008, 6123
DNA327009, 6124
DNA327010, 6128
DNA327011, 6130
DNA327012, 6131
DNA327013, 6132
DNA327014, 6134
DNA327015, 6136
DNA327016, 6138
DNA327017, 6140
DNA327018, 6142
DNA327019, 6143
DNA327020, 6145
DNA327021, 6146
DNA327022, 6151
DNA327023, 6152
DNA327024, 6153
DNA327025, 6155
DNA327026, 6157
DNA327027, 6158
DNA327028, 6159
DNA327029, 6161
DNA327030, 6163

DNA327031, 6165
DNA327032, 6167
DNA327033, 6169
DNA327034, 6170
DNA327035, 6172
DNA327036, 6173
DNA327037, 6174
DNA327038, 6176
DNA327039, 6177
DNA327040, 6179
DNA327041, 6183
DNA327042, 6185
DNA327043, 6189
DNA327044, 6192
DNA327045, 6194
DNA327046, 6196
DNA327047, 6199
DNA327048, 6201
DNA327049, 6203
DNA327050, 6204
DNA327051, 6206
DNA327052, 6207
DNA327053, 6209
DNA327054, 6210
DNA327055, 6212
DNA327056, 6216
DNA327057, 6218
DNA327058, 6220
DNA327059, 6222
DNA327060, 6224
DNA327061, 6226
DNA327062, 6227
DNA327063, 6228
DNA327064, 6229
DNA327065, 6232
DNA327066, 6233
DNA327067, 6235
DNA327068, 6237
DNA327069, 6238
DNA327070, 6241
DNA327071, 6242
DNA327072, 6244
DNA327073, 6246
DNA327074, 6248
DNA327075, 6250
DNA327076, 6251
DNA327077, 6253
DNA327078, 6255
DNA327079, 6256
DNA327080, 6259
DNA327081, 6261
DNA327082, 6263
DNA327083, 6265
DNA327084, 6267
DNA327085, 6268
DNA327086, 6269

WO 2004/030615

PCT/US2003/028547

DNA327087, 6274
DNA327088, 6275
DNA327089, 6276
DNA327090, 6278
DNA327091, 6280
DNA327092, 6281
DNA327093, 6282
DNA327094, 6284
DNA327095, 6289
DNA327096, 6291
DNA327097, 6293
DNA327098, 6295
DNA327099, 6297
DNA327100, 6299
DNA327101, 6300
DNA327102, 6302
DNA327103, 6304
DNA327104, 6306
DNA327105, 6308
DNA327106, 6310
DNA327107, 6311
DNA327108, 6313
DNA327109, 6315
DNA327110, 6316
DNA327111, 6320
DNA327112, 6323
DNA327113, 6325
DNA327114, 6326
DNA327115, 6328
DNA327116, 6329
DNA327117, 6330
DNA327118, 6336
DNA327119, 6346
DNA327120, 6348
DNA327121, 6349
DNA327122, 6350
DNA327123, 6351
DNA327124, 6352
DNA327125, 6353
DNA327126, 6354
DNA327127, 6355
DNA66475, 4796
DNA75863, 3245
DNA76504, 6270
DNA79101, 3678
DNA79129, 1352
DNA79313, 3524
DNA82328, 624
DNA83020, 1671
DNA83022, 2495
DNA83046, 558
DNA83085, 173
DNA83141, 2361
DNA83154, 5590
DNA83170, 5679
DNA83180, 3476

DNA88051, 898
DNA88084, 5511
DNA88100, 1089
DNA88114, 3452
DNA88176, 3333
DNA88239, 5791
DNA88261, 4579
DNA88281, 5050
DNA88350, 2796
DNA88378, 4845
DNA88430, 4963
DNA88457, 5040
DNA88547, 1223
DNA88554, 4903
DNA88562, 2961
DNA88569, 5789
DNA89239, 1327
DNA89242, 2695
DNA97285, 3175
DNA97290, 4887
DNA97293, 4421
DNA97298, 5734
DNA97300, 4687

WO 2004/030615

PCT/US2003/028547

PRO Index (to Figure number)

PRO, 1189	PRO12520, 1025
PRO10002, 487	PRO12565, 1146
PRO10194, 2441	PRO12573, 3527
PRO10297, 1479	PRO12618, 45
PRO10360, 1923	PRO12683, 4399
PRO10400, 4928	PRO12774, 4306
PRO10404, 3952	PRO12779, 1154
PRO10485, 5127	PRO12792, 807
PRO10498, 967	PRO12797, 2035
PRO10602, 1207	PRO12800, 5503
PRO10685, 1633	PRO12806, 4954
PRO10692, 644	PRO12813, 3014
PRO10723, 6245	PRO12822, 5429
PRO10760, 211	PRO12838, 2547
PRO1077, 5094	PRO12839, 3758
PRO10824, 2652	PRO12841, 1067
PRO10838, 3657	PRO12845, 6023
PRO10849, 1709	PRO1285, 1665
PRO10935, 6279	PRO12851, 2905
PRO11048, 1285	PRO12878, 3250
PRO11077, 1571	PRO12886, 6021
PRO1108, 2532	PRO12892, 5477
PRO1112, 2003	PRO12902, 3467
PRO11139, 2981	PRO12916, 4080
PRO11197, 833	PRO1314, 1239
PRO11213, 3655	PRO1555, 2457
PRO11262, 3172	PRO1707, 625
PRO11265, 2589	PRO1720, 5782
PRO11403, 902, 4970	PRO1869, 3909
PRO11582, 556	PRO188, 530
PRO11601, 3521	PRO1910, 2835
PRO11691, 3186	PRO1927, 1847
PRO1182, 646	PRO19615, 1822
PRO119, 2229	PRO19933, 2109
PRO11982, 3915	PRO201, 5209
PRO1204, 4797	PRO20117, 3257, 3259
PRO12077, 1420	PRO20136, 49
PRO12130, 5315	PRO2018, 3246
PRO12134, 6006	PRO2042, 2496
PRO12135, 5897	PRO2054, 4066
PRO12187, 3412	PRO2065, 5780
PRO12198, 4142	PRO2066, 4049
PRO12199, 682	PRO2077, 1217
PRO12224, 3205	PRO2109, 5591
PRO12265, 4937	PRO2146, 899
PRO12324, 5704	PRO21481, 2669
PRO124, 3121	PRO2172, 1090
PRO12416, 1733	PRO21728, 5837
PRO12448, 3385	PRO21773, 3666
PRO12460, 5722	PRO21887, 4783
PRO12468, 2185	PRO21924, 3481
PRO1248, 565	PRO2198, 4639
PRO12490, 6055	PRO22196, 94

WO 2004/030615

PCT/US2003/028547

PRO22262, 168
PRO22304, 147
PRO224, 5217
PRO22481, 6028
PRO22613, 5284
PRO22637, 4569
PRO2267, 5051
PRO2269, 61
PRO22771, 1625
PRO22897, 2339
PRO22907, 2634, 2636
PRO231, 329
PRO23123, 999
PRO23124, 949, 951
PRO23201, 2615
PRO23231, 6059
PRO23238, 5589
PRO23248, 2568
PRO23300, 586
PRO23362, 2194
PRO23364, 2948
PRO2355, 4512
PRO2373, 6125
PRO23746, 13
PRO23794, 5251
PRO23797, 2024, 2151
PRO23845, 5394
PRO23942, 429
PRO24002, 5748
PRO24021, 6317
PRO24028, 855
PRO24075, 4531
PRO24077, 5761
PRO24091, 978
PRO2420, 5790
PRO24831, 3307
PRO24851, 577
PRO24856, 125
PRO25115, 4878
PRO25245, 6312
PRO25302, 5882
PRO2537, 6271
PRO2549, 3679
PRO2551, 1353
PRO2555, 3525
PRO2560, 5096
PRO2561, 1672
PRO2569, 559
PRO2570, 2477
PRO2583, 174
PRO25845, 3298
PRO25849, 1853
PRO25881, 5498
PRO25985, 3156
PRO2604, 2362
PRO2610, 981

PRO2615, 5680
PRO26194, 82
PRO2622, 3477
PRO26228, 983
PRO2644, 5512
PRO2660, 3453
PRO2665, 922
PRO2672, 4550
PRO2685, 3334
PRO2711, 5792
PRO2718, 5282
PRO2719, 4580
PRO2720, 4219
PRO2732, 4175
PRO2733, 2443
PRO2758, 2797
PRO2769, 4846
PRO2788, 4964
PRO2799, 5041
PRO283, 3664
PRO2837, 1224
PRO2839, 4904
PRO2841, 3741, 3743
PRO2842, 2962
PRO2846, 3661
PRO2851, 177
PRO28687, 5880
PRO287, 1277
PRO2871, 3995
PRO2875, 2974
PRO2906, 1328
PRO2907, 2696
PRO292, 3134
PRO29371, 5329
PRO302, 4918
PRO303, 4409
PRO329, 504
PRO3344, 2484
PRO33679, 368
PRO33717, 3963
PRO33818, 2773
PRO34043, 6205
PRO34073, 3052
PRO34151, 5479
PRO34323, 5259
PRO34473, 2783
PRO3449, 3601
PRO34531, 6076
PRO34544, 1676
PRO34557, 4183
PRO34584, 6186
PRO36020, 1741
PRO36047, 1490
PRO36055, 1331
PRO36058, 1735
PRO36093, 2768

WO 2004/030615

PCT/US2003/028547

PRO36094, 2175
PRO36095, 3474
PRO36112, 4043
PRO36118, 6339
PRO36134, 2507
PRO36184, 6215
PRO36215, 3377
PRO36263, 6335
PRO36272, 357
PRO3629, 4355, 4357
PRO36305, 1960
PRO36316, 1958
PRO3632, 3176
PRO36328, 3977
PRO3637, 4888
PRO36372, 1829
PRO36373, 1129
PRO36382, 1447
PRO36383, 1512
PRO36384, 1516
PRO3640, 4422
PRO36417, 5948
PRO3645, 5735
PRO36468, 554
PRO3647, 4688
PRO36474, 5518
PRO36477, 3730
PRO36491, 3490
PRO36543, 3207
PRO36568, 3993
PRO36588, 410
PRO36680, 3005
PRO36693, 2656
PRO36723, 272
PRO36725, 106
PRO36735, 1096
PRO36787, 4096
PRO36800, 2459
PRO36808, 2671
PRO36841, 1919
PRO36852, 4821
PRO36872, 5922
PRO36879, 2263
PRO36881, 1792
PRO36891, 742
PRO36959, 2566
PRO36963, 5490
PRO36970, 3456
PRO37010, 1109
PRO37012, 5976
PRO37023, 2394
PRO37024, 5957
PRO37073, 2987
PRO37080, 5936
PRO37082, 475
PRO37083, 6160

PRO37091, 1765
PRO37109, 4225
PRO37221, 5746
PRO37234, 3499
PRO37256, 437
PRO37316, 3867
PRO37335, 1690
PRO37476, 6333
PRO37518, 4940
PRO37534, 4890
PRO37535, 385
PRO37540, 4990
PRO37547, 4743
PRO37551, 3221
PRO37555, 3594
PRO37557, 3629
PRO37628, 685
PRO37634, 3725
PRO37635, 2965
PRO37636, 1574
PRO37644, 6273
PRO37653, 815
PRO37654, 3589
PRO37667, 1887
PRO37669, 4171
PRO37675, 924
PRO37676, 158
PRO37697, 4627
PRO37709, 551
PRO37712, 5353
PRO37730, 2513
PRO37731, 2243
PRO37743, 5233
PRO37764, 4934
PRO37770, 1166
PRO37783, 1813
PRO37784, 3985
PRO37791, 4793
PRO37806, 498
PRO37811, 5682
PRO37905, 1943
PRO37935, 5772
PRO37937, 3721
PRO37938, 2461
PRO37951, 5164
PRO37954, 2692
PRO37961, 4343
PRO37967, 595
PRO37972, 3077
PRO37991, 804
PRO37992, 347
PRO38008, 699
PRO38010, 3459
PRO38021, 6217
PRO38022, 4162
PRO38028, 2667

WO 2004/030615

PCT/US2003/028547

PRO38038, 1509
PRO38040, 375
PRO38066, 5810
PRO38070, 1962
PRO38101, 5565
PRO38119, 6286
PRO38152, 6148
PRO38227, 4892
PRO38258, 793
PRO38284, 37
PRO38311, 4359
PRO38336, 4842
PRO38380, 6322
PRO38387, 2100
PRO38392, 2207
PRO38406, 6198
PRO38464, 4336
PRO38480, 4373
PRO38496, 5133
PRO38730, 6343
PRO38852, 4215
PRO39030, 6105
PRO39127, 6182
PRO39201, 4983
PRO39530, 4643
PRO39648, 3009
PRO39773, 2399
PRO4, 2535
PRO41882, 2366
PRO42022, 6225
PRO42208, 4519
PRO4348, 3577
PRO4379, 4179
PRO4426, 3632
PRO44999, 579
PRO45014, 2183
PRO4544, 219
PRO4547, 650
PRO4569, 5577
PRO4583, 189
PRO4586, 6071
PRO4605, 1450
PRO4650, 5273
PRO4666, 3682
PRO4676, 1599
PRO4710, 1678
PRO4729, 4709
PRO47354, 5516
PRO4738, 4799
PRO4749, 2983
PRO4756, 5377
PRO4763, 458
PRO4789, 5995
PRO4793, 3848
PRO4798, 2071
PRO4801, 3314

PRO4813, 5845
PRO4814, 4582
PRO4832, 1150
PRO4833, 2991
PRO48357, 1082
PRO4836, 4111
PRO4841, 3479
PRO4852, 5775
PRO4870, 3312
PRO4872, 6082
PRO4873, 3684
PRO4884, 1950
PRO4885, 6345
PRO4900, 3050
PRO4904, 4064, 5495
PRO4908, 1780
PRO4912, 2275
PRO4914, 617
PRO4917, 712
PRO4918, 765
PRO49182, 4705
PRO49209, 1371
PRO49256, 6004
PRO49262, 1628
PRO49278, 6069
PRO49298, 3330
PRO49310, 4720
PRO49316, 995
PRO49352, 6046
PRO49409, 500
PRO49457, 604
PRO49639, 4488
PRO49642, 343
PRO49648, 2741
PRO49653, 5628
PRO49675, 5886
PRO49685, 1156
PRO49722, 1317
PRO49726, 3469
PRO4984, 1909
PRO49869, 2694
PRO49875, 3778
PRO49879, 4375
PRO49881, 6319
PRO49883, 6258
PRO49888, 4899
PRO49967, 4578
PRO50083, 5891
PRO50095, 1133
PRO50134, 5940
PRO50165, 3114
PRO50409, 4209
PRO50438, 4266
PRO50481, 4748
PRO50582, 1927
PRO50596, 860

WO 2004/030615

PCT/US2003/028547

PRO50658, 4613
PRO50756, 3110
PRO51109, 1273
PRO51119, 6102
PRO51121, 3512
PRO51389, 2055
PRO51539, 200
PRO51565, 5514
PRO51586, 5147
PRO51744, 5057
PRO51767, 5388
PRO51771, 5435
PRO51775, 4363
PRO51815, 4371
PRO51836, 546
PRO51851, 1643
PRO51901, 2747
PRO52010, 4855
PRO52083, 1438
PRO52101, 5507
PRO52119, 5966
PRO52449, 403
PRO52492, 3416
PRO52537, 2924
PRO54594, 4204
PRO57307, 3327
PRO57854, 3102
PRO57901, 5594
PRO57917, 4060
PRO57942, 5815
PRO58006, 1855
PRO58042, 5313
PRO58046, 5123
PRO58092, 3899
PRO58118, 268
PRO58140, 1196
PRO58155, 5874
PRO58177, 1257
PRO58198, 6127
PRO58207, 3285
PRO58213, 1688
PRO58219, 1647
PRO58232, 5990
PRO58259, 1271
PRO58263, 2553
PRO58292, 5299
PRO58308, 1063
PRO58328, 1098
PRO58348, 3094
PRO58410, 3865
PRO58437, 2370
PRO58440, 3688
PRO58446, 5268
PRO58523, 3209
PRO58543, 747
PRO58606, 3300

PRO58642, 3897
PRO58702, 5207
PRO58784, 1100
PRO58837, 3592
PRO58875, 6240
PRO58939, 2877
PRO58974, 471
PRO58984, 1893
PRO58986, 1387
PRO58991, 5235
PRO58993, 1804
PRO59001, 3817
PRO59022, 6243
PRO59040, 1851
PRO59042, 3824
PRO59043, 3056
PRO59061, 6012
PRO59074, 2372
PRO59084, 3296
PRO59099, 128
PRO59136, 795
PRO59142, 5649, 5651
PRO59168, 6154
PRO59220, 5361
PRO59230, 2551
PRO59262, 3440
PRO59264, 5505
PRO59285, 6080
PRO59305, 4844
PRO59309, 4806
PRO59313, 959
PRO59321, 2663
PRO59328, 4912
PRO59332, 289
PRO59339, 5677
PRO59351, 2856
PRO59365, 1998
PRO59380, 2397
PRO59384, 752
PRO59441, 6139
PRO59491, 4508
PRO59504, 1094
PRO59544, 762
PRO59546, 230
PRO59558, 704
PRO59579, 2674
PRO59629, 3381
PRO59647, 3551
PRO59669, 5904
PRO59717, 2105
PRO59721, 3272
PRO59725, 462
PRO59785, 3728
PRO59868, 6188
PRO59895, 935
PRO59913, 1722

WO 2004/030615

PCT/US2003/028547

PRO60006, 2752
PRO60008, 3282
PRO60070, 4102
PRO60115, 2807
PRO60121, 5053
PRO60123, 3393
PRO60127, 2661
PRO6018, 395
PRO60207, 1698
PRO60261, 520
PRO60298, 203
PRO60311, 3345
PRO60321, 2601
PRO60325, 4450
PRO60333, 5626
PRO60360, 2349
PRO60397, 882
PRO60438, 1867
PRO60475, 2735
PRO60499, 4262
PRO60542, 1397
PRO60575, 4087
PRO60579, 2181
PRO60603, 5427
PRO60634, 3556
PRO60666, 3391
PRO60674, 5202
PRO60741, 1336
PRO60753, 872
PRO60781, 2715
PRO60800, 5073
PRO60815, 84
PRO60847, 3216
PRO60860, 236
PRO60924, 3575
PRO60945, 5743
PRO60956, 1495
PRO60979, 4813
PRO60991, 3087
PRO61085, 4268
PRO61113, 5070
PRO61125, 195
PRO61129, 5569
PRO61146, 397
PRO61219, 4260
PRO61238, 3323
PRO61246, 5003
PRO61250, 90
PRO61271, 6231
PRO61308, 5575
PRO61325, 781
PRO61327, 5786
PRO61349, 5616
PRO61458, 5422
PRO61470, 6288
PRO61498, 5739

PRO61502, 3067
PRO61575, 5449
PRO61638, 349
PRO61661, 5024
PRO61679, 43
PRO61688, 2250
PRO61721, 2900
PRO61744, 6141
PRO61761, 689
PRO61799, 4361
PRO61812, 2237
PRO61824, 2247
PRO61870, 1183
PRO61897, 2795
PRO61938, 6191
PRO61948, 4477
PRO61977, 5278
PRO61999, 3913
PRO62039, 5116
PRO62065, 5893
PRO62069, 2865
PRO62075, 5442
PRO62077, 516
PRO62099, 4070
PRO62108, 2492
PRO62110, 4517
PRO62112, 5242
PRO62135, 1831
PRO62153, 1171
PRO62212, 5524
PRO62225, 5179
PRO62236, 2781
PRO62239, 750
PRO62244, 2177
PRO62273, 3764
PRO62302, 5162
PRO62328, 6000
PRO62389, 181
PRO62466, 6327
PRO62500, 5407
PRO62518, 193
PRO62529, 341
PRO62531, 5200
PRO62574, 453
PRO62582, 5543
PRO62588, 6150
PRO62607, 637
PRO62617, 2882
PRO62760, 931
PRO62770, 663
PRO62780, 4666
PRO62786, 745
PRO62849, 293
PRO62852, 4301
PRO62882, 4321
PRO62893, 652

WO 2004/030615

PCT/US2003/028547

PRO62899, 5103
PRO62927, 865
PRO62981, 4717
PRO63000, 2724
PRO63009, 2233
PRO63052, 1972
PRO63068, 4565
PRO63082, 1680
PRO63226, 5238
PRO63253, 1905
PRO63299, 6341
PRO6360, 1077
PRO6373, 2213
PRO65, 848
PRO66265, 4670
PRO66275, 3901
PRO66279, 2127
PRO66282, 2129
PRO69461, 3302
PRO69463, 32
PRO69471, 3840
PRO69473, 3027, 3760
PRO69475, 2266
PRO69486, 5906
PRO69496, 2702
PRO69506, 1953
PRO69513, 5015
PRO69518, 5280
PRO69521, 1901
PRO69523, 3011
PRO69528, 3237
PRO69531, 906
PRO69533, 5669
PRO69541, 5655
PRO69542, 2764
PRO69549, 3461
PRO69554, 1583
PRO69560, 5686
PRO69561, 4920
PRO69568, 3254
PRO69584, 1970
PRO69595, 4243
PRO69617, 4521
PRO69635, 3138
PRO69674, 3219
PRO69681, 1301
PRO69682, 4901
PRO69684, 4779
PRO70011, 2704
PRO70138, 1968
PRO70258, 656
PRO70276, 4447
PRO70290, 2762
PRO703, 380
PRO70327, 1637, 1639
PRO70331, 6030

PRO70333, 541
PRO70383, 6035
PRO70385, 5551
PRO70393, 2008
PRO70433, 351
PRO70449, 4729
PRO70453, 3621
PRO70536, 1460
PRO70544, 2033
PRO70595, 2681
PRO70675, 991
PRO70694, 3786
PRO70703, 4976
PRO70754, 439
PRO70810, 5639
PRO70812, 4700
PRO70989, 3828, 3830
PRO70993, 1719
PRO71031, 3433, 3435
PRO71057, 2997
PRO71085, 5563
PRO71088, 1947
PRO71089, 5641
PRO71091, 2591
PRO71093, 370
PRO71095, 1964
PRO71096, 3888
PRO71097, 5831
PRO71103, 1148
PRO71106, 1875
PRO71111, 2436
PRO71112, 221
PRO71120, 3718
PRO71125, 1985, 1987
PRO71130, 4576
PRO71133, 2255
PRO71136, 2309
PRO71141, 4715
PRO71142, 1913
PRO71145, 6039
PRO71146, 372
PRO71211, 2343
PRO71242, 5974
PRO7143, 4986
PRO730, 4274
PRO7427, 2239
PRO7445, 2594
PRO80480, 5
PRO80481, 7
PRO80482, 9
PRO80483, 11
PRO80484, 16
PRO80485, 18
PRO80487, 21
PRO80488, 23
PRO80489, 25

WO 2004/030615

PCT/US2003/028547

PRO80490, 27
PRO80492, 30
PRO80493, 35
PRO80494, 39
PRO80497, 47
PRO80498, 51
PRO80499, 53
PRO80501, 56
PRO80505, 63
PRO80506, 65
PRO80510, 70
PRO80511, 72
PRO80512, 74
PRO80517, 80
PRO80518, 86
PRO80519, 88
PRO80520, 92
PRO80521, 96
PRO80524, 100
PRO80527, 104
PRO80528, 108
PRO80530, 111
PRO80533, 115
PRO80534, 117
PRO80535, 119
PRO80536, 121
PRO80537, 123
PRO80542, 132
PRO80547, 138
PRO80550, 143
PRO80553, 149
PRO80554, 151
PRO80555, 153
PRO80557, 156
PRO80558, 160
PRO80559, 162
PRO80560, 164
PRO80561, 166
PRO80562, 170
PRO80563, 172
PRO80565, 179
PRO80567, 184
PRO80568, 186
PRO80570, 191
PRO80571, 197
PRO80574, 205
PRO80575, 207
PRO80576, 209
PRO80579, 215
PRO80580, 217
PRO80581, 223
PRO80582, 225
PRO80583, 227
PRO80584, 232
PRO80585, 234
PRO80586, 238

PRO80587, 240
PRO80588, 242
PRO80591, 246
PRO80592, 248
PRO80593, 252
PRO80595, 255
PRO80597, 258
PRO80599, 261
PRO80600, 263
PRO80602, 266
PRO80603, 270
PRO80604, 274
PRO80607, 278
PRO80611, 283
PRO80612, 285
PRO80613, 287
PRO80614, 291
PRO80617, 297
PRO80618, 299
PRO80619, 301
PRO80620, 303
PRO80621, 305
PRO80622, 307
PRO80623, 309
PRO80624, 311
PRO80625, 313
PRO80627, 316
PRO80630, 320
PRO80631, 322
PRO80633, 325
PRO80638, 333
PRO80639, 335
PRO80640, 337
PRO80641, 339
PRO80642, 345
PRO80644, 355
PRO80645, 359
PRO80646, 362
PRO80648, 365
PRO80651, 378
PRO80652, 382
PRO80654, 387
PRO80656, 390
PRO80657, 393
PRO80658, 399
PRO80659, 401
PRO80660, 405
PRO80661, 407
PRO80664, 413
PRO80665, 415
PRO80666, 417
PRO80667, 419
PRO80668, 421
PRO80669, 423
PRO80670, 425
PRO80671, 427

WO 2004/030615

PCT/US2003/028547

PRO80672, 431
PRO80675, 435
PRO80676, 441
PRO80677, 443
PRO80678, 445
PRO80679, 447
PRO80680, 449
PRO80684, 456
PRO80685, 460
PRO80686, 464
PRO80688, 467
PRO80689, 469
PRO80693, 478
PRO80694, 480
PRO80695, 482
PRO80699, 489
PRO80700, 491
PRO80704, 496
PRO80705, 502
PRO80706, 506
PRO80707, 508
PRO80708, 510
PRO80709, 512
PRO80710, 514
PRO80711, 518
PRO80714, 526
PRO80715, 528
PRO80717, 533
PRO80719, 536
PRO80720, 539
PRO80725, 549
PRO80730, 563
PRO80734, 570
PRO80735, 572
PRO80736, 574
PRO80740, 584
PRO80741, 588
PRO80742, 590
PRO80745, 597
PRO80752, 607
PRO80753, 609
PRO80754, 611
PRO80755, 613
PRO80756, 615
PRO80759, 621
PRO80760, 623
PRO80761, 627
PRO80762, 629
PRO80763, 631
PRO80764, 633
PRO80765, 635
PRO80767, 640
PRO80770, 648
PRO80771, 654
PRO80772, 658
PRO80773, 660

PRO80775, 666
PRO80776, 668
PRO80778, 671
PRO80779, 673
PRO80780, 675
PRO80781, 677
PRO80782, 679
PRO80785, 687
PRO80786, 691
PRO80787, 693
PRO80788, 695
PRO80789, 697
PRO80790, 702
PRO80791, 708
PRO80792, 710
PRO80793, 714
PRO80796, 718
PRO80797, 720
PRO80798, 722
PRO80799, 724
PRO80802, 728
PRO80803, 730
PRO80804, 732
PRO80806, 735
PRO80807, 737
PRO80808, 739
PRO80811, 754
PRO80812, 756
PRO80813, 758
PRO80814, 760
PRO80816, 767
PRO80817, 769
PRO80820, 774
PRO80823, 778
PRO80827, 786
PRO80830, 790
PRO80832, 797
PRO80833, 799
PRO80835, 802
PRO80837, 809
PRO80838, 811
PRO80839, 813
PRO80842, 819
PRO80843, 821
PRO80846, 826
PRO80847, 828
PRO80848, 830
PRO80850, 835
PRO80851, 837
PRO80853, 840
PRO80856, 844
PRO80857, 846
PRO80860, 852
PRO80866, 863
PRO80868, 868
PRO80869, 870

WO 2004/030615

PCT/US2003/028547

PRO80870, 874
PRO80871, 876
PRO80873, 879
PRO80875, 884
PRO80876, 886
PRO80877, 888
PRO80878, 890
PRO80879, 892
PRO80881, 895
PRO80882, 897
PRO80883, 904
PRO80884, 908
PRO80888, 913
PRO80889, 915
PRO80890, 917
PRO80891, 919
PRO80900, 937
PRO80901, 939
PRO80903, 943
PRO80904, 945
PRO80905, 947
PRO80906, 953
PRO80908, 956
PRO80910, 961
PRO80911, 963
PRO80915, 972
PRO80916, 974
PRO80917, 976
PRO80920, 987
PRO80921, 989
PRO80924, 997
PRO80925, 1001
PRO80926, 1003
PRO80927, 1005
PRO80929, 1008
PRO80930, 1010
PRO80932, 1013
PRO80933, 1015
PRO80934, 1017
PRO80935, 1019
PRO80936, 1021
PRO80937, 1023
PRO80938, 1027
PRO80941, 1031
PRO80942, 1033
PRO80943, 1035
PRO80945, 1038
PRO80949, 1044
PRO80950, 1046
PRO80951, 1048
PRO80952, 1050
PRO80953, 1052
PRO80954, 1054
PRO80955, 1056
PRO80956, 1058
PRO80958, 1061

PRO80959, 1065
PRO80960, 1069
PRO80961, 1071
PRO80962, 1073
PRO80966, 1080
PRO80967, 1084
PRO80969, 1087
PRO80970, 1092
PRO80971, 1102
PRO80972, 1104
PRO80974, 1107
PRO80975, 1111
PRO80977, 1114
PRO80978, 1116
PRO80979, 1118
PRO80983, 1124
PRO80984, 1126
PRO80988, 1135
PRO80990, 1138
PRO80993, 1142
PRO80994, 1144
PRO80995, 1152
PRO80996, 1158
PRO80997, 1160
PRO80999, 1164
PRO81000, 1168
PRO81002, 1173
PRO81003, 1175
PRO81004, 1177
PRO81005, 1179
PRO81006, 1181
PRO81007, 1185
PRO81010, 1191
PRO81012, 1194
PRO81015, 1200
PRO81022, 1210
PRO81023, 1212
PRO81025, 1215
PRO81026, 1219
PRO81028, 1222
PRO81029, 1226
PRO81030, 1228
PRO81031, 1230
PRO81033, 1233
PRO81034, 1236
PRO81036, 1241
PRO81040, 1247
PRO81041, 1249
PRO81042, 1251
PRO81043, 1253
PRO81046, 1259
PRO81047, 1261
PRO81053, 1269
PRO81056, 1279
PRO81057, 1281
PRO81058, 1283

WO 2004/030615

PCT/US2003/028547

PRO81059, 1287
PRO81064, 1293
PRO81068, 1298
PRO81070, 1303
PRO81071, 1305
PRO81072, 1307
PRO81073, 1309
PRO81074, 1311
PRO81079, 1319
PRO81080, 1321
PRO81082, 1324
PRO81083, 1326
PRO81086, 1334
PRO81088, 1339
PRO81090, 1342
PRO81093, 1346
PRO81095, 1349
PRO81096, 1351
PRO81097, 1355
PRO81098, 1357
PRO81102, 1362
PRO81106, 1367
PRO81107, 1373
PRO81108, 1375
PRO81109, 1377
PRO81110, 1379
PRO81111, 1381
PRO81112, 1383
PRO81113, 1385
PRO81114, 1389
PRO81115, 1391
PRO81116, 1393
PRO81117, 1395
PRO81118, 1399
PRO81119, 1401
PRO81120, 1403
PRO81121, 1405
PRO81122, 1407
PRO81123, 1409
PRO81124, 1411
PRO81127, 1415
PRO81131, 1422
PRO81134, 1426
PRO81135, 1428
PRO81137, 1431
PRO81141, 1436
PRO81146, 1444
PRO81148, 1454
PRO81150, 1458
PRO81151, 1462
PRO81156, 1467
PRO81163, 1475
PRO81166, 1481
PRO81169, 1486
PRO81170, 1488
PRO81171, 1492

PRO81174, 1498
PRO81176, 1501
PRO81177, 1503
PRO81178, 1505
PRO81179, 1507
PRO81181, 1514
PRO81182, 1518
PRO81184, 1521
PRO81185, 1523
PRO81188, 1527
PRO81189, 1529
PRO81195, 1536
PRO81196, 1538
PRO81199, 1542
PRO81202, 1546
PRO81213, 1558
PRO81214, 1560
PRO81216, 1563
PRO81219, 1566
PRO81221, 1569
PRO81223, 1576
PRO81224, 1578
PRO81225, 1580
PRO81227, 1585
PRO81230, 1589
PRO81234, 1594
PRO81238, 1601
PRO81239, 1603
PRO81240, 1605
PRO81241, 1607
PRO81246, 1613
PRO81248, 1616
PRO81249, 1618
PRO81250, 1620
PRO81254, 1630
PRO81256, 1635
PRO81259, 1645
PRO81260, 1649
PRO81261, 1651
PRO81262, 1653
PRO81264, 1657
PRO81265, 1659
PRO81266, 1661
PRO81269, 1667
PRO81272, 1674
PRO81273, 1682
PRO81274, 1684
PRO81275, 1686
PRO81276, 1692
PRO81277, 1694
PRO81278, 1696
PRO81280, 1703
PRO81281, 1705
PRO81282, 1707
PRO81286, 1715
PRO81287, 1717

WO 2004/030615

PCT/US2003/028547

PRO81289, 1725
PRO81290, 1727
PRO81291, 1729
PRO81292, 1731
PRO81293, 1737
PRO81294, 1739
PRO81295, 1743
PRO81296, 1745
PRO81297, 1747
PRO81298, 1749
PRO81299, 1751
PRO81300, 1753
PRO81301, 1755
PRO81302, 1757
PRO81303, 1759
PRO81304, 1761
PRO81305, 1763
PRO81306, 1767
PRO81307, 1769
PRO81308, 1771
PRO81309, 1773
PRO81310, 1775
PRO81311, 1777
PRO81313, 1782
PRO81314, 1784
PRO81315, 1786
PRO81316, 1788
PRO81317, 1790
PRO81318, 1794
PRO81319, 1796
PRO81323, 1801
PRO81325, 1806
PRO81327, 1809
PRO81330, 1815
PRO81336, 1825
PRO81337, 1827
PRO81338, 1833
PRO81339, 1835
PRO81340, 1837
PRO81341, 1839
PRO81345, 1844
PRO81347, 1849
PRO81354, 1864
PRO81355, 1869
PRO81356, 1873
PRO81359, 1881
PRO81362, 1885
PRO81363, 1889
PRO81364, 1891
PRO81365, 1895
PRO81366, 1897
PRO81367, 1899
PRO81368, 1903
PRO81369, 1907
PRO81370, 1911
PRO81371, 1915

PRO81372, 1917
PRO81375, 1925
PRO81377, 1930
PRO81379, 1933
PRO81380, 1935
PRO81387, 1945
PRO81394, 1966
PRO81395, 1974
PRO81396, 1976
PRO81397, 1978
PRO81398, 1980
PRO81399, 1982
PRO81400, 1989
PRO81401, 1991
PRO81402, 1993
PRO81404, 1996
PRO81406, 2001
PRO81407, 2005
PRO81409, 2010
PRO81410, 2012
PRO81411, 2014
PRO81414, 2018
PRO81415, 2020
PRO81416, 2022
PRO81417, 2026
PRO81418, 2028
PRO81419, 2030
PRO81421, 2038
PRO81422, 2040
PRO81424, 2043
PRO81426, 2046
PRO81427, 2048
PRO81429, 2051
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PRO81435, 2061
PRO81436, 2063
PRO81439, 2067
PRO81441, 2073
PRO81443, 2076
PRO81444, 2078
PRO81446, 2082
PRO81447, 2084
PRO81448, 2086
PRO81449, 2088
PRO81453, 2093
PRO81454, 2095
PRO81455, 2097
PRO81457, 2102
PRO81462, 2112
PRO81464, 2115
PRO81465, 2117
PRO81467, 2120
PRO81471, 2125
PRO81474, 2133
PRO81476, 2136
PRO81477, 2138

WO 2004/030615

PCT/US2003/028547

PRO81481, 2143
PRO81486, 2149
PRO81487, 2153
PRO81490, 2156
PRO81491, 2158
PRO81494, 2162
PRO81495, 2164
PRO81496, 2166
PRO81498, 2169
PRO81499, 2171
PRO81500, 2173
PRO81501, 2179
PRO81502, 2187
PRO81503, 2189
PRO81505, 2192
PRO81506, 2196
PRO81508, 2199
PRO81509, 2201
PRO81514, 2209
PRO81515, 2211
PRO81516, 2215
PRO81517, 2217
PRO81520, 2221
PRO81521, 2223
PRO81523, 2227
PRO81524, 2231
PRO81525, 2235
PRO81526, 2241
PRO81529, 2252
PRO81531, 2257
PRO81534, 2261
PRO81536, 2268
PRO81537, 2270
PRO81538, 2272
PRO81540, 2277
PRO81541, 2279
PRO81544, 2283
PRO81545, 2285
PRO81546, 2287
PRO81547, 2289
PRO81548, 2291
PRO81550, 2294
PRO81551, 2296
PRO81552, 2298
PRO81556, 2303
PRO81557, 2305
PRO81558, 2307
PRO81561, 2314
PRO81566, 2320
PRO81569, 2324
PRO81571, 2327
PRO81572, 2330
PRO81573, 2332
PRO81574, 2334
PRO81575, 2336
PRO81578, 2341

PRO81579, 2345
PRO81580, 2347
PRO81584, 2354
PRO81585, 2356
PRO81586, 2358
PRO81587, 2360
PRO81588, 2364
PRO81589, 2368
PRO81590, 2374
PRO81591, 2377
PRO81592, 2379
PRO81594, 2382
PRO81595, 2384
PRO81598, 2388
PRO81599, 2390
PRO81600, 2392
PRO81602, 2401
PRO81605, 2405
PRO81607, 2408
PRO81608, 2410
PRO81609, 2412
PRO81611, 2415
PRO81614, 2419
PRO81615, 2421
PRO81617, 2424
PRO81618, 2426
PRO81619, 2428
PRO81621, 2431
PRO81625, 2438
PRO81627, 2445
PRO81629, 2448
PRO81630, 2450
PRO81631, 2452
PRO81634, 2463
PRO81635, 2465
PRO81637, 2468
PRO81641, 2474
PRO81643, 2481
PRO81645, 2486
PRO81647, 2489
PRO81649, 2494
PRO81650, 2498
PRO81651, 2500
PRO81652, 2502
PRO81653, 2504
PRO81654, 2509
PRO81655, 2511
PRO81657, 2516
PRO81658, 2518
PRO81659, 2520
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PRO81661, 2524
PRO81664, 2528
PRO81668, 2537
PRO81669, 2539
PRO81671, 2542

WO 2004/030615

PCT/US2003/028547

PRO81673, 2545
PRO81674, 2549
PRO81675, 2555
PRO81685, 2570
PRO81687, 2573
PRO81689, 2576
PRO81690, 2578
PRO81691, 2580
PRO81695, 2585
PRO81696, 2587
PRO81699, 2597
PRO81700, 2599
PRO81701, 2603
PRO81704, 2607
PRO81705, 2610
PRO81708, 2617
PRO81711, 2621
PRO81714, 2624
PRO81719, 2630
PRO81720, 2632
PRO81722, 2639
PRO81725, 2643
PRO81729, 2648
PRO81730, 2650
PRO81731, 2654
PRO81732, 2658
PRO81734, 2665
PRO81736, 2678
PRO81738, 2683
PRO81739, 2685
PRO81740, 2687
PRO81742, 2690
PRO81743, 2698
PRO81746, 2706
PRO81748, 2709
PRO81751, 2713
PRO81752, 2717
PRO81753, 2719
PRO81754, 2721
PRO81759, 2729
PRO81760, 2731
PRO81761, 2733
PRO81762, 2737
PRO81763, 2739
PRO81764, 2743
PRO81765, 2745
PRO81766, 2749
PRO81768, 2754
PRO81771, 2758
PRO81775, 2770
PRO81778, 2776
PRO81780, 2779
PRO81781, 2785
PRO81783, 2788
PRO81785, 2791
PRO81786, 2793

PRO81792, 2805
PRO81794, 2810
PRO81795, 2812
PRO81796, 2814
PRO81797, 2816
PRO81800, 2821
PRO81801, 2823
PRO81804, 2827
PRO81805, 2829
PRO81806, 2831
PRO81809, 2837
PRO81811, 2840
PRO81812, 2842
PRO81813, 2844
PRO81815, 2848
PRO81816, 2850
PRO81817, 2853
PRO81819, 2858
PRO81821, 2861
PRO81822, 2863
PRO81823, 2867
PRO81824, 2869
PRO81826, 2872
PRO81831, 2880
PRO81832, 2884
PRO81833, 2886
PRO81834, 2888
PRO81835, 2890
PRO81836, 2892
PRO81837, 2894
PRO81838, 2896
PRO81841, 2903
PRO81842, 2907
PRO81846, 2912
PRO81848, 2915
PRO81849, 2917
PRO81851, 2920
PRO81855, 2928
PRO81858, 2932
PRO81861, 2936
PRO81862, 2938
PRO81863, 2940
PRO81865, 2943
PRO81867, 2946
PRO81868, 2950
PRO81869, 2954
PRO81870, 2956
PRO81871, 2958
PRO81872, 2960
PRO81874, 2967
PRO81875, 2969
PRO81877, 2972
PRO81881, 2979
PRO81882, 2985
PRO81883, 2989
PRO81884, 2993

WO 2004/030615

PCT/US2003/028547

PRO81885, 2995
PRO81887, 3001
PRO81888, 3003
PRO81889, 3007
PRO81893, 3018
PRO81895, 3021
PRO81896, 3023
PRO81897, 3025
PRO81899, 3030
PRO81900, 3032
PRO81901, 3034
PRO81902, 3036
PRO81903, 3038
PRO81904, 3040
PRO81905, 3043
PRO81907, 3046
PRO81908, 3048
PRO81909, 3054
PRO81912, 3060
PRO81913, 3062
PRO81914, 3064
PRO81916, 3069
PRO81917, 3071
PRO81922, 3079
PRO81923, 3081
PRO81924, 3083
PRO81925, 3085
PRO81926, 3090
PRO81927, 3092
PRO81928, 3096
PRO81929, 3098
PRO81930, 3100
PRO81932, 3105
PRO81934, 3108
PRO81935, 3112
PRO81936, 3116
PRO81937, 3118
PRO81939, 3123
PRO81941, 3126
PRO81942, 3128
PRO81943, 3130
PRO81944, 3132
PRO81945, 3140
PRO81946, 3143
PRO81947, 3145
PRO81948, 3147
PRO81950, 3150
PRO81953, 3154
PRO81954, 3158
PRO81955, 3160
PRO81956, 3162
PRO81957, 3164
PRO81958, 3166
PRO81959, 3168
PRO81962, 3174
PRO81964, 3179

PRO81965, 3181
PRO81970, 3189
PRO81971, 3191
PRO81977, 3198
PRO81978, 3200
PRO81980, 3203
PRO81981, 3211
PRO81982, 3213
PRO81988, 3226
PRO81990, 3229
PRO81991, 3231
PRO81992, 3233
PRO81993, 3235
PRO81994, 3239
PRO81995, 3241
PRO81996, 3243
PRO81999, 3252
PRO82002, 3262
PRO82004, 3265
PRO82005, 3267
PRO82009, 3274
PRO82011, 3277
PRO82013, 3280
PRO82018, 3290
PRO82019, 3292
PRO82023, 3305
PRO82024, 3309
PRO82027, 3317
PRO82028, 3319
PRO82029, 3321
PRO82032, 3332
PRO82034, 3338
PRO82035, 3340
PRO82037, 3343
PRO82038, 3347
PRO82040, 3351
PRO82042, 3354
PRO82043, 3356
PRO82045, 3360
PRO82046, 3362
PRO82050, 3368
PRO82051, 3370
PRO82052, 3372
PRO82054, 3375
PRO82055, 3379
PRO82056, 3383
PRO82057, 3387
PRO82058, 3389
PRO82060, 3396
PRO82064, 3402
PRO82066, 3405
PRO82068, 3408
PRO82069, 3410
PRO82072, 3419
PRO82073, 3421
PRO82074, 3423

WO 2004/030615

PCT/US2003/028547

PRO82075, 3425
PRO82078, 3431
PRO82080, 3438
PRO82082, 3443
PRO82083, 3445
PRO82084, 3447
PRO82085, 3449
PRO82091, 3464
PRO82093, 3471
PRO82097, 3484
PRO82099, 3487
PRO82101, 3492
PRO82104, 3497
PRO82106, 3502
PRO82107, 3505
PRO82109, 3508
PRO82110, 3510
PRO82111, 3514
PRO82112, 3516
PRO82113, 3518
PRO82115, 3523
PRO82117, 3530
PRO82120, 3534
PRO82122, 3537
PRO82125, 3541
PRO82127, 3544
PRO82129, 3547
PRO82130, 3549
PRO82131, 3553
PRO82133, 3558
PRO82137, 3563
PRO82138, 3565
PRO82139, 3567
PRO82140, 3569
PRO82143, 3573
PRO82152, 3587
PRO82155, 3597
PRO82158, 3603
PRO82159, 3605
PRO82160, 3607
PRO82161, 3609
PRO82162, 3611
PRO82163, 3613
PRO82164, 3615
PRO82165, 3617
PRO82166, 3619
PRO82167, 3623
PRO82168, 3625
PRO82169, 3627
PRO82174, 3637
PRO82175, 3639
PRO82179, 3644
PRO82181, 3647
PRO82182, 3649
PRO82183, 3651
PRO82184, 3653

PRO82188, 3670
PRO82190, 3673
PRO82191, 3675
PRO82192, 3677
PRO82194, 3686
PRO82195, 3690
PRO82196, 3692
PRO82197, 3694
PRO82198, 3696
PRO82199, 3698
PRO82201, 3701
PRO82202, 3703
PRO82204, 3706
PRO82206, 3709
PRO82207, 3711
PRO82208, 3713
PRO82210, 3716
PRO82212, 3723
PRO82213, 3733
PRO82214, 3735
PRO82215, 3738
PRO82218, 3745
PRO82219, 3747
PRO82220, 3749
PRO82221, 3751
PRO82223, 3756
PRO82224, 3762
PRO82227, 3768
PRO82228, 3770
PRO82232, 3776
PRO82233, 3780
PRO82234, 3782
PRO82235, 3784
PRO82237, 3789
PRO82238, 3791
PRO82239, 3793
PRO82240, 3795
PRO82243, 3799
PRO82244, 3801
PRO82245, 3803
PRO82247, 3806
PRO82248, 3808
PRO82250, 3811
PRO82252, 3813
PRO82253, 3815
PRO82255, 3820
PRO82256, 3822
PRO82259, 3832
PRO82263, 3838
PRO82264, 3842
PRO82265, 3844
PRO82266, 3846
PRO82267, 3850
PRO82268, 3852
PRO82269, 3854
PRO82272, 3858

WO 2004/030615

PCT/US2003/028547

PRO82273, 3860
PRO82275, 3863
PRO82278, 3871
PRO82279, 3873
PRO82280, 3875
PRO82283, 3879
PRO82285, 3882
PRO82287, 3885
PRO82289, 3890
PRO82290, 3892
PRO82291, 3894
PRO82295, 3905
PRO82296, 3907
PRO82297, 3911
PRO82300, 3919
PRO82302, 3922
PRO82305, 3927
PRO82306, 3929
PRO82311, 3934
PRO82312, 3936
PRO82314, 3939
PRO82315, 3941
PRO82316, 3943
PRO82317, 3945
PRO82318, 3947
PRO82321, 3954
PRO82322, 3956
PRO82325, 3961
PRO82326, 3965
PRO82329, 3970
PRO82330, 3972
PRO82331, 3974
PRO82333, 3979
PRO82334, 3982
PRO82338, 3989
PRO82342, 3998
PRO82343, 4000
PRO82344, 4002
PRO82345, 4004
PRO82347, 4007
PRO82348, 4009
PRO82349, 4011
PRO82350, 4013
PRO82351, 4015
PRO82352, 4017
PRO82355, 4021
PRO82356, 4023
PRO82357, 4026
PRO82358, 4028
PRO82359, 4030
PRO82364, 4036
PRO82365, 4038
PRO82367, 4041
PRO82369, 4047
PRO82370, 4051
PRO82371, 4053

PRO82373, 4056
PRO82374, 4058
PRO82375, 4062
PRO82381, 4076
PRO82382, 4078
PRO82383, 4083
PRO82384, 4085
PRO82385, 4089
PRO82388, 4093
PRO82391, 4099
PRO82393, 4104
PRO82395, 4107
PRO82396, 4109
PRO82397, 4113
PRO82400, 4117
PRO82408, 4126
PRO82409, 4128
PRO82411, 4131
PRO82415, 4137
PRO82417, 4140
PRO82418, 4144
PRO82419, 4146
PRO82421, 4149
PRO82422, 4151
PRO82423, 4153
PRO82424, 4155
PRO82425, 4158
PRO82428, 4164
PRO82429, 4166
PRO82431, 4169
PRO82432, 4173
PRO82433, 4177
PRO82434, 4181
PRO82435, 4185
PRO82437, 4188
PRO82438, 4190
PRO82439, 4192
PRO82440, 4194
PRO82441, 4196
PRO82442, 4198
PRO82444, 4201
PRO82446, 4206
PRO82448, 4212
PRO82450, 4217
PRO82453, 4223
PRO82454, 4227
PRO82455, 4229
PRO82456, 4231
PRO82457, 4233
PRO82458, 4235
PRO82460, 4238
PRO82461, 4240
PRO82465, 4247
PRO82466, 4249
PRO82469, 4253
PRO82470, 4255

WO 2004/030615

PCT/US2003/028547

PRO82472, 4258
PRO82473, 4264
PRO82475, 4271
PRO82477, 4276
PRO82479, 4280
PRO82482, 4284
PRO82485, 4288
PRO82487, 4291
PRO82489, 4294
PRO82491, 4297
PRO82492, 4299
PRO82493, 4303
PRO82495, 4308
PRO82499, 4313
PRO82501, 4316
PRO82502, 4318
PRO82505, 4324
PRO82508, 4328
PRO82509, 4330
PRO82510, 4332
PRO82513, 4339
PRO82514, 4341
PRO82515, 4345
PRO82516, 4347
PRO82517, 4349
PRO82518, 4351
PRO82521, 4365
PRO82522, 4367
PRO82523, 4369
PRO82524, 4377
PRO82525, 4379
PRO82526, 4381
PRO82527, 4383
PRO82528, 4385
PRO82529, 4387
PRO82530, 4389
PRO82531, 4391
PRO82532, 4393
PRO82533, 4395
PRO82534, 4397
PRO82535, 4401
PRO82536, 4403
PRO82537, 4405
PRO82538, 4407
PRO82540, 4412
PRO82542, 4415
PRO82543, 4417
PRO82544, 4419
PRO82546, 4424
PRO82548, 4428
PRO82551, 4433
PRO82554, 4437
PRO82555, 4439
PRO82556, 4441
PRO82557, 4443
PRO82558, 4445

PRO82560, 4452
PRO82562, 4455
PRO82563, 4457
PRO82564, 4459
PRO82567, 4464
PRO82568, 4466
PRO82570, 4469
PRO82571, 4471
PRO82572, 4473
PRO82573, 4475
PRO82576, 4481
PRO82579, 4486
PRO82582, 4492
PRO82583, 4494
PRO82584, 4496
PRO82585, 4499
PRO82586, 4501
PRO82587, 4503
PRO82589, 4506
PRO82590, 4510
PRO82592, 4515
PRO82593, 4523
PRO82594, 4525
PRO82597, 4529
PRO82598, 4533
PRO82599, 4536
PRO82602, 4540
PRO82603, 4542
PRO82606, 4546
PRO82607, 4548
PRO82608, 4552
PRO82609, 4554
PRO82611, 4557
PRO82612, 4559
PRO82615, 4563
PRO82616, 4567
PRO82618, 4572
PRO82619, 4574
PRO82621, 4585
PRO82622, 4587
PRO82623, 4589
PRO82624, 4591
PRO82625, 4593
PRO82626, 4595
PRO82627, 4598
PRO82629, 4601
PRO82630, 4603
PRO82631, 4605
PRO82632, 4607
PRO82633, 4609
PRO82634, 4611
PRO82635, 4615
PRO82637, 4618
PRO82638, 4620
PRO82640, 4623
PRO82641, 4625

WO 2004/030615

PCT/US2003/028547

PRO82642, 4629
PRO82643, 4631
PRO82645, 4634
PRO82646, 4636
PRO82654, 4649
PRO82656, 4652
PRO82658, 4655
PRO82659, 4657
PRO82661, 4660
PRO82662, 4662
PRO82663, 4664
PRO82664, 4668
PRO82665, 4673
PRO82667, 4676
PRO82669, 4679
PRO82670, 4681
PRO82671, 4683
PRO82672, 4685
PRO82674, 4690
PRO82675, 4692
PRO82678, 4698
PRO82679, 4702
PRO82683, 4711
PRO82687, 4722
PRO82689, 4726
PRO82691, 4731
PRO82692, 4733
PRO82694, 4736
PRO82695, 4738
PRO82696, 4740
PRO82699, 4746
PRO82702, 4753
PRO82704, 4756
PRO82706, 4759
PRO82707, 4762
PRO82708, 4764
PRO82709, 4766
PRO82712, 4770
PRO82713, 4772
PRO82714, 4774
PRO82715, 4776
PRO82717, 4781
PRO82718, 4785
PRO82719, 4787
PRO82720, 4789
PRO82721, 4791
PRO82722, 4795
PRO82724, 4802
PRO82725, 4804
PRO82726, 4808
PRO82728, 4811
PRO82729, 4815
PRO82730, 4817
PRO82732, 4823
PRO82736, 4828
PRO82737, 4831

PRO82738, 4833
PRO82739, 4835
PRO82740, 4837
PRO82741, 4839
PRO82743, 4848
PRO82745, 4851
PRO82746, 4853
PRO82748, 4858
PRO82749, 4860
PRO82750, 4862
PRO82753, 4866
PRO82754, 4868
PRO82755, 4870
PRO82756, 4872
PRO82757, 4874
PRO82758, 4876
PRO82760, 4882
PRO82761, 4884
PRO82762, 4886
PRO82763, 4894
PRO82764, 4896
PRO82768, 4907
PRO82769, 4909
PRO82771, 4914
PRO82774, 4922
PRO82776, 4925
PRO82778, 4930
PRO82779, 4932
PRO82787, 4947
PRO82788, 4949
PRO82790, 4952
PRO82791, 4956
PRO82792, 4959
PRO82793, 4961
PRO82794, 4966
PRO82795, 4968
PRO82796, 4972
PRO82797, 4974
PRO82799, 4979
PRO82800, 4981
PRO82805, 4993
PRO82807, 4997
PRO82812, 5005
PRO82813, 5007
PRO82814, 5009
PRO82816, 5012
PRO82818, 5017
PRO82825, 5029
PRO82828, 5033
PRO82829, 5035
PRO82831, 5038
PRO82833, 5044
PRO82835, 5047
PRO82840, 5059
PRO82841, 5061
PRO82842, 5063

WO 2004/030615

PCT/US2003/028547

PRO82846, 5068
PRO82850, 5077
PRO82851, 5079
PRO82852, 5081
PRO82855, 5085
PRO82856, 5087
PRO82859, 5091
PRO82861, 5099
PRO82862, 5101
PRO82863, 5105
PRO82864, 5107
PRO82867, 5111
PRO82871, 5118
PRO82872, 5121
PRO82873, 5125
PRO82874, 5129
PRO82877, 5136
PRO82879, 5139
PRO82881, 5142
PRO82882, 5144
PRO82884, 5149
PRO82885, 5151
PRO82886, 5153
PRO82887, 5156
PRO82888, 5158
PRO82892, 5167
PRO82893, 5170
PRO82894, 5172
PRO82895, 5174
PRO82897, 5177
PRO82899, 5182
PRO82901, 5185
PRO82902, 5187
PRO82903, 5189
PRO82904, 5191
PRO82905, 5193
PRO82909, 5198
PRO82910, 5204
PRO82912, 5211
PRO82915, 5215
PRO82917, 5220
PRO82920, 5224
PRO82923, 5228
PRO82925, 5231
PRO82930, 5245
PRO82933, 5249
PRO82934, 5253
PRO82935, 5255
PRO82939, 5263
PRO82940, 5265
PRO82943, 5271
PRO82944, 5275
PRO82947, 5287
PRO82948, 5289
PRO82949, 5291
PRO82950, 5293

PRO82952, 5296
PRO82954, 5301
PRO82956, 5304
PRO82957, 5306
PRO82958, 5309
PRO82962, 5318
PRO82963, 5320
PRO82964, 5322
PRO82965, 5324
PRO82967, 5327
PRO82970, 5333
PRO82971, 5335
PRO82975, 5340
PRO82976, 5342
PRO82977, 5344
PRO82978, 5346
PRO82979, 5348
PRO82980, 5351
PRO82982, 5356
PRO82983, 5359
PRO82984, 5363
PRO82985, 5365
PRO82987, 5368
PRO82991, 5373
PRO82992, 5375
PRO82995, 5381
PRO82998, 5386
PRO82999, 5390
PRO83000, 5392
PRO83002, 5397
PRO83004, 5400
PRO83005, 5402
PRO83007, 5405
PRO83008, 5410
PRO83009, 5412
PRO83010, 5414
PRO83011, 5416
PRO83012, 5418
PRO83013, 5420
PRO83014, 5424
PRO83016, 5431
PRO83017, 5433
PRO83018, 5437
PRO83027, 5452
PRO83029, 5455
PRO83030, 5457
PRO83031, 5459
PRO83035, 5464
PRO83037, 5467
PRO83038, 5469
PRO83039, 5471
PRO83040, 5473
PRO83041, 5475
PRO83042, 5481
PRO83050, 5493
PRO83052, 5500

WO 2004/030615

PCT/US2003/028547

PRO83054, 5509
PRO83056, 5520
PRO83059, 5526
PRO83065, 5533
PRO83066, 5535
PRO83068, 5538
PRO83069, 5540
PRO83071, 5545
PRO83072, 5547
PRO83073, 5553
PRO83074, 5555
PRO83075, 5557
PRO83076, 5559
PRO83077, 5561
PRO83078, 5567
PRO83080, 5572
PRO83082, 5579
PRO83083, 5581
PRO83084, 5583
PRO83085, 5585
PRO83086, 5587
PRO83087, 5596
PRO83089, 5599
PRO83090, 5601
PRO83092, 5604
PRO83093, 5606
PRO83095, 5609
PRO83096, 5611
PRO83098, 5614
PRO83099, 5618
PRO83100, 5620
PRO83101, 5622
PRO83102, 5624
PRO83103, 5630
PRO83104, 5632
PRO83105, 5634
PRO83107, 5637
PRO83108, 5643
PRO83109, 5645
PRO83112, 5653
PRO83113, 5657
PRO83114, 5659
PRO83116, 5662
PRO83117, 5664
PRO83118, 5666
PRO83121, 5672
PRO83125, 5684
PRO83128, 5690
PRO83129, 5692
PRO83130, 5694
PRO83132, 5697
PRO83133, 5699
PRO83135, 5702
PRO83137, 5707
PRO83138, 5709
PRO83139, 5711

PRO83141, 5714
PRO83142, 5716
PRO83143, 5718
PRO83144, 5720
PRO83145, 5724
PRO83146, 5726
PRO83149, 5730
PRO83150, 5732
PRO83152, 5737
PRO83153, 5741
PRO83155, 5751
PRO83156, 5753
PRO83157, 5755
PRO83159, 5758
PRO83161, 5764
PRO83163, 5767
PRO83165, 5770
PRO83167, 5777
PRO83169, 5784
PRO83170, 5788
PRO83174, 5797
PRO83175, 5799
PRO83176, 5801
PRO83177, 5803
PRO83178, 5805
PRO83179, 5807
PRO83180, 5812
PRO83182, 5817
PRO83183, 5820
PRO83184, 5822
PRO83185, 5827
PRO83186, 5829
PRO83187, 5833
PRO83188, 5835
PRO83189, 5839
PRO83190, 5841
PRO83191, 5843
PRO83193, 5848
PRO83194, 5850
PRO83195, 5852
PRO83196, 5854
PRO83197, 5856
PRO83198, 5858
PRO83199, 5860
PRO83200, 5862
PRO83201, 5864
PRO83202, 5866
PRO83203, 5868
PRO83204, 5870
PRO83205, 5872
PRO83210, 5884
PRO83211, 5888
PRO83212, 5895
PRO83213, 5899
PRO83214, 5901
PRO83217, 5909

WO 2004/030615

PCT/US2003/028547

PRO83219, 5912
PRO83222, 5916
PRO83223, 5918
PRO83224, 5920
PRO83233, 5932
PRO83234, 5934
PRO83235, 5938
PRO83236, 5942
PRO83237, 5944
PRO83242, 5952
PRO83244, 5955
PRO83245, 5959
PRO83247, 5962
PRO83252, 5970
PRO83253, 5972
PRO83254, 5978
PRO83255, 5980
PRO83256, 5982
PRO83257, 5984
PRO83260, 5988
PRO83261, 5992
PRO83263, 5997
PRO83265, 6002
PRO83266, 6008
PRO83267, 6010
PRO83270, 6016
PRO83271, 6018
PRO83273, 6026
PRO83274, 6033
PRO83275, 6037
PRO83276, 6041
PRO83278, 6044
PRO83279, 6048
PRO83280, 6050
PRO83282, 6053
PRO83283, 6057
PRO83285, 6062
PRO83288, 6067
PRO83289, 6073
PRO83291, 6078
PRO83292, 6084
PRO83293, 6086
PRO83297, 6092
PRO83300, 6096
PRO83301, 6098
PRO83302, 6100
PRO83304, 6107
PRO83306, 6110
PRO83307, 6112
PRO83309, 6115
PRO83310, 6117
PRO83312, 6120
PRO83316, 6129
PRO83319, 6133
PRO83320, 6135
PRO83321, 6137

PRO83323, 6144
PRO83328, 6156
PRO83331, 6162
PRO83332, 6164
PRO83333, 6166
PRO83334, 6168
PRO83335, 6171
PRO83337, 6175
PRO83339, 6178
PRO83340, 6180
PRO83341, 6184
PRO83343, 6193
PRO83344, 6195
PRO83345, 6200
PRO83346, 6202
PRO83349, 6208
PRO83351, 6211
PRO83352, 6213
PRO83353, 6219
PRO83354, 6221
PRO83355, 6223
PRO83360, 6234
PRO83361, 6236
PRO83365, 6247
PRO83366, 6249
PRO83368, 6252
PRO83369, 6254
PRO83372, 6260
PRO83373, 6262
PRO83374, 6264
PRO83375, 6266
PRO83381, 6277
PRO83383, 6283
PRO83385, 6290
PRO83386, 6292
PRO83387, 6294
PRO83388, 6296
PRO83389, 6298
PRO83391, 6301
PRO83392, 6303
PRO83393, 6305
PRO83394, 6307
PRO83395, 6309
PRO83397, 6314
PRO83400, 6324
PRO83403, 6331
PRO83404, 6337
PRO83405, 6347
PRO868, 1871
PRO9112, 3668
PRO9785, 1369
PRO9819, 2676
PRO983, 5825
PRO9886, 706
PRO9902, 2952
PRO9980, 2479

WO 2004/030615

PCT/US2003/028547

PRO9984, 969
PRO9987, 3753

WO 2004/030615

PCT/US2003/028547

Accession Index (to Figure number)

NM_000018, 4669	NM_000484, 5882
NM_000026, 6068	NM_000505, 1828
NM_000029, 624	NM_000508, 1511
NM_000033, 6342	NM_000509, 1515
NM_000034, 4520	NM_000516, 5830
NM_000039, 3376	NM_000517, 4354
NM_000041, 5511	NM_000521, 1627
NM_000070, 4161	NM_000526, 4816
NM_000075, 3683	NM_000532, 1260
NM_000077, 2655	NM_000554, 5480
NM_000079, 898	NM_000558, 4356
NM_000090, 921	NM_000559, 3142
NM_000107, 3208	NM_000569, 505
NM_000114, 5836	NM_000574, 558
NM_000121, 5258	NM_000576, 847
NM_000126, 4267	NM_000582, 1459
NM_000137, 4300	NM_000592, 1957
NM_000143, 636	NM_000598, 2228
NM_000146, 5562	NM_000602, 2361
NM_000154, 4967	NM_000612, 3120
NM_000156, 5122	NM_000638, 4763
NM_000165, 2099	NM_000661, 1425
NM_000177, 2796	NM_000666, 1172
NM_000178, 5738	NM_000687, 5736
NM_000179, 744	NM_000688, 1167
NM_000182, 713	NM_000700, 2695
NM_000183, 711	NM_000701, 312
NM_000184, 3144	NM_000743, 4259
NM_000196, 4547	NM_000754, 5956
NM_000213, 4963	NM_000760, 173
NM_000221, 701	NM_000785, 3687
NM_000224, 3593	NM_000787, 2830
NM_000227, 5040	NM_000795, 3384
NM_000228, 553	NM_000801, 5648
NM_000239, 3729	NM_000852, 3297
NM_000250, 4903	NM_000858, 612
NM_000251, 741	NM_000893, 1327
NM_000268, 5994	NM_000895, 3763
NM_000269, 4889	NM_000930, 2534
NM_000274, 3076	NM_000931, 2536
NM_000284, 6138	NM_000942, 4218
NM_000291, 6230	NM_000954, 2868
NM_000358, 1671	NM_000964, 4820
NM_000365, 3460	NM_000967, 6061
NM_000368, 2806	NM_000969, 284
NM_000385, 2262	NM_000970, 3781
NM_000386, 4843	NM_000971, 2569
NM_000396, 356	NM_000972, 2826
NM_000404, 1089	NM_000973, 2633
NM_000407, 5947	NM_000975, 87
NM_000422, 4807	NM_000976, 2780
NM_000425, 6334	NM_000977, 4633
NM_000447, 594	NM_000978, 4801

WO 2004/030615

PCT/US2003/028547

NM_000979, 5571
NM_000980, 5334
NM_000981, 4798
NM_000982, 3091
NM_000983, 34
NM_000985, 5067
NM_000986, 1206
NM_000987, 4714
NM_000989, 2588
NM_000990, 3155
NM_000991, 5613
NM_000992, 1170
NM_000993, 832
NM_000994, 1064
NM_000997, 1570
NM_000998, 966
NM_001000, 6278
NM_001002, 3827
NM_001003, 4228
NM_001005, 3331
NM_001006, 1506
NM_001007, 6224
NM_001009, 5633
NM_001010, 2651
NM_001011, 643
NM_001012, 210
NM_001016, 2111
NM_001017, 3171
NM_001018, 5126
NM_001020, 5426
NM_001021, 4283
NM_001022, 5468
NM_001023, 2552
NM_001024, 5847
NM_001025, 1632
NM_001026, 2980
NM_001028, 3361
NM_001029, 3656
NM_001030, 440
NM_001034, 651
NM_001038, 3478
NM_001043, 4487
NM_001050, 4841
NM_001064, 1159
NM_001065, 3480
NM_001068, 1079
NM_001069, 2050
NM_001084, 2369
NM_001087, 994
NM_001098, 6079
NM_001101, 2174
NM_001102, 4040
NM_001122, 2649
NM_001134, 1446
NM_001154, 1489
NM_001157, 2990

NM_001168, 4985
NM_001190, 5568
NM_001199, 2495
NM_001207, 1624
NM_001211, 4139
NM_001218, 4203
NM_001235, 3333
NM_001238, 5374
NM_001247, 5703
NM_001255, 194
NM_001262, 229
NM_001273, 3468
NM_001274, 3411
NM_001275, 4065
NM_001283, 2365
NM_001287, 4372
NM_001288, 1969
NM_001293, 3337
NM_001294, 5508
NM_001313, 1396
NM_001319, 5141
NM_001320, 1971
NM_001324, 5814
NM_001325, 6239
NM_001333, 2736
NM_001344, 3984
NM_001350, 1942
NM_001363, 6318
NM_001407, 1132
NM_001415, 6143
NM_001416, 4687
NM_001418, 3163
NM_001428, 31
NM_001436, 5436
NM_001444, 2575
NM_001450, 836
NM_001463, 916
NM_001465, 1573
NM_001467, 3359
NM_001469, 6081
NM_001494, 2891
NM_001500, 2052
NM_001517, 1997
NM_001521, 689
NM_001530, 4016
NM_001536, 5539
NM_001539, 2660
NM_001540, 2308
NM_001553, 1435
NM_001554, 269
NM_001560, 6270
NM_001567, 3322
NM_001568, 2596
NM_001569, 6332
NM_001571, 5542
NM_001605, 4564

WO 2004/030615

PCT/US2003/028547

NM_001607, 1097
NM_001610, 3206
NM_001613, 3008
NM_001622, 1330
NM_001628, 2423
NM_001641, 3997
NM_001644, 3511
NM_001647, 1352
NM_001648, 5590
NM_001659, 3550
NM_001662, 2398
NM_001667, 3284
NM_001673, 2355
NM_001687, 5115
NM_001688, 308
NM_001696, 5941
NM_001697, 5892
NM_001710, 1959
NM_001734, 3452
NM_001743, 5494
NM_001747, 806
NM_001751, 3137
NM_001753, 2391
NM_001757, 5894
NM_001760, 1898
NM_001762, 2274
NM_001780, 3663
NM_001791, 81
NM_001816, 5478
NM_001819, 5679
NM_001827, 2714
NM_001831, 2506
NM_001833, 2689
NM_001842, 2668
NM_001853, 5853
NM_001861, 4614
NM_001862, 827
NM_001878, 392
NM_001907, 4579
NM_001909, 3133
NM_001920, 3740
NM_001930, 5267
NM_001935, 894
NM_001944, 5050
NM_001959, 950
NM_001961, 5178
NM_001964, 1689
NM_001969, 4098
NM_001970, 4697
NM_001975, 3458
NM_001983, 5502
NM_001985, 5593
NM_002003, 2834
NM_002004, 422
NM_002011, 1836
NM_002014, 3439

NM_002015, 3896
NM_002018, 4719
NM_002028, 4010
NM_002046, 3473
NM_002047, 2265
NM_002075, 3463
NM_002079, 3066
NM_002083, 4012
NM_002084, 1704
NM_002085, 5112
NM_002086, 4953
NM_002087, 4845
NM_002106, 1478
NM_002109, 1779
NM_002128, 3887
NM_002129, 1522
NM_002130, 1582
NM_002133, 6020
NM_002137, 2210
NM_002157, 930
NM_002161, 2716
NM_002168, 4293
NM_002178, 3600
NM_002211, 2919
NM_002212, 5742
NM_002229, 5272
NM_002265, 4834
NM_002273, 3591
NM_002274, 4814
NM_002275, 4812
NM_002276, 4810
NM_002295, 1108
NM_002305, 6038
NM_002306, 4022
NM_002339, 3115
NM_002340, 5931
NM_002342, 3476
NM_002345, 3752
NM_002355, 3489
NM_002358, 1485
NM_002364, 6147
NM_002385, 5086
NM_002386, 4626
NM_002388, 1866
NM_002396, 5069
NM_002397, 1646
NM_002401, 4933
NM_002411, 3245
NM_002413, 1494
NM_002414, 6124
NM_002415, 5979
NM_002453, 751
NM_002466, 5774
NM_002468, 1095
NM_002473, 6025
NM_002477, 1368

WO 2004/030615

PCT/US2003/028547

NM.002484, 4416
NM.002486, 2734
NM.002489, 2193
NM.002492, 1297
NM.002512, 4887
NM.002520, 1803
NM.002537, 4210
NM.002539, 659
NM.002567, 3816
NM.002568, 2593
NM.002574, 220
NM.002588, 1728
NM.002606, 5900
NM.002615, 4647
NM.002617, 12
NM.002632, 4052
NM.002634, 4939
NM.002638, 5779
NM.002654, 4242
NM.002660, 5771
NM.002668, 6185
NM.002689, 3289
NM.002691, 5580
NM.002707, 681
NM.002712, 1030
NM.002720, 4518
NM.002727, 2961
NM.002730, 5298
NM.002733, 3555
NM.002766, 4975
NM.002787, 2254
NM.002789, 4261
NM.002792, 5838
NM.002793, 2137
NM.002796, 346
NM.002802, 4059
NM.002803, 2378
NM.002809, 4805
NM.002810, 348
NM.002812, 5401
NM.002813, 3837
NM.002815, 4778
NM.002819, 5102
NM.002827, 5809
NM.002846, 980
NM.002854, 1188
NM.002856, 5515
NM.002857, 481
NM.002863, 4029
NM.002870, 438
NM.002878, 4784
NM.002883, 6075
NM.002887, 1800
NM.002913, 1427
NM.002915, 3891
NM.002921, 3002

NM.002923, 540
NM.002934, 3992
NM.002938, 1386
NM.002946, 127
NM.002947, 2188
NM.002948, 1076
NM.002952, 4382
NM.002954, 749
NM.002961, 369
NM.002965, 364
NM.002979, 235
NM.003002, 3390
NM.003021, 5161
NM.003025, 5188
NM.003055, 2947
NM.003064, 5781
NM.003072, 5254
NM.003076, 3568
NM.003088, 2176
NM.003090, 4320
NM.003091, 5654
NM.003092, 5683
NM.003104, 4187
NM.003107, 2032
NM.003123, 4511
NM.003124, 789
NM.003128, 746
NM.003132, 50
NM.003137, 1916
NM.003143, 2435
NM.003145, 409
NM.003146, 3215
NM.003149, 1099
NM.003169, 5428
NM.003181, 2135
NM.003216, 6077
NM.003283, 5608
NM.003287, 2104
NM.003289, 2680
NM.003290, 5312
NM.003295, 3900
NM.003310, 649
NM.003316, 5896
NM.003334, 6167
NM.003349, 5804
NM.003350, 2546
NM.003365, 1134
NM.003366, 4421
NM.003370, 5499
NM.003374, 1677
NM.003375, 2982
NM.003378, 2367
NM.003389, 2728
NM.003400, 761
NM.003401, 1636
NM.003406, 2590

WO 2004/030615

PCT/US2003/028547

NM_003418, 1250
NM_003453, 3864
NM_003461, 2440
NM_003472, 2034
NM_003516, 459
NM_003564, 474
NM_003598, 5556
NM_003617, 497
NM_003624, 5214
NM_003626, 3316
NM_003646, 3197
NM_003662, 6149
NM_003680, 157
NM_003681, 5905
NM_003685, 5203
NM_003687, 1673
NM_003689, 71
NM_003712, 5093
NM_003714, 1812
NM_003720, 5898
NM_003721, 5360
NM_003722, 1335
NM_003729, 288
NM_003735, 1730
NM_003736, 1732
NM_003739, 2883
NM_003752, 4449
NM_003753, 6027
NM_003755, 5234
NM_003756, 2598
NM_003757, 148
NM_003765, 5288
NM_003766, 4865
NM_003779, 468
NM_003780, 199
NM_003787, 5052
NM_003815, 457
NM_003824, 3313
NM_003836, 4088
NM_003837, 2723
NM_003859, 5811
NM_003876, 4708
NM_003877, 3757
NM_003906, 5933
NM_003908, 5734
NM_003915, 5747
NM_003932, 6070
NM_003937, 881
NM_003938, 5148
NM_003971, 4891
NM_003973, 1110
NM_003979, 3498
NM_004000, 306
NM_004004, 3866
NM_004044, 955
NM_004048, 4178

NM_004053, 1900
NM_004060, 1791
NM_004074, 3264
NM_004084, 2476
NM_004085, 6242
NM_004092, 3099
NM_004111, 3253
NM_004117, 1918
NM_004127, 5008
NM_004134, 1693
NM_004135, 6340
NM_004147, 6011
NM_004152, 5154
NM_004159, 1952
NM_004175, 5983
NM_004176, 4742
NM_004178, 3614
NM_004181, 1430
NM_004182, 6174
NM_004193, 3045
NM_004203, 4402
NM_004208, 6285
NM_004217, 4699
NM_004219, 1795
NM_004240, 5206
NM_004247, 4879
NM_004261, 273
NM_004265, 3249
NM_004309, 5002
NM_004322, 3256
NM_004323, 2662
NM_004324, 5564
NM_004335, 5328
NM_004339, 5921
NM_004341, 692
NM_004345, 1128
NM_004360, 4549
NM_004398, 3392
NM_004401, 48
NM_004404, 1034
NM_004435, 2761
NM_004448, 4796
NM_004461, 5279
NM_004483, 4602
NM_004493, 6190
NM_004509, 1012
NM_004510, 1014
NM_004524, 4960
NM_004539, 5072
NM_004547, 1218
NM_004550, 470
NM_004551, 3199
NM_004555, 4586
NM_004573, 4141
NM_004595, 6140
NM_004596, 5448

WO 2004/030615

PCT/US2003/028547

NM.004599, 6085
NM.004618, 4716
NM.004632, 414
NM.004635, 1155
NM.004636, 1149
NM.004637, 1246
NM.004638, 1979
NM.004639, 1973
NM.004640, 1986
NM.004673, 529
NM.004691, 4545
NM.004697, 2751
NM.004699, 6323
NM.004701, 4197
NM.004704, 1182
NM.004706, 5470
NM.004714, 5434
NM.004725, 3093
NM.004728, 2959
NM.004735, 1026
NM.004738, 5824
NM.004739, 3230
NM.004766, 1270
NM.004767, 576
NM.004772, 1650
NM.004781, 44
NM.004794, 6287
NM.004813, 3190
NM.004821, 1787
NM.004844, 1066
NM.004846, 998
NM.004859, 4921
NM.004870, 4689
NM.004889, 2342
NM.004893, 1685
NM.004905, 511
NM.004911, 2442
NM.004928, 5915
NM.004930, 69
NM.004933, 4638
NM.004939, 662
NM.004957, 2775
NM.004960, 4465
NM.004964, 150
NM.004973, 2039
NM.004982, 3526
NM.004990, 3669
NM.004992, 6330
NM.004994, 5791
NM.004995, 3976
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NM.005002, 3448
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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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NM_032023, 2923

WO 2004/030615

PCT/US2003/028547

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NM.032292, 412
NM.032299, 3395
NM.032313, 1437
NM.032322, 4771
NM.032323, 402
NM.032324, 630
NM.032330, 4485
NM.032331, 1318
NM.032333, 2996
NM.032338, 3712
NM.032342, 2746
NM.032343, 1235
NM.032350, 2163
NM.032361, 1814
NM.032376, 4854
NM.032377, 5262
NM.032379, 3346
NM.032383, 1280
NM.032390, 875
NM.032402, 1776
NM.032403, 1774
NM.032486, 4444
NM.032527, 5869
NM.032565, 3914
NM.032626, 4440
NM.032627, 5345
NM.032635, 5393
NM.032636, 296
NM.032637, 1577
NM.032642, 3434
NM.032656, 3851
NM.032667, 3240
NM.032712, 5588
NM.032726, 990
NM.032737, 5157
NM.032738, 503
NM.032747, 3061
NM.032750, 1174
NM.032753, 5173

NM.032756, 222
NM.032792, 5631
NM.032799, 2763
NM.032814, 3812
NM.032822, 785
NM.032827, 810
NM.032864, 245
NM.032871, 3326
NM.032872, 122
NM.032873, 3415
NM.032890, 606
NM.032904, 3794
NM.032905, 2893
NM.032907, 4248
NM.032928, 2860
NM.032929, 2081
NM.032933, 5037
NM.032951, 2284
NM.032953, 2286
NM.032958, 2376
NM.032989, 3258
NM.032997, 2949
NM.032999, 2295
NM.033008, 1176
NM.033010, 1178
NM.033011, 2538
NM.033022, 2978
NM.033046, 796
NM.033070, 5937
NM.033161, 2828
NM.033197, 5729
NM.033219, 2730
NM.033251, 4635
NM.033296, 1404
NM.033301, 2635
NM.033316, 1348
NM.033363, 5417
NM.033410, 4456
NM.033415, 5355
NM.033416, 878
NM.033421, 5787
NM.033440, 60
NM.033534, 15
NM.033544, 4315
NM.033551, 1785
NM.052837, 426
NM.052848, 5451
NM.052859, 1157
NM.052862, 488
NM.052881, 5656
NM.052886, 2602
NM.052936, 6251
NM.052963, 2616
NM.052984, 3685
NM.053043, 2462
NM.053056, 3311

WO 2004/030615

PCT/US2003/028547

NM_053275, 3829
NM_054012, 2822
NM_054013, 1848
NM_054014, 5650
NM_054016, 95
NM_057089, 2363
NM_057161, 1890
NM_057169, 3790
NM_057174, 3188
NM_057182, 5376
NM_058164, 5230
NM_058179, 2703
NM_058192, 4366
NM_058193, 3422
NM_058195, 2653
NM_058196, 2657
NM_058199, 2836
NM_078467, 1912
NM_079423, 3648
NM_079425, 3650
NM_080424, 1016
NM_080425, 5828
NM_080426, 5832
NM_080491, 3342
NM_080592, 696
NM_080594, 4394
NM_080598, 1984
NM_080648, 3999
NM_080649, 4001
NM_080670, 1726
NM_080686, 1981
NM_080687, 3942
NM_080702, 1977
NM_080703, 1975
NM_080796, 5855
NM_080797, 5859
NM_080820, 5693
NM_080822, 4654
NM_106552, 670
NM_130398, 639
NM_130442, 2260
NM_130468, 4143
NM_130898, 434
NM_133330, 1376
NM_133332, 1380
NM_133373, 4885
NM_133375, 4222
NM_133436, 2357
NM_133480, 1051
NM_133481, 1053
NM_133483, 3676
NM_133503, 3742
NM_133504, 3744
NM_133505, 3746
NM_133506, 3750
NM_133507, 3748

NM_133627, 4786
NM_133629, 4790
NM_133630, 4788
NM_133637, 798
NM_133645, 2066
NM_134269, 6009
NM_134323, 3616
NM_134324, 3618
NM_134440, 5358
NM_138385, 1372
NM_138391, 545
NM_138427, 4739
NM_138434, 2451
NM_138443, 5060
NM_138483, 1037
NM_138578, 5713
NM_138614, 1125
NM_138699, 1406
NM_138801, 727
NM_138924, 5124

XM_001289, 524
XM_001299, 33
XM_001389, 1453
XM_001468, 342
XM_001472, 250
XM_001482, 3658
XM_001589, 24
XM_001616, 101
XM_001640, 126
XM_001807, 135
XM_001812, 134
XM_001826, 78
XM_001897, 486
XM_001914, 567
XM_001916, 568
XM_001958, 599
XM_002068, 523
XM_002105, 141
XM_002114, 113
XM_002217, 845
XM_002255, 1361
XM_002435, 700
XM_002447, 877
XM_002480, 680
XM_002540, 1006
XM_002611, 823
XM_002636, 964
XM_002647, 770
XM_002669, 946
XM_002674, 776
XM_002704, 853
XM_002727, 788
XM_002739, 779
XM_002742, 1036
XM_002828, 1143
XM_002854, 1187

WO 2004/030615

PCT/US2003/028547

XM.002855, 1186
XM.002859, 1274
XM.002899, 1127
XM.003213, 1162
XM.003222, 1119
XM.003245, 1136
XM.003305, 1451
XM.003435, 1432
XM.003477, 1530
XM.003511, 1448
XM.003555, 1500
XM.003611, 2083
XM.003716, 1811
XM.003771, 1644
XM.003789, 1712
XM.003825, 1540
XM.003830, 1666
XM.003841, 1699
XM.003869, 1572
XM.003896, 1581
XM.003937, 1710
XM.004009, 1565
XM.004098, 3704
XM.004151, 2065
XM.004256, 2114
XM.004297, 2113
XM.004330, 3194
XM.004379, 2122
XM.004383, 2130
XM.004526, 2110
XM.004627, 2402
XM.004901, 2292
XM.005060, 2605
XM.005086, 1042
XM.005100, 2908
XM.005180, 1332
XM.005305, 2485
XM.005348, 2755
XM.005365, 2760
XM.005490, 2707
XM.005525, 2727
XM.005543, 2666
XM.005675, 3103
XM.005698, 3053
XM.005724, 2878
XM.005938, 3058
XM.005969, 3088
XM.006139, 3127
XM.006170, 3201
XM.006212, 3167
XM.006290, 98
XM.006297, 3196
XM.006424, 3151
XM.006432, 3371
XM.006464, 3355
XM.006467, 3399

XM.006475, 3135
XM.006483, 3136
XM.006529, 3281
XM.006533, 3270
XM.006566, 3849
XM.006578, 3736
XM.006589, 3766
XM.006595, 3835
XM.006694, 3535
XM.006710, 3626
XM.006748, 3536
XM.006826, 3559
XM.006887, 3765
XM.006925, 3485
XM.006936, 3483
XM.006937, 5074
XM.006947, 3482
XM.006958, 3475
XM.007002, 3797
XM.007003, 3796
XM.007199, 3923
XM.007254, 4097
XM.007272, 4081
XM.007288, 3968
XM.007293, 3967
XM.007315, 3958
XM.007316, 3957
XM.007324, 4027
XM.007328, 4024
XM.007441, 4045
XM.007483, 4072
XM.007488, 4005
XM.007491, 3996
XM.007531, 4167
XM.007545, 4156
XM.007623, 4221
XM.007651, 4189
XM.007751, 4129
XM.007963, 4474
XM.007988, 4430
XM.008064, 4509
XM.008065, 4497
XM.008106, 4463
XM.008126, 4353
XM.008150, 4800
XM.008231, 4694
XM.008253, 4926
XM.008323, 4750
XM.008334, 4671
XM.008351, 4856
XM.008401, 4867
XM.008402, 4869
XM.008432, 4902
XM.008441, 4686
XM.008459, 4915
XM.008462, 4777

WO 2004/030615

PCT/US2003/028547

XM.008486, 4760
XM.008509, 4658
XM.008538, 4684
XM.008557, 4650
XM.008579, 4809
XM.008679, 4693
XM.008695, 5089
XM.008723, 5054
XM.008812, 5083
XM.008830, 5597
XM.008851, 5522
XM.008854, 5325
XM.008860, 5485
XM.008878, 5472
XM.008887, 5243
XM.008912, 5453
XM.008985, 5531
XM.009010, 5205
XM.009036, 5486
XM.009063, 5274
XM.009082, 5256
XM.009125, 5484
XM.009126, 5496
XM.009149, 5406
XM.009180, 5378
XM.009203, 5443
XM.009222, 5165
XM.009277, 5113
XM.009279, 5110
XM.009293, 5338
XM.009303, 5310
XM.009330, 5357
XM.009338, 5384
XM.009436, 5705
XM.009450, 5728
XM.009501, 5754
XM.009549, 5816
XM.009622, 5647
XM.009642, 5759
XM.009671, 5823
XM.009672, 5821
XM.009686, 5762
XM.009805, 5919
XM.009947, 6022
XM.009967, 6031
XM.009973, 6042
XM.010000, 6063
XM.010002, 6064
XM.010024, 6087
XM.010029, 6094
XM.010040, 6103
XM.010055, 6108
XM.010117, 6269
XM.010141, 6216
XM.010156, 5266
XM.010178, 6310

XM.010272, 6132
XM.010362, 6274
XM.010378, 6169
XM.010436, 6280
XM.010494, 3429
XM.010615, 253
XM.010636, 451
XM.010664, 133
XM.010682, 581
XM.010712, 182
XM.010732, 593
XM.010778, 925
XM.010852, 938
XM.010858, 1004
XM.010866, 992
XM.010881, 771
XM.010886, 755
XM.010938, 4641
XM.010941, 1433
XM.010953, 1130
XM.010978, 1290
XM.011074, 1320
XM.011089, 5076
XM.011117, 2059
XM.011118, 4941
XM.011129, 1423
XM.011160, 1365
XM.011548, 2411
XM.011618, 2400
XM.011629, 2533
XM.011642, 2586
XM.011650, 66
XM.011657, 2592
XM.011749, 2798
XM.011752, 2786
XM.011769, 2562
XM.011778, 2832
XM.011988, 3260
XM.012124, 3836
XM.012145, 3761
XM.012159, 3494
XM.012162, 3598
XM.012179, 5337
XM.012182, 3638
XM.012184, 3861
XM.012219, 3759
XM.012272, 3543
XM.012284, 2395
XM.012376, 3990
XM.012377, 3983
XM.012398, 4133
XM.012418, 4199
XM.012462, 4322
XM.012487, 4555
XM.012549, 4734
XM.012569, 4461

WO 2004/030615

PCT/US2003/028547

XM.012609, 4945
XM.012615, 4744
XM.012634, 4950
XM.012638, 3874
XM.012642, 4849
XM.012651, 4916
XM.012676, 4675
XM.012741, 5031
XM.012798, 5212
XM.012812, 5370
XM.012860, 5439
XM.012862, 5195
XM.012913, 5114
XM.012931, 5768
XM.012970, 5700
XM.013010, 6066
XM.013015, 6089
XM.013029, 6118
XM.013042, 6207
XM.013060, 6196
XM.013086, 6145
XM.013112, 2530
XM.013127, 2577
XM.015234, 75
XM.015241, 5088
XM.015243, 3148
XM.015258, 2244
XM.015366, 4239
XM.015434, 547
XM.015462, 1208
XM.015468, 3596
XM.015476, 3585
XM.015481, 3580
XM.015516, 6206
XM.015563, 1525
XM.015652, 2937
XM.015697, 5264
XM.015700, 4478
XM.015705, 3214
XM.015717, 257
XM.015755, 5046
XM.015769, 5369
XM.015835, 4311
XM.015840, 3921
XM.015842, 3932
XM.015920, 909
XM.015922, 911
XM.016047, 2604
XM.016076, 4237
XM.016093, 2992
XM.016113, 2712
XM.016125, 6275
XM.016139, 3170
XM.016164, 276
XM.016170, 1554
XM.016199, 600

XM.016288, 880
XM.016308, 2726
XM.016334, 1294
XM.016345, 1799
XM.016351, 3924
XM.016378, 5364
XM.016382, 5036
XM.016410, 5438
XM.016480, 326
XM.016486, 4071
XM.016487, 4068
XM.016605, 3708
XM.016625, 773
XM.016640, 3538
XM.016674, 1652
XM.016700, 2433
XM.016713, 4165
XM.016733, 2256
XM.016843, 766
XM.016857, 1941
XM.016871, 5180
XM.016985, 4213
XM.017080, 3436
XM.017096, 4644
XM.017204, 5240
XM.017234, 4712
XM.017240, 4135
XM.017315, 67
XM.017356, 1291
XM.017364, 1105
XM.017369, 3394
XM.017432, 3895
XM.017442, 2313
XM.017474, 1679
XM.017483, 2280
XM.017508, 3710
XM.017517, 2080
XM.017578, 4980
XM.017591, 1701
XM.017641, 1544
XM.017698, 861
XM.017816, 2581
XM.017831, 2119
XM.017846, 109
XM.017857, 1640
XM.017914, 3953
XM.017925, 1476
XM.017930, 6284
XM.017931, 2659
XM.017971, 4319
XM.017984, 4338
XM.017996, 2711
XM.018006, 2710
XM.018019, 6157
XM.018039, 784
XM.018041, 642

WO 2004/030615

PCT/US2003/028547

XM.018054, 4123
XM.018088, 4472
XM.018108, 6313
XM.018109, 6315
XM.018136, 161
XM.018142, 6232
XM.018149, 1264
XM.018167, 3015
XM.018182, 2098
XM.018205, 64
XM.018241, 6161
XM.018279, 3057
XM.018287, 2595
XM.018301, 763
XM.018332, 314
XM.018359, 2281
XM.018399, 3918
XM.018432, 4331
XM.018473, 1658
XM.018515, 5354
XM.018523, 1359
XM.018534, 4840
XM.018539, 6014
XM.018540, 841
XM.026944, 2787
XM.026951, 2771
XM.026968, 2769
XM.026985, 2766
XM.026987, 2765
XM.027102, 3802
XM.027143, 6106
XM.027161, 1220
XM.027214, 2385
XM.027309, 4329
XM.027313, 226
XM.027365, 4334
XM.027412, 4368
XM.027440, 2505
XM.027558, 4352
XM.027651, 2490
XM.027679, 2488
XM.027825, 4661
XM.027904, 5548
XM.027916, 76
XM.027952, 6353
XM.027963, 936
XM.027964, 1619
XM.027983, 213
XM.028034, 940
XM.028064, 5119
XM.028067, 5117
XM.028151, 4562
XM.028192, 3117
XM.028263, 5488
XM.028267, 5491
XM.028322, 4075

XM.028347, 4074
XM.028358, 4073
XM.028398, 4667
XM.028417, 4678
XM.028643, 3624
XM.028662, 3561
XM.028666, 5383
XM.028672, 5382
XM.028744, 5025
XM.028760, 3554
XM.028783, 5851
XM.028806, 5765
XM.028810, 5766
XM.028834, 5863
XM.028848, 4390
XM.028918, 5867
XM.028966, 5871
XM.029031, 169
XM.029096, 1539
XM.029104, 1314
XM.029132, 1313
XM.029136, 1310
XM.029168, 2841
XM.029187, 6194
XM.029228, 2069
XM.029288, 4067
XM.029369, 1198
XM.029438, 4656
XM.029450, 5404
XM.029455, 5403
XM.029461, 6282
XM.029567, 2609
XM.029631, 3602
XM.029728, 3595
XM.029746, 2128
XM.029805, 3507
XM.029810, 5776
XM.029822, 5778
XM.029842, 176
XM.029844, 145
XM.030044, 5796
XM.030203, 1028
XM.030268, 2543
XM.030274, 2544
XM.030326, 3187
XM.030373, 6233
XM.030417, 1112
XM.030423, 154
XM.030447, 3065
XM.030470, 68
XM.030485, 5159
XM.030529, 862
XM.030582, 883
XM.030621, 5818
XM.030699, 5834
XM.030714, 5145

WO 2004/030615

PCT/US2003/028547

XM.030720, 5137
XM.030721, 5135
XM.030771, 1821
XM.030777, 1823
XM.030782, 1824
XM.030812, 1256
XM.030834, 952
XM.030895, 5465
XM.030901, 5456
XM.030914, 5450
XM.030920, 40
XM.031025, 4032
XM.031074, 4039
XM.031251, 5307
XM.031263, 5305
XM.031273, 5303
XM.031276, 5302
XM.031292, 4295
XM.031320, 1445
XM.031345, 5292
XM.031354, 4292
XM.031404, 4285
XM.031415, 4767
XM.031427, 4769
XM.031466, 4765
XM.031515, 4147
XM.031519, 731
XM.031527, 733
XM.031536, 4758
XM.031554, 4145
XM.031585, 782
XM.031586, 783
XM.031596, 780
XM.031617, 4138
XM.031626, 738
XM.031718, 4159
XM.031807, 3491
XM.031857, 5184
XM.031866, 3041
XM.031890, 3044
XM.031917, 5176
XM.031944, 5066
XM.031949, 3049
XM.031992, 3059
XM.032020, 5281
XM.032121, 2455
XM.032201, 4836
XM.032216, 2454
XM.032269, 1221
XM.032285, 5399
XM.032391, 216
XM.032403, 4180
XM.032443, 3930
XM.032476, 2976
XM.032520, 2970
XM.032553, 1626

XM.032588, 3457
XM.032614, 3462
XM.032710, 5247
XM.032719, 5248
XM.032724, 5252
XM.032759, 1700
XM.032766, 4864
XM.032774, 5257
XM.032782, 5261
XM.032813, 4863
XM.032817, 4861
XM.032852, 4857
XM.032895, 1590
XM.032902, 1588
XM.032930, 6189
XM.032944, 2470
XM.032996, 5943
XM.033015, 5902
XM.033016, 5903
XM.033090, 5946
XM.033147, 6241
XM.033227, 3450
XM.033232, 6351
XM.033251, 3959
XM.033263, 3472
XM.033294, 1123
XM.033337, 3964
XM.033355, 2819
XM.033359, 2818
XM.033360, 2817
XM.033361, 2815
XM.033362, 2811
XM.033380, 2809
XM.033385, 2808
XM.033391, 3969
XM.033424, 2774
XM.033435, 3975
XM.033445, 3980
XM.033457, 2777
XM.033460, 2778
XM.033553, 3991
XM.033595, 3994
XM.033654, 79
XM.033683, 77
XM.033689, 4646
XM.033714, 4645
XM.033813, 5960
XM.033862, 6173
XM.033876, 2383
XM.033878, 6172
XM.033884, 6170
XM.033910, 2134
XM.033912, 2132
XM.033922, 4606
XM.034000, 501
XM.034082, 454

WO 2004/030615

PCT/US2003/028547

XM_034321, 1502
XM_034375, 4460
XM_034377, 5623
XM_034431, 3185
XM_034586, 4376
XM_034590, 4380
XM_034640, 2638
XM_034662, 319
XM_034671, 318
XM_034710, 1466
XM_034713, 1468
XM_034744, 1655
XM_034862, 1675
XM_034890, 4184
XM_034897, 4256
XM_034935, 6201
XM_034952, 857
XM_034953, 4116
XM_035014, 4119
XM_035103, 2824
XM_035107, 2439
XM_035109, 2825
XM_035220, 800
XM_035368, 2626
XM_035370, 2631
XM_035373, 2629
XM_035465, 6123
XM_035485, 3571
XM_035490, 3564
XM_035497, 3562
XM_035572, 1392
XM_035625, 5197
XM_035627, 5196
XM_035636, 5194
XM_035638, 5192
XM_035640, 5034
XM_035662, 2483
XM_035680, 2482
XM_035824, 1402
XM_035919, 5612
XM_035986, 1456
XM_035999, 5907
XM_036002, 1440
XM_036011, 5910
XM_036042, 5913
XM_036087, 5917
XM_036104, 4965
XM_036107, 5923
XM_036115, 4971
XM_036118, 1262
XM_036175, 5924
XM_036299, 155
XM_036339, 3178
XM_036413, 2469
XM_036450, 664
XM_036462, 4827

XM_036465, 4825
XM_036500, 573
XM_036507, 575
XM_036528, 4410
XM_036556, 566
XM_036593, 2939
XM_036659, 4707
XM_036680, 4342
XM_036727, 4134
XM_036744, 433
XM_036755, 5927
XM_036785, 4982
XM_036829, 442
XM_036845, 450
XM_036934, 448
XM_036937, 5969
XM_036938, 1197
XM_037002, 1668
XM_037056, 2107
XM_037101, 873
XM_037108, 831
XM_037147, 3212
XM_037173, 3202
XM_037195, 4988
XM_037196, 4987
XM_037202, 5840
XM_037206, 5842
XM_037217, 5846
XM_037260, 1608
XM_037329, 591
XM_037377, 1300
XM_037381, 1299
XM_037423, 1163
XM_037468, 6114
XM_037474, 6116
XM_037565, 5106
XM_037572, 5109
XM_037600, 1304
XM_037657, 2608
XM_037662, 5372
XM_037682, 5977
XM_037741, 2276
XM_037778, 4244
XM_037797, 5981
XM_037808, 3263
XM_037875, 2045
XM_037945, 5993
XM_037971, 4897
XM_038030, 2855
XM_038049, 2864
XM_038063, 2866
XM_038098, 5343
XM_038146, 5339
XM_038221, 1695
XM_038243, 1341
XM_038308, 3737

WO 2004/030615

PCT/US2003/028547

XM.038371, 3902
XM.038391, 2757
XM.038424, 5018
XM.038536, 2909
XM.038576, 734
XM.038584, 6019
XM.038659, 3533
XM.038791, 3841
XM.038852, 244
XM.038872, 5062
XM.038911, 237
XM.038946, 1840
XM.039165, 1413
XM.039173, 1416
XM.039176, 1417
XM.039225, 4125
XM.039236, 6047
XM.039248, 6051
XM.039306, 4551
XM.039339, 6060
XM.039372, 6065
XM.039395, 3732
XM.039474, 4794
XM.039654, 2646
XM.039702, 4200
XM.039712, 716
XM.039721, 321
XM.039723, 5140
XM.039796, 1292
XM.039805, 1258
XM.039908, 5598
XM.039910, 4721
XM.039921, 4732
XM.039952, 1213
XM.039975, 1783
XM.040009, 377
XM.040066, 6088
XM.040095, 6091
XM.040221, 3707
XM.040267, 2879
XM.040272, 2876
XM.040321, 1524
XM.040498, 2417
XM.040623, 2074
XM.040644, 3734
XM.040709, 315
XM.040752, 1493
XM.040853, 2218
XM.040898, 4100
XM.040942, 4094
XM.040952, 4090
XM.041014, 4086
XM.041020, 2697
XM.041059, 1670
XM.041100, 3503
XM.041209, 3925

XM.041211, 1161
XM.041221, 1410
XM.041235, 4008
XM.041248, 6111
XM.041473, 3928
XM.041484, 3944
XM.041507, 1147
XM.041583, 4957
XM.041678, 5027
XM.041694, 1614
XM.041712, 1592
XM.041872, 5090
XM.041879, 353
XM.041884, 354
XM.041921, 6304
XM.041964, 4680
XM.042018, 5095
XM.042025, 1600
XM.042153, 6348
XM.042155, 6346
XM.042168, 1286
XM.042301, 1474
XM.042326, 1032
XM.042422, 2145
XM.042473, 2148
XM.042618, 1229
XM.042621, 4596
XM.042658, 2561
XM.042695, 1364
XM.042698, 4710
XM.042765, 5701
XM.042781, 2434
XM.042788, 2744
XM.042841, 1072
XM.042852, 3339
XM.042860, 1070
XM.042963, 6295
XM.042967, 537
XM.042968, 6297
XM.043047, 4577
XM.043173, 866
XM.043220, 3111
XM.043340, 1805
XM.043388, 1808
XM.043589, 2998
XM.043605, 2999
XM.043614, 6099
XM.043643, 6250
XM.043771, 1568
XM.044075, 416
XM.044077, 391
XM.044127, 398
XM.044128, 408
XM.044166, 406
XM.044172, 411
XM.044334, 3859

WO 2004/030615

PCT/US2003/028547

XM.044354, 2968
XM.044367, 4938
XM.044372, 4943
XM.044376, 4935
XM.044394, 4927
XM.044426, 4924
XM.044523, 4304
XM.044533, 4307
XM.044565, 4269
XM.044569, 4272
XM.044593, 4278
XM.044608, 5213
XM.044619, 5210
XM.044627, 2563
XM.044866, 2139
XM.044914, 5658
XM.044915, 5660
XM.044932, 3129
XM.044957, 3131
XM.045010, 3821
XM.045044, 4749
XM.045104, 4989
XM.045140, 2973
XM.045151, 5226
XM.045170, 928
XM.045183, 4651
XM.045187, 3833
XM.045283, 757
XM.045290, 1214
XM.045296, 2759
XM.045401, 2403
XM.045418, 5667
XM.045451, 5671
XM.045460, 5674
XM.045499, 3276
XM.045525, 3278
XM.045535, 4751
XM.045551, 4752
XM.045581, 4996
XM.045602, 3856
XM.045612, 3273
XM.045613, 3271
XM.045642, 3269
XM.045667, 3074
XM.045681, 4287
XM.045750, 3157
XM.045802, 3826
XM.045856, 2407
XM.045901, 4852
XM.045952, 2413
XM.045963, 3834
XM.046001, 2414
XM.046035, 4453
XM.046041, 3726
XM.046057, 1443
XM.046090, 5423

XM.046160, 5708
XM.046179, 5710
XM.046313, 5544
XM.046349, 187
XM.046401, 1085
XM.046419, 5578
XM.046450, 201
XM.046464, 522
XM.046472, 5004
XM.046481, 4999
XM.046520, 5689
XM.046551, 212
XM.046557, 208
XM.046565, 204
XM.046642, 3951
XM.046648, 3950
XM.046651, 3949
XM.046743, 3035
XM.046765, 5020
XM.046767, 5022
XM.046769, 5021
XM.046822, 5150
XM.046836, 2722
XM.046863, 2720
XM.046918, 112
XM.046932, 4958
XM.046934, 5160
XM.047007, 5723
XM.047011, 5725
XM.047018, 5727
XM.047024, 6177
XM.047032, 6176
XM.047083, 2521
XM.047175, 690
XM.047374, 5446
XM.047376, 5445
XM.047409, 5444
XM.047436, 4624
XM.047477, 1429
XM.047479, 495
XM.047499, 610
XM.047525, 4632
XM.047545, 616
XM.047561, 1137
XM.047584, 5131
XM.047600, 5132
XM.047964, 1798
XM.048088, 753
XM.048119, 4344
XM.048258, 5385
XM.048286, 3255
XM.048351, 5218
XM.048364, 5219
XM.048404, 6329
XM.048410, 6328
XM.048420, 6325

WO 2004/030615

PCT/US2003/028547

XM_048471, 5082
XM_048479, 2679
XM_048518, 2684
XM_048539, 2686
XM_048603, 3674
XM_048654, 4829
XM_048690, 1007
XM_048780, 57
XM_048859, 2881
XM_048905, 6306
XM_048943, 3640
XM_048957, 3931
XM_048991, 3642
XM_049048, 3652
XM_049108, 820
XM_049113, 822
XM_049116, 818
XM_049141, 3586
XM_049148, 3581
XM_049150, 3659
XM_049197, 3161
XM_049201, 3772
XM_049211, 3771
XM_049226, 2623
XM_049237, 5391
XM_049247, 2618
XM_049282, 5223
XM_049310, 139
XM_049337, 6320
XM_049354, 4275
XM_049372, 4317
XM_049421, 2637
XM_049502, 5236
XM_049561, 5239
XM_049663, 3493
XM_049680, 476
XM_049690, 483
XM_049742, 14
XM_049795, 3082
XM_049899, 2121
XM_049904, 3937
XM_049920, 5482
XM_049931, 4995
XM_049934, 4994
XM_049937, 4818
XM_050074, 3528
XM_050101, 4773
XM_050159, 4880
XM_050194, 4462
XM_050200, 1487
XM_050215, 2525
XM_050236, 5602
XM_050265, 2278
XM_050278, 4103
XM_050293, 2487
XM_050403, 6192

XM_050430, 2389
XM_050435, 5227
XM_050506, 2583
XM_050534, 4348
XM_050552, 1234
XM_050589, 5603
XM_050638, 979
XM_050660, 5330
XM_050731, 2571
XM_050891, 984
XM_050962, 975
XM_050964, 4220
XM_051219, 4479
XM_051264, 1237
XM_051298, 2612
XM_051364, 5290
XM_051430, 3398
XM_051435, 3358
XM_051463, 4230
XM_051471, 6238
XM_051476, 6237
XM_051489, 3367
XM_051518, 1131
XM_051556, 6
XM_051586, 5092
XM_051712, 4025
XM_051716, 3373
XM_051763, 4727
XM_051778, 4600
XM_051860, 4298
XM_051877, 515
XM_052113, 3378
XM_052310, 1060
XM_052313, 1535
XM_052336, 1477
XM_052460, 3714
XM_052474, 3719
XM_052530, 1424
XM_052542, 3755
XM_052626, 1398
XM_052635, 5166
XM_052641, 3769
XM_052661, 5168
XM_052721, 2056
XM_052725, 2784
XM_052786, 3153
XM_052862, 3404
XM_052893, 3825
XM_052974, 608
XM_052989, 817
XM_053074, 5430
XM_053122, 1363
XM_053164, 3641
XM_053183, 58
XM_053206, 2875
XM_053245, 400

WO 2004/030615

PCT/US2003/028547

XM.053323, 1078
XM.053585, 4252
XM.053633, 544
XM.053712, 1074
XM.053717, 4663
XM.053787, 3283
XM.053796, 3288
XM.053952, 3722
XM.053955, 1859
XM.054038, 4832
XM.054098, 6183
XM.054221, 6155
XM.054344, 4973
XM.054474, 2933
XM.054475, 2935
XM.054520, 1047
XM.054566, 5926
XM.054706, 2146
XM.054752, 2849
XM.054763, 2852
XM.054856, 3193
XM.054868, 228
XM.054900, 4309
XM.054978, 295
XM.055013, 3853
XM.055061, 4826
XM.055132, 4514
XM.055195, 4427
XM.055199, 4942
XM.055230, 5336
XM.055254, 954
XM.055369, 3397
XM.055481, 251
XM.055551, 1461
XM.055573, 3086
XM.055641, 2064
XM.055658, 5592
XM.055686, 5163
XM.055771, 4505
XM.055859, 5483
XM.055880, 583
XM.055993, 5646
XM.056035, 5678
XM.056082, 4648
XM.056260, 4438
XM.056286, 5582
XM.056315, 1723
XM.056317, 4077
XM.056346, 3645
XM.056353, 3662
XM.056421, 5175
XM.056481, 3545
XM.056602, 5408
XM.056681, 3700
XM.056730, 4775
XM.056884, 618

XM.056923, 521
XM.056957, 1471
XM.056963, 1793
XM.056970, 628
XM.056996, 3798
XM.057020, 4257
XM.057074, 5260
XM.057150, 4619
XM.057236, 5756
XM.057374, 5793
XM.057492, 1548
XM.057664, 740
XM.057780, 2557
XM.057994, 1541
XM.058039, 1934
XM.058098, 986
XM.058116, 4526
XM.058125, 5635
XM.058210, 4018
XM.058232, 5225
XM.058240, 102
XM.058247, 466
XM.058266, 2144
XM.058267, 1278
XM.058343, 3020
XM.058361, 3078
XM.058405, 552
XM.058406, 3084
XM.058414, 3159
XM.058450, 3352
XM.058505, 3125
XM.058528, 3671
XM.058556, 3773
XM.058567, 3504
XM.058574, 3454
XM.058602, 3022
XM.058611, 3926
XM.058618, 4091
XM.058636, 4118
XM.058646, 3986
XM.058647, 3978
XM.058677, 4061
XM.058684, 4186
XM.058699, 4250
XM.058702, 294
XM.058739, 4621
XM.058745, 4543
XM.058784, 4404
XM.058796, 4337
XM.058830, 4803
XM.058867, 4755
XM.058900, 4730
XM.058918, 5949
XM.058927, 1441
XM.058949, 5463
XM.058967, 5295

WO 2004/030615

PCT/US2003/028547

XM.058968, 2619
XM.058977, 3920
XM.058987, 5570
XM.058990, 5584
XM.058991, 5552
XM.059045, 5419
XM.059052, 5447
XM.059066, 114
XM.059067, 120
XM.059088, 130
XM.059094, 465
XM.059117, 103
XM.059120, 562
XM.059133, 224
XM.059171, 171
XM.059180, 256
XM.059191, 492
XM.059201, 1
XM.059210, 330
XM.059214, 185
XM.059230, 55
XM.059268, 5675
XM.059321, 5607
XM.059335, 6013
XM.059351, 920
XM.059368, 653
XM.059372, 1029
XM.059422, 968
XM.059461, 971
XM.059465, 907
XM.059516, 1266
XM.059557, 1068
XM.059561, 1059
XM.059583, 1252
XM.059593, 1434
XM.059623, 1519
XM.059628, 1442
XM.059633, 1469
XM.059637, 2804
XM.059653, 1596
XM.059669, 1617
XM.059709, 1604
XM.059720, 2914
XM.059741, 2118
XM.059745, 2131
XM.059773, 2141
XM.059776, 2062
XM.059801, 1939
XM.059839, 2430
XM.059876, 2282
XM.059933, 2531
XM.059945, 2838
XM.059961, 2859
XM.059966, 2871
XM.059979, 2644
XM.059986, 2813

XM.059998, 2673
XM.060006, 2647
XM.060012, 4115
XM.060030, 6146
XM.060042, 4281
XM.060067, 1499
XM.060331, 509
XM.060517, 531
XM.060976, 2885
XM.061125, 2931
XM.061126, 2930
XM.062437, 3775
XM.063639, 4234
XM.064091, 4597
XM.065884, 777
XM.066291, 5998
XM.066900, 6261
XM.067264, 1240
XM.067325, 5030
XM.067715, 1169
XM.068164, 1497
XM.068395, 1789
XM.068853, 1714
XM.068919, 2085
XM.068963, 2072
XM.070188, 2480
XM.070203, 2473
XM.070873, 2742
XM.071178, 2705
XM.071580, 1557
XM.071605, 2381
XM.071623, 1439
XM.071801, 4122
XM.071873, 4630
XM.071937, 2152
XM.072173, 5876
XM.072430, 2387
XM.072526, 2857
XM.076414, 1199
XM.083842, 3026
XM.083852, 3141
XM.083864, 3774
XM.083866, 3715
XM.083868, 3590
XM.083892, 3787
XM.083939, 4364
XM.083966, 4923
XM.083983, 4881
XM.084007, 5055
XM.084014, 5246
XM.084023, 5528
XM.084026, 5549
XM.084055, 580
XM.084084, 6090
XM.084110, 1340
XM.084111, 1243

WO 2004/030615

PCT/US2003/028547

XM_084120, 1315
XM_084123, 1263
XM_084129, 1231
XM_084141, 1041
XM_084158, 1465
XM_084168, 1547
XM_084179, 1591
XM_084180, 1781
XM_084204, 2079
XM_084238, 2453
XM_084241, 2337
XM_084270, 2851
XM_084283, 6229
XM_084287, 6203
XM_084288, 6153
XM_084296, 6227
XM_084311, 6350
XM_084359, 3073
XM_084372, 3016
XM_084385, 2944
XM_084413, 3028
XM_084420, 2910
XM_084429, 2911
XM_084450, 2942
XM_084451, 2953
XM_084467, 2994
XM_084477, 3010
XM_084480, 3012
XM_084505, 3080
XM_084514, 3180
XM_084515, 3183
XM_084516, 3182
XM_084517, 3184
XM_084522, 3424
XM_084525, 3428
XM_084527, 3169
XM_084570, 3357
XM_084601, 3353
XM_084610, 3350
XM_084632, 3072
XM_084645, 3731
XM_084654, 3388
XM_084658, 3382
XM_084681, 3195
XM_084702, 3287
XM_084739, 3124
XM_084742, 3122
XM_084770, 3515
XM_084789, 3599
XM_084800, 3783
XM_084801, 3672
XM_084807, 3531
XM_084808, 3818
XM_084824, 3630
XM_084841, 3540
XM_084866, 3557

XM_084884, 3583
XM_084885, 3582
XM_084889, 3814
XM_084901, 3488
XM_084909, 3702
XM_084912, 3705
XM_084918, 3500
XM_084922, 3495
XM_084941, 3788
XM_084946, 3800
XM_084948, 3804
XM_084982, 3870
XM_084997, 3933
XM_084998, 2142
XM_085017, 3893
XM_085044, 3916
XM_085065, 4044
XM_085066, 4033
XM_085068, 1480
XM_085106, 3987
XM_085125, 4031
XM_085127, 4014
XM_085141, 4019
XM_085151, 4050
XM_085162, 4054
XM_085166, 3955
XM_085203, 4130
XM_085204, 4132
XM_085215, 4282
XM_085239, 4254
XM_085249, 4236
XM_085262, 4314
XM_085280, 4289
XM_085283, 4211
XM_085307, 4160
XM_085327, 4622
XM_085340, 4448
XM_085393, 4480
XM_085395, 4482
XM_085408, 4637
XM_085434, 4524
XM_085442, 4513
XM_085445, 4425
XM_085452, 4435
XM_085471, 4558
XM_085475, 4561
XM_085483, 4616
XM_085525, 4323
XM_085531, 4977
XM_085545, 4741
XM_085548, 4735
XM_085563, 4991
XM_085581, 472
XM_085589, 4948
XM_085613, 4724
XM_085627, 4951

WO 2004/030615

PCT/US2003/028547

XM_085636, 4873
XM_085672, 4757
XM_085687, 4659
XM_085691, 4677
XM_085716, 4992
XM_085722, 4745
XM_085735, 5019
XM_085743, 4718
XM_085775, 5058
XM_085779, 5075
XM_085788, 5049
XM_085789, 5043
XM_085790, 5045
XM_085791, 5042
XM_085856, 5501
XM_085862, 5244
XM_085874, 5460
XM_085875, 5461
XM_085876, 5462
XM_085909, 5297
XM_085916, 5285
XM_085917, 5276
XM_085927, 5527
XM_085928, 5489
XM_085934, 5537
XM_085935, 5573
XM_085950, 5487
XM_085971, 5371
XM_085972, 5629
XM_085981, 4599
XM_085986, 5398
XM_086004, 5425
XM_086074, 5311
XM_086101, 5128
XM_086102, 5130
XM_086116, 5331
XM_086132, 304
XM_086138, 282
XM_086142, 557
XM_086151, 46
XM_086164, 277
XM_086165, 279
XM_086166, 281
XM_086167, 280
XM_086178, 4
XM_086180, 19
XM_086204, 38
XM_086228, 1356
XM_086244, 601
XM_086245, 602
XM_086257, 632
XM_086271, 383
XM_086278, 4434
XM_086282, 543
XM_086296, 331
XM_086324, 214

XM_086328, 542
XM_086343, 265
XM_086357, 85
XM_086360, 29
XM_086375, 97
XM_086378, 485
XM_086381, 479
XM_086384, 178
XM_086389, 243
XM_086391, 231
XM_086397, 323
XM_086400, 366
XM_086428, 2161
XM_086431, 589
XM_086432, 592
XM_086444, 136
XM_086481, 490
XM_086484, 494
XM_086485, 493
XM_086494, 538
XM_086515, 324
XM_086518, 317
XM_086543, 190
XM_086552, 432
XM_086564, 388
XM_086567, 430
XM_086586, 52
XM_086587, 54
XM_086648, 5819
XM_086701, 5687
XM_086710, 5670
XM_086715, 5695
XM_086736, 5717
XM_086745, 5712
XM_086759, 5877
XM_086760, 5878
XM_086770, 5914
XM_086773, 5928
XM_086777, 5930
XM_086779, 5064
XM_086805, 5963
XM_086809, 5953
XM_086821, 5985
XM_086830, 6043
XM_086844, 6074
XM_086873, 5964
XM_086875, 6093
XM_086920, 805
XM_086923, 849
XM_086925, 850
XM_086944, 933
XM_086950, 858
XM_086961, 926
XM_086980, 791
XM_087028, 942
XM_087038, 2803

WO 2004/030615

PCT/US2003/028547

XM_087040, 842
XM_087041, 2800
XM_087045, 932
XM_087051, 748
XM_087061, 912
XM_087062, 914
XM_087068, 775
XM_087069, 772
XM_087118, 891
XM_087122, 839
XM_087151, 683
XM_087162, 985
XM_087166, 993
XM_087181, 965
XM_087193, 726
XM_087195, 725
XM_087206, 669
XM_087211, 743
XM_087218, 1011
XM_087240, 901
XM_087254, 1302
XM_087268, 1203
XM_087278, 1358
XM_087284, 1075
XM_087289, 1323
XM_087295, 1322
XM_087297, 1360
XM_087322, 1312
XM_087331, 1211
XM_087341, 1267
XM_087342, 1265
XM_087346, 1115
XM_087349, 1106
XM_087359, 1343
XM_087370, 1101
XM_087392, 1333
XM_087410, 1347
XM_087448, 1184
XM_087480, 3000
XM_087498, 1463
XM_087514, 1483
XM_087527, 1455
XM_087583, 1418
XM_087588, 1120
XM_087597, 1549
XM_087599, 1551
XM_087600, 1553
XM_087601, 1550
XM_087610, 1597
XM_087611, 1595
XM_087614, 1564
XM_087621, 1711
XM_087635, 1660
XM_087637, 1662
XM_087652, 1713
XM_087659, 1537

XM_087686, 1543
XM_087710, 3247
XM_087713, 1559
XM_087745, 1656
XM_087773, 1816
XM_087790, 1631
XM_087823, 1858
XM_087834, 2123
XM_087836, 2124
XM_087853, 2090
XM_087855, 2089
XM_087939, 2000
XM_087945, 1990
XM_087955, 3857
XM_087960, 1883
XM_087990, 1936
XM_087991, 2154
XM_088009, 3106
XM_088020, 1621
XM_088073, 2386
XM_088099, 2416
XM_088103, 2418
XM_088105, 2409
XM_088107, 605
XM_088119, 2422
XM_088122, 2420
XM_088135, 2446
XM_088180, 2352
XM_088239, 2297
XM_088264, 2195
XM_088294, 2529
XM_088316, 2611
XM_088321, 2628
XM_088323, 2574
XM_088325, 2572
XM_088336, 2519
XM_088338, 2515
XM_088370, 2613
XM_088399, 2559
XM_088401, 2560
XM_088422, 2839
XM_088426, 2833
XM_088459, 2847
XM_088461, 2870
XM_088472, 1472
XM_088550, 2640
XM_088552, 2641
XM_088553, 2642
XM_088563, 2672
XM_088569, 2748
XM_088571, 2750
XM_088587, 4120
XM_088588, 4114
XM_088589, 4121
XM_088592, 6311
XM_088619, 6151

WO 2004/030615

PCT/US2003/028547

XM_088622, 6152
XM_088630, 6209
XM_088637, 2700
XM_088638, 768
XM_088665, 6158
XM_088688, 6220
XM_088689, 6218
XM_088710, 6253
XM_088736, 6265
XM_088738, 6267
XM_088739, 6268
XM_088745, 6289
XM_088747, 6128
XM_088788, 338
XM_088863, 286
XM_088945, 507
XM_089030, 622
XM_089138, 254
XM_089514, 3019
XM_089551, 3006
XM_090218, 3542
XM_090413, 3779
XM_090458, 3767
XM_090833, 638
XM_090914, 4082
XM_090991, 4191
XM_091076, 1091
XM_091100, 4263
XM_091108, 4124
XM_091159, 4157
XM_091270, 4483
XM_091399, 4590
XM_091420, 4544
XM_091786, 3426
XM_091886, 5595
XM_091938, 5221
XM_091981, 5586
XM_091984, 5396
XM_092042, 5108
XM_092046, 5341
XM_092049, 5380
XM_092135, 672
XM_092158, 918
XM_092346, 944
XM_092489, 867
XM_092517, 676
XM_092545, 970
XM_092760, 5696
XM_092888, 5986
XM_092966, 6113
XM_093050, 6212
XM_093130, 6226
XM_093219, 6299
XM_093241, 6228
XM_093423, 1308
XM_093487, 1255

XM_093546, 1201
XM_093624, 1083
XM_094243, 1797
XM_094440, 1561
XM_094741, 1862
XM_094855, 2060
XM_095146, 2432
XM_095371, 2475
XM_095545, 2514
XM_095667, 2554
XM_096038, 3699
XM_096060, 4241
XM_096146, 3539
XM_096149, 661
XM_096155, 5967
XM_096156, 5968
XM_096169, 1022
XM_096172, 787
XM_096195, 1190
XM_096198, 1117
XM_096203, 1464
XM_096303, 6256
XM_096486, 3315
XM_096520, 3165
XM_096544, 3119
XM_096566, 3680
XM_096572, 3819
XM_096597, 3739
XM_096606, 3608
XM_096620, 3578
XM_096630, 3486
XM_096661, 3441
XM_096744, 4034
XM_096772, 3966
XM_096842, 4245
XM_096844, 4286
XM_097043, 4984
XM_097193, 5001
XM_097195, 5000
XM_097204, 4754
XM_097232, 5048
XM_097274, 5510
XM_097275, 5521
XM_097300, 5222
XM_097365, 5440
XM_097420, 5134
XM_097453, 2068
XM_097519, 561
XM_097565, 249
XM_097639, 352
XM_097649, 198
XM_097713, 5800
XM_097727, 5773
XM_097731, 5795
XM_097749, 5644
XM_097772, 5731

WO 2004/030615

PCT/US2003/028547

XM_097807, 5929
XM_097817, 5925
XM_097833, 5950
XM_097886, 5971
XM_097976, 715
XM_098004, 729
XM_098047, 962
XM_098048, 960
XM_098109, 1345
XM_098111, 1245
XM_098154, 1232
XM_098158, 1103
XM_098173, 1227
XM_098248, 1384
XM_098351, 1609
XM_098352, 1611
XM_098354, 1610
XM_098362, 1634
XM_098387, 1778
XM_098405, 1534
XM_098468, 2108
XM_098599, 619
XM_098654, 2447
XM_098669, 2466
XM_098747, 2582
XM_098761, 2564
XM_098913, 2843
XM_098943, 2725
XM_098995, 6302
XM_099467, 363
XM_102377, 4432
XM_103946, 665
XM_104983, 6263
XM_105236, 1289
XM_105658, 1325
XM_106246, 1520
XM_106739, 1562
XM_107825, 2225
XM_109162, 3075
XM_113223, 3268
XM_113224, 3275
XM_113226, 3400
XM_113229, 3366
XM_113230, 3363
XM_113238, 3152
XM_113266, 4202
XM_113268, 4207
XM_113291, 4429
XM_113293, 4467
XM_113299, 4504
XM_113303, 5013
XM_113310, 4723
XM_113315, 4944
XM_113324, 4674
XM_113325, 4703
XM_113328, 4695

XM_113330, 5011
XM_113334, 4819
XM_113343, 5028
XM_113348, 5316
XM_113352, 5294
XM_113360, 386
XM_113361, 598
XM_113369, 361
XM_113374, 140
XM_113379, 473
XM_113380, 5749
XM_113390, 929
XM_113395, 1193
XM_113397, 1244
XM_113405, 1140
XM_113408, 1296
XM_113409, 1202
XM_113410, 1088
XM_113417, 1254
XM_113422, 1329
XM_113425, 1452
XM_113452, 1556
XM_113454, 1841
XM_113463, 1654
XM_113467, 1720
XM_113468, 1845
XM_113476, 1860
XM_113531, 2526
XM_113532, 2627
XM_113540, 2548
XM_113557, 2493
XM_113564, 2846
XM_113585, 6122
XM_113615, 2927
XM_113702, 3862
XM_113712, 3635
XM_113719, 3560
XM_113726, 3584
XM_113730, 3519
XM_113737, 3855
XM_113739, 3437
XM_113752, 3946
XM_113759, 4105
XM_113823, 4163
XM_113836, 4326
XM_113840, 4608
XM_113843, 4420
XM_113845, 4418
XM_113853, 4570
XM_113855, 4560
XM_113874, 4431
XM_113876, 4426
XM_113882, 4640
XM_113892, 4978
XM_113901, 4653
XM_113919, 4905

WO 2004/030615

PCT/US2003/028547

XM.113929, 4696
XM.113931, 4706
XM.113938, 4824
XM.113943, 5010
XM.113945, 4998
XM.113951, 4962
XM.113988, 5229
XM.114004, 5349
XM.114018, 5097
XM.114024, 5560
XM.114025, 5530
XM.114027, 5366
XM.114030, 560
XM.114044, 129
XM.114055, 384
XM.114062, 3
XM.114097, 376
XM.114098, 360
XM.114109, 525
XM.114125, 259
XM.114137, 634
XM.114153, 484
XM.114154, 5875
XM.114163, 5794
XM.114165, 5813
XM.114174, 5673
XM.114178, 5706
XM.114185, 5889
XM.114209, 6024
XM.114215, 816
XM.114229, 838
XM.114247, 824
XM.114266, 851
XM.114267, 856
XM.114298, 957
XM.114301, 1225
XM.114309, 1242
XM.114323, 1141
XM.114328, 1344
XM.114356, 1288
XM.114364, 1122
XM.114368, 1510
XM.114401, 1496
XM.114424, 1473
XM.114426, 1470
XM.114434, 1555
XM.114435, 1552
XM.114437, 1567
XM.114439, 1586
XM.114440, 1587
XM.114442, 1584
XM.114453, 1819
XM.114457, 1817
XM.114469, 1623
XM.114482, 1683
XM.114492, 2106

XM.114497, 2058
XM.114555, 2429
XM.114578, 2444
XM.114602, 2404
XM.114613, 2625
XM.114617, 2517
XM.114618, 2523
XM.114640, 2556
XM.114646, 2756
XM.114649, 2873
XM.114655, 2854
XM.114661, 2677
XM.114662, 2688
XM.114669, 2845
XM.114677, 2802
XM.114678, 2801
XM.114679, 2799
XM.114686, 2699
XM.114692, 6354
XM.114708, 6291
XM.114720, 6130
XM.114724, 6119
XM.114798, 233
XM.114862, 3104
XM.114894, 2977
XM.114981, 3139
XM.115031, 3286
XM.115062, 3364
XM.115063, 3365
XM.115081, 3177
XM.115117, 3570
XM.115140, 3634
XM.115197, 3809
XM.115215, 3948
XM.115352, 4333
XM.115480, 4910
XM.115603, 5466
XM.115615, 5395
XM.115672, 869
XM.115706, 1039
XM.115722, 1040
XM.115825, 1002
XM.115846, 5691
XM.115874, 6281
XM.115886, 6131
XM.115890, 6136
XM.115923, 6259
XM.115924, 6121
XM.116034, 1338
XM.116058, 1295
XM.116071, 1204
XM.116072, 1205
XM.116204, 1532
XM.116205, 1533
XM.116247, 1484
XM.116285, 1408

WO 2004/030615

PCT/US2003/028547

XM.116307, 1691	XM.165451, 1268
XM.116340, 1807	XM.165465, 1531
XM.116365, 1856	XM.165470, 1528
XM.116427, 1648	XM.165473, 1482
XM.116439, 1593	XM.165483, 1818
XM.116447, 1606	XM.165484, 1820
XM.116465, 1716	XM.165488, 1615
XM.116511, 1857	XM.165499, 2057
XM.116514, 1861	XM.165514, 2579
XM.116524, 2140	XM.165530, 6355
XM.116806, 2789	XM.165533, 6235
XM.116818, 2738	XM.165551, 2913
XM.116853, 1139	XM.165555, 2889
XM.116856, 1810	XM.165557, 2897
XM.116863, 2975	XM.165560, 2925
XM.116913, 3845	XM.165563, 2926
XM.116926, 3451	XM.165567, 2921
XM.117061, 4913	XM.165571, 3407
XM.117066, 4768	XM.165584, 3414
XM.117096, 5084	XM.165586, 3413
XM.117118, 5379	XM.165592, 3401
XM.117122, 5183	XM.165598, 3303
XM.117128, 5605	XM.165600, 3310
XM.117159, 2	XM.165610, 3222
XM.117181, 534	XM.165611, 3217
XM.117184, 163	XM.165612, 3223
XM.117185, 582	XM.165616, 3325
XM.117196, 641	XM.165627, 3335
XM.117209, 5688	XM.165628, 3341
XM.117264, 736	XM.165631, 3328
XM.117311, 1337	XM.165636, 3903
XM.117351, 1412	XM.165639, 3917
XM.117387, 1622	XM.165645, 4534
XM.117398, 1641	XM.165647, 4528
XM.117444, 2471	XM.165648, 4537
XM.117449, 2160	XM.165649, 4527
XM.117452, 2472	XM.165656, 4484
XM.117481, 2406	XM.165657, 4493
XM.117487, 2622	XM.165658, 4489
XM.117519, 2874	XM.165669, 2091
XM.117539, 6352	XM.165692, 2159
XM.117555, 6349	XM.165698, 1949
XM.117692, 28	XM.165717, 1954
XM.118637, 4251	XM.165728, 2036
XM.165390, 3427	XM.165738, 1999
XM.165410, 4583	XM.165740, 1865
XM.165411, 4413	XM.165743, 1937
XM.165418, 4713	XM.165747, 1948
XM.165421, 4701	XM.165749, 2037
XM.165422, 4704	XM.165758, 2013
XM.165432, 5541	XM.165764, 2011
XM.165438, 144	XM.165765, 1988
XM.165439, 620	XM.165770, 1951
XM.165442, 59	XM.165771, 1983
XM.165443, 477	XM.165772, 1876
XM.165448, 723	XM.165777, 2044

WO 2004/030615

PCT/US2003/028547

XM.165794, 1921
XM.165799, 2006
XM.165801, 1956
XM.165809, 2016
XM.165836, 2350
XM.165839, 2346
XM.165841, 2197
XM.165860, 2167
XM.165867, 2249
XM.165870, 2245
XM.165872, 2253
XM.165876, 2258
XM.165877, 2240
XM.165882, 2248
XM.165888, 2934
XM.165890, 2929
XM.165891, 2941
XM.165903, 3633
XM.165905, 3579
XM.165906, 3532
XM.165910, 3465
XM.165921, 4127
XM.165923, 4325
XM.165954, 5026
XM.165960, 5347
XM.165963, 5367
XM.165975, 327
XM.165976, 373
XM.165977, 264
XM.165978, 532
XM.165981, 290
XM.165983, 275
XM.165984, 175
XM.165994, 927
XM.165998, 893
XM.166007, 910
XM.166008, 900
XM.166011, 1121
XM.166014, 1275
XM.166015, 1192
XM.166017, 1350
XM.166026, 1669
XM.166027, 1663
XM.166028, 1842
XM.166029, 1802
XM.166037, 1612
XM.166042, 2054
XM.166049, 2147
XM.166063, 2540
XM.166064, 2558
XM.166078, 6142
XM.166081, 6255
XM.166093, 2984
XM.166125, 2966
XM.166157, 2922
XM.166174, 3409

XM.166177, 3406
XM.166181, 3403
XM.166196, 3308
XM.166232, 3227
XM.166234, 3224
XM.166235, 3293
XM.166236, 3294
XM.166239, 3349
XM.166253, 3336
XM.166266, 3904
XM.166273, 3886
XM.166277, 4532
XM.166282, 4491
XM.166285, 4490
XM.166288, 5071
XM.166303, 2092
XM.166310, 2101
XM.166327, 2157
XM.166333, 1932
XM.166336, 2021
XM.166340, 1882
XM.166349, 1872
XM.166353, 2002
XM.166357, 2049
XM.166360, 1938
XM.166361, 2009
XM.166362, 1884
XM.166363, 1940
XM.166376, 2004
XM.166381, 1992
XM.166392, 2019
XM.166401, 1995
XM.166402, 1896
XM.166406, 2015
XM.166412, 1910
XM.166417, 1914
XM.166419, 1920
XM.166425, 1888
XM.166446, 2042
XM.166457, 1878
XM.166459, 1931
XM.166469, 1879
XM.166480, 1955
XM.166482, 2351
XM.166485, 2353
XM.166494, 2224
XM.166504, 2222
XM.166505, 2202
XM.166506, 2200
XM.166509, 2219
XM.166512, 2205
XM.166513, 2220
XM.166514, 2203
XM.166515, 2204
XM.166521, 2198
XM.166523, 2170

WO 2004/030615

PCT/US2003/028547

XM_166531, 2190
XM_166540, 2191,
XM_166541, 2168
XM_166594, 2230
XM_166599, 20
XM_166605, 3506
XM_166629, 2988
XM_166665, 2918
XM_166717, 2906
XM_166743, 3418
XM_167008, 5080
XM_167016, 2087
XM_167027, 2094
XM_167037, 2096
XM_167046, 2150
XM_167128, 2023
XM_167161, 2025
XM_167169, 1868
XM_167179, 2031
XM_167196, 2041
XM_167225, 2047
XM_167339, 2264
XM_167363, 5065
XM_167366, 1209
XM_167374, 2898
XM_167395, 2963
XM_167411, 2901
XM_167414, 2904
XM_167433, 3324
XM_167437, 3192
XM_167439, 3876
XM_167453, 4538
XM_167456, 4541
XM_167476, 2321
XM_167477, 2325
XM_167483, 2328
XM_167484, 2329
XM_167494, 2273
XM_167498, 2301
XM_167500, 2299
XM_167502, 2312
XM_167504, 2300
XM_167518, 3754
XM_167530, 5529
XM_167538, 5945
XM_167558, 2645
XM_167626, 2887
XM_167716, 3244
XM_167726, 3248
XM_167747, 3234
XM_167748, 3228
XM_167780, 3417
XM_167804, 3291
XM_167853, 3318
XM_167892, 3883
XM_167906, 3877

XM_167911, 3868
XM_167918, 3869
XM_168054, 2103
XM_168070, 1928
XM_168104, 1994
XM_168123, 1877
XM_168181, 2322
XM_168251, 2323
XM_168354, 2271
XM_168378, 2269
XM_168435, 2316
XM_168450, 2315
XM_168454, 2302
XM_168461, 2311
XM_168464, 2317
XM_168470, 2310
XM_168548, 2375
XM_168572, 2380
XM_168586, 2360
XM_169414, 3880
XM_169540, 5078
XM_170195, 2267
XM_170427, 2318

WO 2004/030615

PCT/US2003/028547

Source Index (to Figure number)

gen.NM_000018,4669	gen.NM_000484,5882
gen.NM_000026,6068	gen.NM_000505,1828
gen.NM_000029,624	gen.NM_000508,1511
gen.NM_000033,6342	gen.NM_000509,1515
gen.NM_000034,4520	gen.NM_000516,5830
gen.NM_000039,3376	gen.NM_000517,4354
gen.NM_000041,5511	gen.NM_000521,1627
gen.NM_000070,4161	gen.NM_000526,4816
gen.NM_000075,3683	gen.NM_000532,1260
gen.NM_000077,2655	gen.NM_000554,5480
gen.NM_000079,898	gen.NM_000558,4356
gen.NM_000090,921	gen.NM_000559,3142
gen.NM_000107,3208	gen.NM_000569,505
gen.NM_000114,5836	gen.NM_000574,558
gen.NM_000121,5258	gen.NM_000576,847
gen.NM_000126,4267	gen.NM_000582,1459
gen.NM_000137,4300	gen.NM_000592,1957
gen.NM_000143,636	gen.NM_000598,2228
gen.NM_000146,5562	gen.NM_000602,2361
gen.NM_000154,4967	gen.NM_000612,3120
gen.NM_000156,5122	gen.NM_000638,4763
gen.NM_000165,2099	gen.NM_000661,1425
gen.NM_000177,2796	gen.NM_000666,1172
gen.NM_000178,5738	gen.NM_000687,5736
gen.NM_000179,744	gen.NM_000688,1167
gen.NM_000182,713	gen.NM_000700,2695
gen.NM_000183,711	gen.NM_000701,312
gen.NM_000184,3144	gen.NM_000743,4259
gen.NM_000196,4547	gen.NM_000754,5956
gen.NM_000213,4963	gen.NM_000760,173
gen.NM_000221,701	gen.NM_000785,3687
gen.NM_000224,3593	gen.NM_000787,2830
gen.NM_000227,5040	gen.NM_000795,3384
gen.NM_000228,553	gen.NM_000801,5648
gen.NM_000239,3729	gen.NM_000852,3297
gen.NM_000250,4903	gen.NM_000858,612
gen.NM_000251,741	gen.NM_000893,1327
gen.NM_000268,5994	gen.NM_000895,3763
gen.NM_000269,4889	gen.NM_000930,2534
gen.NM_000274,3076	gen.NM_000931,2536
gen.NM_000284,6138	gen.NM_000942,4218
gen.NM_000291,6230	gen.NM_000954,2868
gen.NM_000358,1671	gen.NM_000964,4820
gen.NM_000365,3460	gen.NM_000967,6061
gen.NM_000368,2806	gen.NM_000969,284
gen.NM_000385,2262	gen.NM_000970,3781
gen.NM_000386,4843	gen.NM_000971,2569
gen.NM_000396,356	gen.NM_000972,2826
gen.NM_000404,1089	gen.NM_000973,2633
gen.NM_000407,5947	gen.NM_000975,87
gen.NM_000422,4807	gen.NM_000976,2780
gen.NM_000425,6334	gen.NM_000977,4633
gen.NM_000447,594	gen.NM_000978,4801

WO 2004/030615

PCT/US2003/028547

gen.NM_000979,5571
gen.NM_000980,5334
gen.NM_000981,4798
gen.NM_000982,3091
gen.NM_000983,34
gen.NM_000985,5067
gen.NM_000986,1206
gen.NM_000987,4714
gen.NM_000989,2588
gen.NM_000990,3155
gen.NM_000991,5613
gen.NM_000992,1170
gen.NM_000993,832
gen.NM_000994,1064
gen.NM_000997,1570
gen.NM_000998,966
gen.NM_001000,6278
gen.NM_001002,3827
gen.NM_001003,4228
gen.NM_001005,3331
gen.NM_001006,1506
gen.NM_001007,6224
gen.NM_001009,5633
gen.NM_001010,2651
gen.NM_001011,643
gen.NM_001012,210
gen.NM_001016,2111
gen.NM_001017,3171
gen.NM_001018,5126
gen.NM_001020,5426
gen.NM_001021,4283
gen.NM_001022,5468
gen.NM_001023,2552
gen.NM_001024,5847
gen.NM_001025,1632
gen.NM_001026,2980
gen.NM_001028,3361
gen.NM_001029,3656
gen.NM_001030,440
gen.NM_001034,651
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WO 2004/030615

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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gen.XM_165983,275
gen.XM_165984,175
gen.XM_165994,927
gen.XM_165998,893
gen.XM_166007,910
gen.XM_166008,900
gen.XM_166011,1121
gen.XM_166014,1275
gen.XM_166015,1192
gen.XM_166017,1350
gen.XM_166026,1669
gen.XM_166027,1663
gen.XM_166028,1842
gen.XM_166029,1802
gen.XM_166037,1612
gen.XM_166042,2054
gen.XM_166049,2147
gen.XM_166063,2540
gen.XM_166064,2558
gen.XM_166078,6142
gen.XM_166081,6255
gen.XM_166093,2984
gen.XM_166125,2966
gen.XM_166157,2922
gen.XM_166174,3409

gen.XM_166177,3406
gen.XM_166181,3403
gen.XM_166196,3308
gen.XM_166232,3227
gen.XM_166234,3224
gen.XM_166235,3293
gen.XM_166236,3294
gen.XM_166239,3349
gen.XM_166253,3336
gen.XM_166266,3904
gen.XM_166273,3886
gen.XM_166277,4532
gen.XM_166282,4491
gen.XM_166285,4490
gen.XM_166288,5071
gen.XM_166303,2092
gen.XM_166310,2101
gen.XM_166327,2157
gen.XM_166333,1932
gen.XM_166336,2021
gen.XM_166340,1882
gen.XM_166349,1872
gen.XM_166353,2002
gen.XM_166357,2049
gen.XM_166360,1938
gen.XM_166361,2009
gen.XM_166362,1884
gen.XM_166363,1940
gen.XM_166376,2004
gen.XM_166381,1992
gen.XM_166392,2019
gen.XM_166401,1995
gen.XM_166402,1896
gen.XM_166406,2015
gen.XM_166412,1910
gen.XM_166417,1914
gen.XM_166419,1920
gen.XM_166425,1888
gen.XM_166446,2042
gen.XM_166457,1878
gen.XM_166459,1931
gen.XM_166469,1879
gen.XM_166480,1955
gen.XM_166482,2351
gen.XM_166485,2353
gen.XM_166494,2224
gen.XM_166504,2222
gen.XM_166505,2202
gen.XM_166506,2200
gen.XM_166509,2219
gen.XM_166512,2205
gen.XM_166513,2220
gen.XM_166514,2203
gen.XM_166515,2204
gen.XM_166521,2198
gen.XM_166523,2170

WO 2004/030615

PCT/US2003/028547

gen.XM_166531,2190
gen.XM_166540,2191
gen.XM_166541,2168
gen.XM_166594,2230
gen.XM_166599,20
gen.XM_166605,3506
gen.XM_166629,2988
gen.XM_166665,2918
gen.XM_166717,2906
gen.XM_166743,3418
gen.XM_167008,5080
gen.XM_167016,2087
gen.XM_167027,2094
gen.XM_167037,2096
gen.XM_167046,2150
gen.XM_167128,2023
gen.XM_167161,2025
gen.XM_167169,1868
gen.XM_167179,2031
gen.XM_167196,2041
gen.XM_167225,2047
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gen.XM_167363,5065
gen.XM_167366,1209
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gen.XM_167414,2904
gen.XM_167433,3324
gen.XM_167437,3192
gen.XM_167439,3876
gen.XM_167453,4538
gen.XM_167456,4541
gen.XM_167476,2321
gen.XM_167477,2325
gen.XM_167483,2328
gen.XM_167484,2329
gen.XM_167494,2273
gen.XM_167498,2301
gen.XM_167500,2299
gen.XM_167502,2312
gen.XM_167504,2300
gen.XM_167518,3754
gen.XM_167530,5529
gen.XM_167538,5945
gen.XM_167558,2645
gen.XM_167626,2887
gen.XM_167716,3244
gen.XM_167726,3248
gen.XM_167747,3234
gen.XM_167748,3228
gen.XM_167780,3417
gen.XM_167804,3291
gen.XM_167853,3318
gen.XM_167892,3883
gen.XM_167906,3877

gen.XM_167911,3868
gen.XM_167918,3869
gen.XM_168054,2103
gen.XM_168070,1928
gen.XM_168104,1994
gen.XM_168123,1877
gen.XM_168181,2322
gen.XM_168251,2323
gen.XM_168354,2271
gen.XM_168378,2269
gen.XM_168435,2316
gen.XM_168450,2315
gen.XM_168454,2302
gen.XM_168461,2311
gen.XM_168464,2317
gen.XM_168470,2310
gen.XM_168548,2375
gen.XM_168572,2380
gen.XM_168586,2360
gen.XM_169414,3880
gen.XM_169540,5078
gen.XM_170195,2267
gen.XM_170427,2318

WO 2004/030615

PCT/US2003/028547

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "TAT polypeptide" and "TAT" as used herein and when immediately followed by a numerical designation, refer to various polypeptides, wherein the complete designation (i.e., TAT/number) refers to specific polypeptide sequences as described herein. The terms "TAT/number polypeptide" and "TAT/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides, polypeptide variants and fragments of native sequence polypeptides and polypeptide variants (which are further defined herein). The TAT polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "TAT polypeptide" refers to each individual TAT/number polypeptide disclosed herein. All disclosures in this specification which refer to the "TAT polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, formation of TAT binding oligopeptides to or against, formation of TAT binding organic molecules to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "TAT polypeptide" also includes variants of the TAT/number polypeptides disclosed herein.

A "native sequence TAT polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding TAT polypeptide derived from nature. Such native sequence TAT polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence TAT polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific TAT polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In certain embodiments of the invention, the native sequence TAT polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons (if indicated) are shown in bold font and underlined in the figures. Nucleic acid residues indicated as "N" in the accompanying figures are any nucleic acid residue. However, while the TAT polypeptides disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the TAT polypeptides.

The TAT polypeptide "extracellular domain" or "ECD" refers to a form of the TAT polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a TAT polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the TAT polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an

WO 2004/030615

PCT/US2003/028547

extracellular domain of a TAT polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various TAT polypeptides disclosed herein may be shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"TAT polypeptide variant" means a TAT polypeptide, preferably an active TAT polypeptide, as defined herein having at least about 80% amino acid sequence identity with a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Such TAT polypeptide variants include, for instance, TAT polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a TAT polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity, to a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide sequence as disclosed herein. Ordinarily, TAT variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600 amino acids in length, or more. Optionally, TAT variant polypeptides will have no more than one conservative amino acid substitution as compared to the native TAT polypeptide sequence, alternatively no more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 conservative amino acid substitution as compared to the native TAT polypeptide sequence.

"Percent (%) amino acid sequence identity" with respect to the TAT polypeptide sequences identified

WO 2004/030615

PCT/US2003/028547

herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific TAT polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "TAT", wherein "TAT" represents the amino acid sequence of a hypothetical TAT polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "TAT" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

"TAT variant polynucleotide" or "TAT variant nucleic acid sequence" means a nucleic acid molecule

WO 2004/030615

PCT/US2003/028547

which encodes a TAT polypeptide, preferably an active TAT polypeptide, as defined herein and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Ordinarily, a TAT variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, TAT variant polynucleotides are at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

"Percent (%) nucleic acid sequence identity" with respect to TAT-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the TAT nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison

WO 2004/030615

PCT/US2003/028547

parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

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$$100 \text{ times the fraction } W/Z$$

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where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "TAT-DNA", wherein "TAT-DNA" represents a hypothetical TAT-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "TAT-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides. Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

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In other embodiments, TAT variant polynucleotides are nucleic acid molecules that encode a TAT polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length TAT polypeptide as disclosed herein. TAT variant polypeptides may be those that are encoded by a TAT variant polynucleotide.

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The term "full-length coding region" when used in reference to a nucleic acid encoding a TAT polypeptide refers to the sequence of nucleotides which encode the full-length TAT polypeptide of the invention (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures). The term "full-length coding region" when used in reference to an ATCC deposited nucleic acid refers to the TAT polypeptide-encoding portion of the cDNA that is inserted into the vector deposited with the ATCC (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures).

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"Isolated," when used to describe the various TAT polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or,

35

WO 2004/030615

PCT/US2003/028547

preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the TAT polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" TAT polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium

WO 2004/030615

PCT/US2003/028547

chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) overnight hybridization in a solution that employs 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1 % sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1 % SDS, and 10% dextran sulfate at 42°C, with a 10 minute wash at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) followed by a 10 minute high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a TAT polypeptide or anti-TAT antibody fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

"Active" or "activity" for the purposes herein refers to form(s) of a TAT polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring TAT, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring TAT other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native TAT polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native TAT polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native TAT polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a TAT polypeptide may comprise contacting a TAT polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities

WO 2004/030615

PCT/US2003/028547

normally associated with the TAT polypeptide.

"Treating" or "treatment" or "alleviation" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. A subject or mammal is successfully "treated" for a TAT polypeptide-expressing cancer if, after receiving a therapeutic amount of an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule according to the methods of the present invention, the patient shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of cancer cells or absence of the cancer cells; reduction in the tumor size; inhibition (i.e., slow to some extent and preferably stop) of cancer cell infiltration into peripheral organs including the spread of cancer into soft tissue and bone; inhibition (i.e., slow to some extent and preferably stop) of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief to some extent, one or more of the symptoms associated with the specific cancer; reduced morbidity and mortality, and improvement in quality of life issues. To the extent the anti-TAT antibody or TAT binding oligopeptide may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. Reduction of these signs or symptoms may also be felt by the patient.

The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician. For cancer therapy, efficacy can be measured, for example, by assessing the time to disease progression (TTP) and/or determining the response rate (RR). Metastasis can be determined by staging tests and by bone scan and tests for calcium level and other enzymes to determine spread to the bone. CT scans can also be done to look for spread to the pelvis and lymph nodes in the area. Chest X-rays and measurement of liver enzyme levels by known methods are used to look for metastasis to the lungs and liver, respectively. Other routine methods for monitoring the disease include transrectal ultrasonography (TRUS) and transrectal needle biopsy (TRNB).

For bladder cancer, which is a more localized cancer, methods to determine progress of disease include urinary cytologic evaluation by cystoscopy, monitoring for presence of blood in the urine, visualization of the urothelial tract by sonography or an intravenous pyelogram, computed tomography (CT) and magnetic resonance imaging (MRI). The presence of distant metastases can be assessed by CT of the abdomen, chest x-rays, or radionuclide imaging of the skeleton.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of the treatment of, alleviating the symptoms of or diagnosis of a cancer refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous

WO 2004/030615

PCT/US2003/028547

(concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN[®], polyethylene glycol (PEG), and PLURONICS[®].

By "solid phase" or "solid support" is meant a non-aqueous matrix to which an antibody, TAT binding oligopeptide or TAT binding organic molecule of the present invention can adhere or attach. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a TAT polypeptide, an antibody thereto or a TAT binding oligopeptide) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small" molecule or "small" organic molecule is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide, antibody, TAT binding oligopeptide, TAT binding organic molecule or an agonist or antagonist thereof as disclosed herein is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

The term "therapeutically effective amount" refers to an amount of an antibody, polypeptide, TAT binding oligopeptide, TAT binding organic molecule or other drug effective to "treat" a disease or disorder in a subject or mammal. In the case of cancer, the therapeutically effective amount of the drug may reduce the number of cancer cells; reduce the tumor size; inhibit (i.e., slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. See the definition herein of "treating". To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic.

A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide

WO 2004/030615

PCT/US2003/028547

or TAT binding organic molecule is an amount capable of inhibiting the growth of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

5 A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule is an amount capable of causing the destruction of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

10 The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-TAT monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-TAT antibody compositions with polyepitopic specificity, polyclonal antibodies, single chain anti-TAT antibodies, and fragments of anti-TAT antibodies (see below) as long as they exhibit the desired biological or immunological activity. The term "immunoglobulin" (Ig) is used interchangeable with antibody herein.

15 An "isolated antibody" is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid
20 sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

25 The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains (an IgM antibody consists of 5 of the basic heterotetramer unit along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain). In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to a H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more
30 disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ϵ isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain (C_L) at its other end. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_{H1}). Particular amino acid
35 residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the

WO 2004/030615

PCT/US2003/028547

different classes of antibodies, see, e.g., Basic and Clinical Immunology, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α , δ , ϵ , γ , and μ , respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, e.g., humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

The term "variable" refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and define specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable domains. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-12 amino acids long. The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (e.g. around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L , and around about 1-35 (H1), 50-65 (H2) and 95-102 (H3) in the V_H ; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (e.g. residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the V_L , and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the V_H ; Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)).

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations which include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies.

WO 2004/030615

PCT/US2003/028547

The modifier "monoclonal" is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies useful in the present invention may be prepared by the hybridoma methodology first described by Kohler et al., Nature, 256:495 (1975), or may be made using recombinant DNA methods in bacterial, eukaryotic animal or plant cells (see, e.g., U.S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991), for example.

The monoclonal antibodies herein include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see U.S. Patent No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (e.g. Old World Monkey, Ape etc), and human constant region sequences.

An "intact" antibody is one which comprises an antigen-binding site as well as a C_L and at least heavy chain constant domains, C_H1, C_H2 and C_H3. The constant domains may be native sequence constant domains (e.g. human native sequence constant domains) or amino acid sequence variant thereof. Preferably, the intact antibody has one or more effector functions.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (see U.S. Patent No. 5,641,870, Example 2; Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain (C_H1). Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large F(ab')₂ fragment which roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having additional few residues at the carboxy terminus of the C_H1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides.

WO 2004/030615

PCT/US2003/028547

The effector functions of antibodies are determined by sequences in the Fc region, which region is also the part recognized by Fc receptors (FcR) found on certain types of cells.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

"Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, *infra*.

The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10 residues) between the V_H and V_L domains such that inter-chain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, i.e., fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

"Humanized" forms of non-human (*e.g.*, rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., *Nature* 321:522-525 (1986); Riechmann et al., *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992).

A "species-dependent antibody," *e.g.*, a mammalian anti-human IgE antibody, is an antibody which

WO 2004/030615

PCT/US2003/028547

has a stronger binding affinity for an antigen from a first mammalian species than it has for a homologue of that antigen from a second mammalian species. Normally, the species-dependent antibody "bind specifically" to a human antigen (i.e., has a binding affinity (Kd) value of no more than about 1×10^{-7} M, preferably no more than about 1×10^{-8} and most preferably no more than about 1×10^{-9} M) but has a binding affinity for a homologue of the antigen from a second non-human mammalian species which is at least about 50 fold, or at least about 500 fold, or at least about 1000 fold, weaker than its binding affinity for the human antigen. The species-dependent antibody can be of any of the various types of antibodies as defined above, but preferably is a humanized or human antibody.

A "TAT binding oligopeptide" is an oligopeptide that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in Synthetic Peptides as Antigens, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

WO 2004/030615

PCT/US2003/028547

A "TAT binding organic molecule" is an organic molecule other than an oligopeptide or antibody as defined herein that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585).

An antibody, oligopeptide or other organic molecule "which binds" an antigen of interest, e.g. a tumor-associated polypeptide antigen target, is one that binds the antigen with sufficient affinity such that the antibody, oligopeptide or other organic molecule is useful as a diagnostic and/or therapeutic agent in targeting a cell or tissue expressing the antigen, and does not significantly cross-react with other proteins. In such embodiments, the extent of binding of the antibody, oligopeptide or other organic molecule to a "non-target" protein will be less than about 10% of the binding of the antibody, oligopeptide or other organic molecule to its particular target protein as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA). With regard to the binding of an antibody, oligopeptide or other organic molecule to a target molecule, the term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a K_d for the target of at least about 10^{-4} M, alternatively at least about 10^{-5} M, alternatively at least about 10^{-6} M, alternatively at least about 10^{-7} M, alternatively at least about 10^{-8} M, alternatively at least about 10^{-9} M, alternatively at least about 10^{-10} M, alternatively at least about 10^{-11} M, alternatively at least about 10^{-12} M, or greater. In one embodiment, the term "specific binding" refers to binding where a molecule binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

An antibody, oligopeptide or other organic molecule that "inhibits the growth of tumor cells expressing a TAT polypeptide" or a "growth inhibitory" antibody, oligopeptide or other organic molecule is one which results in measurable growth inhibition of cancer cells expressing or overexpressing the appropriate TAT polypeptide. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferred growth inhibitory anti-TAT antibodies, oligopeptides or organic molecules inhibit growth of TAT-expressing tumor cells by greater

WO 2004/030615

PCT/US2003/028547

than 20%, preferably from about 20% to about 50%, and even more preferably, by greater than 50% (e.g., from about 50% to about 100%) as compared to the appropriate control, the control typically being tumor cells not treated with the antibody, oligopeptide or other organic molecule being tested. In one embodiment, growth inhibition can be measured at an antibody concentration of about 0.1 to 30 $\mu\text{g/ml}$ or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. Growth inhibition of tumor cells *in vivo* can be determined in various ways such as is described in the Experimental Examples section below. The antibody is growth inhibitory *in vivo* if administration of the anti-TAT antibody at about 1 $\mu\text{g/kg}$ to about 100 mg/kg body weight results in reduction in tumor size or tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

An antibody, oligopeptide or other organic molecule which "induces apoptosis" is one which induces programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). The cell is usually one which overexpresses a TAT polypeptide. Preferably the cell is a tumor cell, e.g., a prostate, breast, ovarian, stomach, endometrial, lung, kidney, colon, bladder cell. Various methods are available for evaluating the cellular events associated with apoptosis. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the antibody, oligopeptide or other organic molecule which induces apoptosis is one which results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay.

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies "arm" the cytotoxic cells and are absolutely required for such killing. The primary cells for mediating ADCC, NK cells, express Fc γ RIII only, whereas monocytes express Fc γ RI, Fc γ RII and Fc γ RIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, Annu. Rev. Immunol. 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, e.g., in a animal model such as that disclosed in Clynes et al.

WO 2004/030615

PCT/US2003/028547

(USA) 95:652-656 (1998).

"Fc receptor" or "FcR" describes a receptor that binds to the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the Fc γ RI, Fc γ RII and Fc γ RIII subclasses, including allelic variants and alternatively spliced forms of these receptors. Fc γ RII receptors include Fc γ RIIA (an "activating receptor") and Fc γ RIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor Fc γ RIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor Fc γ RIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see review M. in Daëron, Annu. Rev. Immunol. 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991); Capel et al., Immunomethods 4:25-34 (1994); and de Haas et al., J. Lab. Clin. Med. 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)).

"Human effector cells" are leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least Fc γ RIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred. The effector cells may be isolated from a native source, e.g., from blood.

"Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement activation, a CDC assay, e.g., as described in Gazzano-Santoro et al., J. Immunol. Methods 202:163 (1996), may be performed.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are

WO 2004/030615

PCT/US2003/028547

associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

"Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

5 An antibody, oligopeptide or other organic molecule which "induces cell death" is one which causes a viable cell to become nonviable. The cell is one which expresses a TAT polypeptide, preferably a cell that overexpresses a TAT polypeptide as compared to a normal cell of the same tissue type. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferably, the cell is a cancer cell, e.g., a breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, thyroid, pancreatic or bladder cell. Cell death *in vitro* may be determined in the absence of complement and immune effector cells to distinguish cell death induced by 10 antibody-dependent cell-mediated cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC). Thus, the assay for cell death may be performed using heat inactivated serum (i.e., in the absence of complement) and in the absence of immune effector cells. To determine whether the antibody, oligopeptide or other organic molecule is able to induce cell death, loss of membrane integrity as evaluated by uptake of propidium iodide (PI), trypan blue (see Moore et al. Cytotechnology 17:1-11 (1995)) or 7AAD can be assessed relative to 15 untreated cells. Preferred cell death-inducing antibodies, oligopeptides or other organic molecules are those which induce PI uptake in the PI uptake assay in BT474 cells.

A "TAT-expressing cell" is a cell which expresses an endogenous or transfected TAT polypeptide either on the cell surface or in a secreted form. A "TAT-expressing cancer" is a cancer comprising cells that 20 have a TAT polypeptide present on the cell surface or that produce and secrete a TAT polypeptide. A "TAT-expressing cancer" optionally produces sufficient levels of TAT polypeptide on the surface of cells thereof, such that an anti-TAT antibody, oligopeptide or other organic molecule can bind thereto and have a therapeutic effect with respect to the cancer. In another embodiment, a "TAT-expressing cancer" optionally produces and secretes sufficient levels of TAT polypeptide, such that an anti-TAT antibody, oligopeptide or other organic 25 molecule antagonist can bind thereto and have a therapeutic effect with respect to the cancer. With regard to the latter, the antagonist may be an antisense oligonucleotide which reduces, inhibits or prevents production and secretion of the secreted TAT polypeptide by tumor cells. A cancer which "overexpresses" a TAT polypeptide is one which has significantly higher levels of TAT polypeptide at the cell surface thereof, or produces and secretes, compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene 30 amplification or by increased transcription or translation. TAT polypeptide overexpression may be determined in a diagnostic or prognostic assay by evaluating increased levels of the TAT protein present on the surface of a cell, or secreted by the cell (e.g., via an immunohistochemistry assay using anti-TAT antibodies prepared against an isolated TAT polypeptide which may be prepared using recombinant DNA technology from an isolated nucleic acid encoding the TAT polypeptide; FACS analysis, etc.). Alternatively, or additionally, one 35 may measure levels of TAT polypeptide-encoding nucleic acid or mRNA in the cell, e.g., via fluorescent *in situ* hybridization using a nucleic acid based probe corresponding to a TAT-encoding nucleic acid or the complement

WO 2004/030615

PCT/US2003/028547

thereof; (FISH; see WO98/45479 published October, 1998), Southern blotting, Northern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR). One may also study TAT polypeptide overexpression by measuring shed antigen in a biological fluid such as serum, e.g. using antibody-based assays (see also, e.g., U.S. Patent No. 4,933,294 issued June 12, 1990; WO91/05264 published April 18, 1991; U.S. Patent 5,401,638 issued March 28, 1995; and Sias et al., J. Immunol. Methods 132:73-80 (1990)). Aside from the above assays, various *in vivo* assays are available to the skilled practitioner. For example, one may expose cells within the body of the patient to an antibody which is optionally labeled with a detectable label, e.g., a radioactive isotope, and binding of the antibody to cells in the patient can be evaluated, e.g., by external scanning for radioactivity or by analyzing a biopsy taken from a patient previously exposed to the antibody.

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody, oligopeptide or other organic molecule so as to generate a "labeled" antibody, oligopeptide or other organic molecule. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., ^{211}At , ^{131}I , ^{125}I , ^{90}Y , ^{186}Re , ^{188}Re , ^{153}Sm , ^{212}Bi , ^{32}P and radioactive isotopes of Lu), chemotherapeutic agents e.g. methotrexate, adriamycin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A tumoricidal agent causes destruction of tumor cells.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a TAT-expressing cancer cell, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of TAT-expressing cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such

WO 2004/030615

PCT/US2003/028547

as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in The Molecular Basis of Cancer, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

"Doxorubicin" is an anthracycline antibiotic. The full chemical name of doxorubicin is (8S-cis)-10-[(3-amino-2,3,6-trideoxy- α -L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor- α and - β ; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF- β ; platelet-growth factor; transforming growth factors (TGFs) such as TGF- α and TGF- β ; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon - α , - β , and - γ ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1a, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF- α or TNF- β ; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

WO 2004/030615**PCT/US2003/028547**

The term "package insert" is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, contraindications and/or warnings concerning the use of such therapeutic products.

WO 2004/030615

PCT/US2003/028547

Table 1

```

/*
*
* C-C increased from 12 to 15
* Z is average of EQ
5  * B is average of ND
* match with stop is _M; stop-stop = 0; J (joker) match = 0
*/
#define _M      -8      /* value of a match with a stop */

10 int _day[26][26] = {
/*  A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

40

45

50

```

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

10
#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
#define DINS1       1       /* penalty per base */
15
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
20
    short           n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short  x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16-1 */

struct diag {
25
    int             score;      /* score at last jmp */
    long            offset;     /* offset of prev block */
    short           ijmp;       /* current jmp index */
    struct jmp      jp;         /* list of jmps */
};

30
struct path {
    int             spc;        /* number of leading spaces */
    short           n[JMPS]; /* size of jmp (gap) */
    int             x[JMPS]; /* loc of jmp (last elem before gap) */
};

35
char            *ofile;        /* output file name */
char            *name[2];      /* seq names: getseqs() */
char            *prog;         /* prog name for err msgs */
char            *seq[2];       /* seqs: getseqs() */
40
int             dmax;          /* best diag: nw() */
int             dmax0;         /* final diag */
int             dna;           /* set if dna: main() */
int             endgaps;       /* set if penalizing end gaps */
int             gapx, gapy;     /* total gaps in seqs */
45
int             len0, len1;     /* seq lens */
int             ngapx, ngapy;   /* total size of gaps */
int             smax;          /* max score: nw() */
int             *xbm;          /* bitmap for matching */
long            offset;        /* current offset in jmp file */
50
struct diag      *dx;          /* holds diagonals */
struct path      pp[2];        /* holds path for seqs */

char            *calloc(), *malloc(), *index(), *strcpy();
char            *getseq(), *g_calloc();

```

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
5 * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
15 #include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

20 static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
25 1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)                                main
30 {
    int    ac;
    char   *av[];

    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                /* 1 to penalize endgaps */
    ofile = "align.out";        /* output file */

50     nw();                    /* fill in the matrix, get the possible jmps */
    readjmps();                /* get the actual jmps */
    print();                    /* print stats, alignment */

    cleanup(0);                /* unlink any tmp files */

```

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
5  * a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw()
{
10  char      *px, *py;      /* seqs and ptrs */
int          *ndely, *dely; /* keep track of dely */
int          ndelx, delx;   /* keep track of delx */
int          *tmp;         /* for swapping row0, row1 */
int          mis;          /* score for each type */
15  int          ins0, ins1; /* insertion penalties */
register      id;           /* diagonal index */
register      ij;           /* jmp index */
register      *col0, *col1; /* score for curr, last row */
register      xx, yy;       /* index into seqs */
20
dx = (struct diag *)g_calloc("to get diags", len0 + len1 + 1, sizeof(struct diag));
ndely = (int *)g_calloc("to get ndely", len1 + 1, sizeof(int));
dely = (int *)g_calloc("to get dely", len1 + 1, sizeof(int));
col0 = (int *)g_calloc("to get col0", len1 + 1, sizeof(int));
25  col1 = (int *)g_calloc("to get col1", len1 + 1, sizeof(int));
ins0 = (dna)? DINS0 : PINS0;
ins1 = (dna)? DINS1 : PINS1;
smax = -10000;
if (endgaps) {
30  for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
col0[yy] = dely[yy] = col0[yy-1] - ins1;
ndely[yy] = yy;
}
col0[0] = 0; /* Waterman Bull Math Biol 84 */
35  }
else
for (yy = 1; yy <= len1; yy++)
dely[yy] = -ins0;
/* fill in match matrix
*/
40  for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
/* initialize first entry in col
*/
if (endgaps) {
45  if (xx == 1)
col1[0] = delx = -(ins0 + ins1);
else
col1[0] = delx = col0[0] - ins1;
ndelx = xx;
50  }
else {
col1[0] = 0;
delx = -ins0;
ndelx = 0;
55  }
}

```

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
  mis = col0[yy-1];
  if (dna)
    mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
  else
    mis += _day[*px-'A'][*py-'A'];

  /* update penalty for del in x seq;
   * favor new del over ongong del
   * ignore MAXGAP if weighting endgaps
   */
  if (endgaps || ndely[yy] < MAXGAP) {
    if (col0[yy] - ins0 >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else {
      dely[yy] -= ins1;
      ndely[yy]++;
    }
  } else {
    if (col0[yy] - (ins0+ins1) >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else
      ndely[yy]++;
  }

  /* update penalty for del in y seq;
   * favor new del over ongong del
   */
  if (endgaps || ndelx < MAXGAP) {
    if (col1[yy-1] - ins0 >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else {
      delx -= ins1;
      ndelx++;
    }
  } else {
    if (col1[yy-1] - (ins0+ins1) >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else
      ndelx++;
  }

  /* pick the maximum score; we're favoring
   * mis over any del and delx over dely
   */

  id = xx - yy + len1 - 1;
  if (mis >= delx && mis >= dely[yy])
    col1[yy] = mis;

```

...nw

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```

else if (delx >= dely[yy]) {
    coll[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (ldna || (ndelx >= MAXJMP
5      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = ndelx;
    dx[id].jp.x[ij] = xx;
    dx[id].score = delx;
}
else {
    coll[yy] = dely[yy];
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (ldna || (ndely[yy] >= MAXJMP
20      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = -ndely[yy];
    dx[id].jp.x[ij] = xx;
    dx[id].score = dely[yy];
}
35 if (xx == len0 && yy < len1) {
    /* last col
    */
    if (endgaps)
        coll[yy] -= ins0+ins1*(len1-yy);
    if (coll[yy] > smax) {
        smax = coll[yy];
        dmax = id;
    }
}
45 }
if (endgaps && xx < len0)
    coll[yy-1] -= ins0+ins1*(len0-xx);
if (coll[yy-1] > smax) {
    smax = coll[yy-1];
    dmax = id;
}
50 }
tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
55 (void) free((char *)col0);
(void) free((char *)coll);
}

```

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
10 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3   /* space between name or num and seq */

20 extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25 print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
50         lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
55     }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

print

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')**getmat**

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)
    int    lx, ly;          /* "core" (minus endgaps) */
    int    firstgap, lastgap; /* leading trailing overlap */
{
    int    nm, i0, i1, siz0, siz1;
10    char    outx[32];
    double    pct;
    register    n0, n1;
    register char    *p0, *p1;
    /* get total matches, score
15    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
20    n1 = pp[0].spc + 1;
    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
25            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
30            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A'] & xbm[*p1-'A'])
35                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
40            p0++;
            p1++;
        }
    }

45    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
    if (endgaps)
50        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*((double)nm)/((double)lx);
    fprintf(fx, "\n");
55    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);

```


WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

...getmat

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapx, (dna)? "base": "residue", (ngapx == 1)? "": "s");
    fprintf(fx, "%s", outx);
    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
            ngapy, (dna)? "base": "residue", (ngapy == 1)? "": "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base": "residue", (firstgap == 1)? "": "s",
            lastgap, (dna)? "base": "residue", (lastgap == 1)? "": "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}
static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */
/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(name[i]);
        if (nn > lmax)
            lmax = nn;
        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

pr_align

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```

5      for (nn = nm = 0, more = 1; more; ) {
        for (i = more = 0; i < 2; i++) {
            /*
            * do we have more of this sequence?
            */
            if (!*ps[i])
                continue;
            more++;
            if (pp[i].spc) { /* leading space */
                *po[i]++ = ' ';
                pp[i].spc--;
            }
            else if (siz[i]) { /* in a gap */
                *po[i]++ = '-';
                siz[i]--;
            }
            else { /* we're putting a seq element
                    */
                *po[i] = *ps[i];
                if (islower(*ps[i]))
                    *ps[i] = toupper(*ps[i]);
                po[i]++;
                ps[i]++;
                /*
                * are we at next gap for this seq?
                */
                if (ni[i] == pp[i].x[ij[i]]) {
                    /*
                    * we need to merge all gaps
                    * at this location
                    */
                    siz[i] = pp[i].n[ij[i] + +];
                    while (ni[i] == pp[i].x[ij[i]])
                        siz[i] += pp[i].n[ij[i] + +];
                }
                ni[i]++;
            }
        }
        if (++nn == olen || !more && nn) {
            dumpblock();
            for (i = 0; i < 2; i++)
                po[i] = out[i];
            nn = 0;
        }
    }
    /*
    * dump a block of lines, including numbers, stars: pr_align()
    */
    static
    dumpblock()
    {
        register i;
        for (i = 0; i < 2; i++)
            *po[i]-- = '\0';
    }

```

...pr_align

dumpblock

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')**...dumpblock**

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
              putline(i);
10         if (i == 0 && *out[1])
                    fprintf(fx, star);
              if (i == 1)
                  nums(i);
          }
      }
15  }
  /*
  * put out a number line: dumpblock()
  */
20  static
  nums(ix)
      int      ix;      /* index in out[] holding seq line */
  {
      char      nline[P_LINE];
      register  i, j;
      register char *pn, *px, *py;
      for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
          *pn = ' ';
      for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
30         if (*py == ' ' || *py == '-')
            *pn = ' ';
            else {
                if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                    j = (i < 0)? -i : i;
                    for (px = pn; j /= 10, px--)
                        *px = j%10 + '0';
                    if (i < 0)
                        *px = '-';
                }
                else
                    *pn = ' ';
                i++;
            }
        }
45     *pn = '\0';
        nc[ix] = i;
        for (pn = nline; *pn; pn++)
            (void) putc(*pn, fx);
        (void) putc('\n', fx);
50     }
    /*
    * put out a line (name, [num], seq, [num]): dumpblock()
    */
    static
55     putline(ix)
        int      ix;
    {

```

nums**putline**

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

...putline

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

10     /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
   static
25  stars()
  {
      int          i;
      register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
          return;
      px = star;
      for (i = lmax+P_SPC; i; i--)
35         *px++ = ' ';

      for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
          if (isalpha(*p0) && isalpha(*p1)) {
40             if (xbm[*p0-'A']&xbm[*p1-'A']) {
                 cx = '*';
                 nm++;
             }
             else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                 cx = '.';
             else
                 cx = ' ';
          }
          else
50             cx = ' ';
          *px++ = cx;
      }
      *px++ = '\n';
      *px = '\0';
55  }

```

stars

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;
10     py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
15     if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
20
```

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

10 char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jumps */
FILE      *fj;
int        cleanup();                          /* cleanup tmp file */
long       lseek();

15 /*
 * remove any tmp file if we blow
 */
cleanup(i)                                     cleanup
{
    int      i;
20     {
        if (fj)
            (void) unlink(jname);
        exit(i);
    }
}
/*
25 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30 char    *
getseq(file, len)                             getseq
{
    char    *file;      /* file name */
    int     *len;       /* seq len */

35     {
        char    line[1024], *pseq;
        register char *px, *py;
        int     natgc, tlen;
        FILE    *fp;
40         if ((fp = fopen(file, "r")) == 0) {
            fprintf(stderr, "%s: can't read %s\n", prog, file);
            exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
45             if (*line == ';' || *line == '<' || *line == '>')
                continue;
            for (px = line; *px != '\n'; px++)
                if (isupper(*px) || islower(*px))
                    tlen++;
50         }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
            fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
            exit(1);
        }
55         pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);
5 while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10         if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
            natgc++;
15     }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
20 dna = natgc > (tlen/3);
    return(pseq+4);
}
char *
g_alloc(msg, nx, sz)                                g_alloc
25 char *msg; /* program, calling routine */
    int nx, sz; /* number and size of elements */
{
    char *px, *calloc();
    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
30         if (*msg) {
            fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
35     return(px);
}

/*
* get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
*/
40 readjmps()
{
    int fd = -1;
    int siz, i0, i1;
45 register i, j, xx;
    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
50             cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
55         while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)

```

readjmps

WO 2004/030615

PCT/US2003/028547

Table 1 (cont')**...readjumps**

```

5         if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
            break;
10     if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
    if (j >= 0) {
15        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1 */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
        /* ignore MAXGAP when doing endgaps */
25        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
        }
        else if (siz > 0) { /* gap in first seq */
30            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
        /* ignore MAXGAP when doing endgaps */
35        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
    }
    else
40        break;
}
/* reverse the order of jumps */
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
45 }
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
50 }
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
55    offset = 0;
}

```


WO 2004/030615

PCT/US2003/028547

Table 1 (cont')

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)                                writejumps
    int    ix;
    {
        char    *mktemp();
10         if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15         if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
20         (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }
}
```

WO 2004/030615

PCT/US2003/028547

Table 2

TAT	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

15	TAT	XXXXXXXXXXXX	(Length = 10 amino acids)
	Comparison Protein	XXXXXXXXYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

20 (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

5 divided by 10 = 50%

Table 4

25	TAT-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
	Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) =
6 divided by 14 = 42.9%

WO 2004/030615

PCT/US2003/028547

Table 5

TAT-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Anti-TAT Antibodies

15 In one embodiment, the present invention provides anti-TAT antibodies which may find use herein as therapeutic and/or diagnostic agents. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

20 Polyclonal antibodies are preferably raised in animals by multiple subcutaneous (sc) or intraperitoneal (ip) injections of the relevant antigen and an adjuvant. It may be useful to conjugate the relevant antigen (especially when synthetic peptides are used) to a protein that is immunogenic in the species to be immunized. For example, the antigen can be conjugated to keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, or soybean trypsin inhibitor, using a bifunctional or derivatizing agent, e.g., maleimidobenzoyl sulfosuccinimide ester (conjugation through cysteine residues), N-hydroxysuccinimide (through lysine residues), glutaraldehyde, succinic anhydride, SOCl₂, or R¹N=C=NR, where R and R¹ are different alkyl groups.

25 Animals are immunized against the antigen, immunogenic conjugates, or derivatives by combining, e.g., 100 µg or 5 µg of the protein or conjugate (for rabbits or mice, respectively) with 3 volumes of Freund's complete adjuvant and injecting the solution intradermally at multiple sites. One month later, the animals are boosted with 1/5 to 1/10 the original amount of peptide or conjugate in Freund's complete adjuvant by subcutaneous injection at multiple sites. Seven to 14 days later, the animals are bled and the serum is assayed
30 for antibody titer. Animals are boosted until the titer plateaus. Conjugates also can be made in recombinant cell culture as protein fusions. Also, aggregating agents such as alum are suitably used to enhance the immune response.

2. Monoclonal Antibodies

35 Monoclonal antibodies may be made using the hybridoma method first described by Kohler et al., Nature, 256:495 (1975), or may be made by recombinant DNA methods (U.S. Patent No. 4,816,567).

In the hybridoma method, a mouse or other appropriate host animal, such as a hamster, is immunized

WO 2004/030615

PCT/US2003/028547

as described above to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. After immunization, lymphocytes are isolated and then fused with a myeloma cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)).

5 The hybridoma cells thus prepared are seeded and grown in a suitable culture medium which medium preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells (also referred to as fusion partner). For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the selective culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances
10 prevent the growth of HGPRT-deficient cells.

 Preferred fusion partner myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a selective medium that selects against the unfused parental cells. Preferred myeloma cell lines are murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center,
15 San Diego, California USA, and SP-2 and derivatives e.g., X63-Ag8-653 cells available from the American Type Culture Collection, Manassas, Virginia, USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); and Brodeur et al., Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

20 Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA).

 The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis described in Munson et al., Anal. Biochem., 107:220 (1980).
25

 Once hybridoma cells that produce antibodies of the desired specificity, affinity, and/or activity are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may
30 be grown *in vivo* as ascites tumors in an animal e.g., by i.p. injection of the cells into mice.

 The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional antibody purification procedures such as, for example, affinity chromatography (e.g., using protein A or protein G-Sepharose) or ion-exchange chromatography, hydroxylapatite chromatography, gel electrophoresis, dialysis, etc.

35 DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the

WO 2004/030615

PCT/US2003/028547

heavy and light chains of murine antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese Hamster Ovary (CHO) cells, or myeloma cells that do not otherwise produce antibody protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. Review articles on recombinant expression in bacteria of DNA encoding the antibody include Skerra et al., Curr. Opin. in Immunol., 5:256-262 (1993) and Plückthun, Immunol. Revs. 130:151-188 (1992).

In a further embodiment, monoclonal antibodies or antibody fragments can be isolated from antibody phage libraries generated using the techniques described in McCafferty et al., Nature, 348:552-554 (1990). Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991) describe the isolation of murine and human antibodies, respectively, using phage libraries. Subsequent publications describe the production of high affinity (nM range) human antibodies by chain shuffling (Marks et al., Bio/Technology, 10:779-783 (1992)), as well as combinatorial infection and *in vivo* recombination as a strategy for constructing very large phage libraries (Waterhouse et al., Nuc. Acids. Res. 21:2265-2266 (1993)). Thus, these techniques are viable alternatives to traditional monoclonal antibody hybridoma techniques for isolation of monoclonal antibodies.

The DNA that encodes the antibody may be modified to produce chimeric or fusion antibody polypeptides, for example, by substituting human heavy chain and light chain constant domain (C_H and C_L) sequences for the homologous murine sequences (U.S. Patent No. 4,816,567; and Morrison, et al., Proc. Natl Acad. Sci. USA, 81:6851 (1984)), or by fusing the immunoglobulin coding sequence with all or part of the coding sequence for a non-immunoglobulin polypeptide (heterologous polypeptide). The non-immunoglobulin polypeptide sequences can substitute for the constant domains of an antibody, or they are substituted for the variable domains of one antigen-combining site of an antibody to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for an antigen and another antigen-combining site having specificity for a different antigen.

3. Human and Humanized Antibodies

The anti-TAT antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are

WO 2004/030615

PCT/US2003/028547

those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important to reduce antigenicity and HAMA response (human anti-mouse antibody) when the antibody is intended for human therapeutic use. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable domain sequences. The human V domain sequence which is closest to that of the rodent is identified and the human framework region (FR) within it accepted for the humanized antibody (Sims et al., J. Immunol. 151:2296 (1993); Chothia et al., J. Mol. Biol., 196:901 (1987)). Another method uses a particular framework region derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (Carter et al., Proc. Natl. Acad. Sci. USA, 89:4285 (1992); Presta et al., J. Immunol. 151:2623 (1993)).

It is further important that antibodies be humanized with retention of high binding affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the hypervariable region residues are directly and most substantially involved in influencing antigen binding.

WO 2004/030615

PCT/US2003/028547

Various forms of a humanized anti-TAT antibody are contemplated. For example, the humanized antibody may be an antibody fragment, such as a Fab, which is optionally conjugated with one or more cytotoxic agent(s) in order to generate an immunoconjugate. Alternatively, the humanized antibody may be an intact antibody, such as an intact IgG1 antibody.

As an alternative to humanization, human antibodies can be generated. For example, it is now possible to produce transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array into such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g., Jakobovits et al., Proc. Natl. Acad. Sci. USA, 90:2551 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggemann et al., Year in Immuno. 7:33 (1993); U.S. Patent Nos. 5,545,806, 5,569,825, 5,591,669 (all of GenPharm); 5,545,807; and WO 97/17852.

Alternatively, phage display technology (McCafferty et al., Nature 348:552-553 [1990]) can be used to produce human antibodies and antibody fragments *in vitro*, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. According to this technique, antibody V domain genes are cloned in-frame into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats, reviewed in, e.g., Johnson, Kevin S. and Chiswell, David J., Current Opinion in Structural Biology 3:564-571 (1993). Several sources of V-gene segments can be used for phage display. Clackson et al. Nature, 352:624-628 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens (including self-antigens) can be isolated essentially following the techniques described by Marks et al., J. Mol. Biol. 222:581-597 (1991), or Griffith et al., EMBO J. 12:725-734 (1993). See, also, U.S. Patent Nos. 5,565,332 and 5,573,905.

As discussed above, human antibodies may also be generated by *in vitro* activated B cells (see U.S. Patents 5,567,610 and 5,229,275).

4. Antibody fragments

In certain circumstances there are advantages of using antibody fragments, rather than whole antibodies. The smaller size of the fragments allows for rapid clearance, and may lead to improved access to solid tumors.

Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, e.g., Morimoto et al., Journal of Biochemical and Biophysical Methods 24:107-117 (1992); and Brennan et al., Science, 229:81 (1985)).

WO 2004/030615

PCT/US2003/028547

However, these fragments can now be produced directly by recombinant host cells. Fab, Fv and ScFv antibody fragments can all be expressed in and secreted from *E. coli*, thus allowing the facile production of large amounts of these fragments. Antibody fragments can be isolated from the antibody phage libraries discussed above. Alternatively, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form F(ab')₂ fragments (Carter et al., Bio/Technology 10:163-167 (1992)). According to another approach, F(ab')₂ fragments can be isolated directly from recombinant host cell culture. Fab and F(ab')₂ fragment with increased in vivo half-life comprising a salvage receptor binding epitope residues are described in U.S. Patent No. 5,869,046. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner. In other embodiments, the antibody of choice is a single chain Fv fragment (scFv). See WO 93/16185; U.S. Patent No. 5,571,894; and U.S. Patent No. 5,587,458. Fv and sFv are the only species with intact combining sites that are devoid of constant regions; thus, they are suitable for reduced nonspecific binding during in vivo use. sFv fusion proteins may be constructed to yield fusion of an effector protein at either the amino or the carboxy terminus of an sFv. See Antibody Engineering, ed. Borrebaeck, supra. The antibody fragment may also be a "linear antibody", e.g., as described in U.S. Patent 5,641,870 for example. Such linear antibody fragments may be monospecific or bispecific.

5. Bispecific Antibodies

Bispecific antibodies are antibodies that have binding specificities for at least two different epitopes. Exemplary bispecific antibodies may bind to two different epitopes of a TAT protein as described herein. Other such antibodies may combine a TAT binding site with a binding site for another protein. Alternatively, an anti-TAT arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD3), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16), so as to focus and localize cellular defense mechanisms to the TAT-expressing cell. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express TAT. These antibodies possess a TAT-binding arm and an arm which binds the cytotoxic agent (e.g., saporin, anti-interferon-α, vinca alkaloid, ricin A chain, methotrexate or radioactive isotope hapten). Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g., F(ab')₂ bispecific antibodies).

WO 96/16673 describes a bispecific anti-ErbB2/anti-FcγRIII antibody and U.S. Patent No. 5,837,234 discloses a bispecific anti-ErbB2/anti-FcγRI antibody. A bispecific anti-ErbB2/Fc α antibody is shown in WO98/02463. U.S. Patent No. 5,821,337 teaches a bispecific anti-ErbB2/anti-CD3 antibody.

Methods for making bispecific antibodies are known in the art. Traditional production of full length bispecific antibodies is based on the co-expression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (Millstein et al., Nature 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829, and in Traunecker et al., EMBO J. 10:3655-3659 (1991).

WO 2004/030615

PCT/US2003/028547

According to a different approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. Preferably, the fusion is with an Ig heavy chain constant domain, comprising at least part of the hinge, C_H2, and C_H3 regions. It is preferred to have the first heavy-chain constant region (C_H1) containing the site necessary for light chain bonding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host cell. This provides for greater flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yield of the desired bispecific antibody. It is, however, possible to insert the coding sequences for two or all three polypeptide chains into a single expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios have no significant affect on the yield of the desired chain combination.

In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. This approach is disclosed in WO 94/04690. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology 121:210 (1986).

According to another approach described in U.S. Patent No. 5,731,168, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the C_H3 domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g., tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g., alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies include cross-linked or "heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360, WO 92/200373, and EP 03089). Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Patent No. 4,676,980, along with a number of cross-linking techniques.

Techniques for generating bispecific antibodies from antibody fragments have also been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate

WO 2004/030615

PCT/US2003/028547

F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent, sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Recent progress has facilitated the direct recovery of Fab'-SH fragments from *E. coli*, which can be chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175: 217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a V_H connected to a V_L by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber et al., *J. Immunol.*, 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

6. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

7. Multivalent Antibodies

WO 2004/030615

PCT/US2003/028547

A multivalent antibody may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibodies of the present invention can be multivalent antibodies (which are other than of the IgM class) with three or more antigen binding sites (e.g. tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid encoding the polypeptide chains of the antibody. The multivalent antibody can comprise a dimerization domain and three or more antigen binding sites. The preferred dimerization domain comprises (or consists of) an Fc region or a hinge region. In this scenario, the antibody will comprise an Fc region and three or more antigen binding sites amino-terminal to the Fc region. The preferred multivalent antibody herein comprises (or consists of) three to about eight, but preferably four, antigen binding sites. The multivalent antibody comprises at least one polypeptide chain (and preferably two polypeptide chains), wherein the polypeptide chain(s) comprise two or more variable domains. For instance, the polypeptide chain(s) may comprise $VD1-(X1)_n-VD2-(X2)_n-Fc$, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is one polypeptide chain of an Fc region, X1 and X2 represent an amino acid or polypeptide, and n is 0 or 1. For instance, the polypeptide chain(s) may comprise: VH-CH1-flexible linker-VH-CH1-Fc region chain; or VH-CH1-VH-CH1-Fc region chain. The multivalent antibody herein preferably further comprises at least two (and preferably four) light chain variable domain polypeptides. The multivalent antibody herein may, for instance, comprise from about two to about eight light chain variable domain polypeptides. The light chain variable domain polypeptides contemplated here comprise a light chain variable domain and, optionally, further comprise a CL domain.

8. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, e.g., so as to enhance antigen-dependent cell-mediated cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. This may be achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med. 176:1191-1195 (1992) and Shopes, B. J., Immunol. 148:2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al., Cancer Research 53:2560-2565 (1993). Alternatively, an antibody can be engineered which has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design 3:219-230 (1989).

To increase the serum half life of the antibody, one may incorporate a salvage receptor binding epitope into the antibody (especially an antibody fragment) as described in U.S. Patent 5,739,277, for example. As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (e.g., IgG₁, IgG₂, IgG₃, or IgG₄) that is responsible for increasing the *in vivo* serum half-life of the IgG molecule.

9. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic

WO 2004/030615

PCT/US2003/028547

agent such as a chemotherapeutic agent, a growth inhibitory agent, a toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re. Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminopentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

Conjugates of an antibody and one or more small molecule toxins, such as a calicheamicin, maytansinoids, a tricothene, and CC1065, and the derivatives of these toxins that have toxin activity, are also contemplated herein.

Maytansine and maytansinoids

In one preferred embodiment, an anti-TAT antibody (full length or fragments) of the invention is conjugated to one or more maytansinoid molecules.

Maytansinoids are mitototic inhibitors which act by inhibiting tubulin polymerization. Maytansine was first isolated from the east African shrub *Maytenus serrata* (U.S. Patent No. 3,896,111). Subsequently, it was discovered that certain microbes also produce maytansinoids, such as maytansinol and C-3 maytansinol esters (U.S. Patent No. 4,151,042). Synthetic maytansinol and derivatives and analogues thereof are disclosed, for example, in U.S. Patent Nos. 4,137,230; 4,248,870; 4,256,746; 4,260,608; 4,265,814; 4,294,757; 4,307,016; 4,308,268; 4,308,269; 4,309,428; 4,313,946; 4,315,929; 4,317,821; 4,322,348; 4,331,598; 4,361,650; 4,364,866; 4,424,219; 4,450,254; 4,362,663; and 4,371,533, the disclosures of which are hereby expressly incorporated by reference.

Maytansinoid-antibody conjugates

In an attempt to improve their therapeutic index, maytansine and maytansinoids have been conjugated to antibodies specifically binding to tumor cell antigens. Immunoconjugates containing maytansinoids and their therapeutic use are disclosed, for example, in U.S. Patent Nos. 5,208,020, 5,416,064 and European Patent EP

WO 2004/030615

PCT/US2003/028547

0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al., Proc. Natl. Acad. Sci. USA 93:8618-8623 (1996) described immunoconjugates comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer. The conjugate was found to be highly cytotoxic towards cultured colon cancer cells, and showed antitumor activity in an *in vivo* tumor growth assay. Chari et al., Cancer Research 52:127-131 (1992) describe immunoconjugates in which a
5 maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/*neu* oncogene. The cytotoxicity of the TA.1-maytansinoid conjugate was tested *in vitro* on the human breast cancer cell line SK-BR-3, which expresses 3×10^5 HER-2 surface antigens per cell. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansinoid drug, which could be increased by increasing the number of
10 maytansinoid molecules per antibody molecule. The A7-maytansinoid conjugate showed low systemic cytotoxicity in mice.

Anti-TAT polypeptide antibody-maytansinoid conjugates (immunoconjugates)

Anti-TAT antibody-maytansinoid conjugates are prepared by chemically linking an anti-TAT antibody to a maytansinoid molecule without significantly diminishing the biological activity of either the antibody or the
15 maytansinoid molecule. An average of 3-4 maytansinoid molecules conjugated per antibody molecule has shown efficacy in enhancing cytotoxicity of target cells without negatively affecting the function or solubility of the antibody, although even one molecule of toxin/antibody would be expected to enhance cytotoxicity over the use of naked antibody. Maytansinoids are well known in the art and can be synthesized by known techniques or isolated from natural sources. Suitable maytansinoids are disclosed, for example, in U.S. Patent No.
20 5,208,020 and in the other patents and nonpatent publications referred to hereinabove. Preferred maytansinoids are maytansinol and maytansinol analogues modified in the aromatic ring or at other positions of the maytansinol molecule, such as various maytansinol esters.

There are many linking groups known in the art for making antibody-maytansinoid conjugates, including, for example, those disclosed in U.S. Patent No. 5,208,020 or EP Patent 0 425 235 B1, and Chari
25 et al., Cancer Research 52:127-131 (1992). The linking groups include disulfide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups, or esterase labile groups, as disclosed in the above-identified patents, disulfide and thioether groups being preferred.

Conjugates of the antibody and maytansinoid may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-
30 maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). Particularly preferred coupling agents
35 include N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP) (Carlsson et al. Biochem. J. 173:723-737 [1978]) and N-succinimidyl-4-(2-pyridylthio)pentanoate (SPP) to provide for a disulfide linkage.

WO 2004/030615

PCT/US2003/028547

The linker may be attached to the maytansinoid molecule at various positions, depending on the type of the link. For example, an ester linkage may be formed by reaction with a hydroxyl group using conventional coupling techniques. The reaction may occur at the C-3 position having a hydroxyl group, the C-14 position modified with hydroxymethyl, the C-15 position modified with a hydroxyl group, and the C-20 position having a hydroxyl group. In a preferred embodiment, the linkage is formed at the C-3 position of maytansinol or a maytansinol analogue.

Calicheamicin

Another immunoconjugate of interest comprises an anti-TAT antibody conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family, see U.S. patents 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ_1^I , α_2^I , α_3^I , N-acetyl- γ_1^I , PSAG and θ_1^I (Hinman et al., Cancer Research 53:3336-3342 (1993), Lode et al., Cancer Research 58:2925-2928 (1998) and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug that the antibody can be conjugated is QFA which is an antifolate. Both calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody mediated internalization greatly enhances their cytotoxic effects.

Other cytotoxic agents

Other antitumor agents that can be conjugated to the anti-TAT antibodies of the invention include BCNU, streptozocin, vincristine and 5-fluorouracil, the family of agents known collectively LL-E33288 complex described in U.S. patents 5,053,394, 5,770,710, as well as esperamicins (U.S. patent 5,877,296).

Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, WO 93/21232 published October 28, 1993.

The present invention further contemplates an immunoconjugate formed between an antibody and a compound with nucleolytic activity (e.g., a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

For selective destruction of the tumor, the antibody may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugated anti-TAT antibodies. Examples include At^{211} , I^{131} , I^{125} , Y^{90} , Re^{186} , Re^{188} , Sm^{153} , Bi^{212} , P^{32} , Pb^{212} and radioactive isotopes of Lu. When the conjugate is used for diagnosis, it may comprise a radioactive atom for scintigraphic studies, for example $\text{tc}^{99\text{m}}$ or I^{123} , or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance

WO 2004/030615

PCT/US2003/028547

imaging, mri), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as ^{99m}Tc or ^{123}I , ^{186}Re , ^{188}Re and ^{111}In can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57 can be used to incorporate iodine-123. "Monoclonal Antibodies in Immunosciography" (Chatal, CRC Press 1989) describes other methods in detail.

Conjugates of the antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science* 238:1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026. The linker may be a "cleavable linker" facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., *Cancer Research* 52:127-131 (1992); U.S. Patent No. 5,208,020) may be used.

Alternatively, a fusion protein comprising the anti-TAT antibody and cytotoxic agent may be made, e.g., by recombinant techniques or peptide synthesis. The length of DNA may comprise respective regions encoding the two portions of the conjugate either adjacent one another or separated by a region encoding a linker peptide which does not destroy the desired properties of the conjugate.

In yet another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) which is conjugated to a cytotoxic agent (e.g., a radionucleotide).

10. Immunoliposomes

The anti-TAT antibodies disclosed herein may also be formulated as immunoliposomes. A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., *Proc. Natl. Acad. Sci. USA* 82:3688 (1985); Hwang et al., *Proc. Natl. Acad. Sci. USA* 77:4030 (1980); U.S. Pat. Nos. 4,485,045 and 4,544,545;

WO 2004/030615

PCT/US2003/028547

and WO97/38731 published October 23, 1997. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., *J. Biol. Chem.* 257:286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon et al., *J. National Cancer Inst.* 81(19):1484 (1989).

B. TAT Binding Oligopeptides

TAT binding oligopeptides of the present invention are oligopeptides that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., *Proc. Natl. Acad. Sci. U.S.A.*, 81:3998-4002 (1984); Geysen et al., *Proc. Natl. Acad. Sci. U.S.A.*, 82:178-182 (1985); Geysen et al., in *Synthetic Peptides as Antigens*, 130-149 (1986); Geysen et al., *J. Immunol. Meth.*, 102:259-274 (1987); Schoofs et al., *J. Immunol.*, 140:611-616 (1988), Cwirla, S. E. et al. (1990) *Proc. Natl. Acad. Sci. USA*, 87:6378; Lowman, H.B. et al. (1991) *Biochemistry*, 30:10832; Clackson, T. et al. (1991) *Nature*, 352: 624; Marks, J. D. et al. (1991), *J. Mol. Biol.*, 222:581; Kang, A.S. et al. (1991) *Proc. Natl. Acad. Sci. USA*, 88:8363, and Smith, G. P. (1991) *Current Opin. Biotechnol.*, 2:668).

In this regard, bacteriophage (phage) display is one well known technique which allows one to screen large oligopeptide libraries to identify member(s) of those libraries which are capable of specifically binding to a polypeptide target. Phage display is a technique by which variant polypeptides are displayed as fusion proteins to the coat protein on the surface of bacteriophage particles (Scott, J.K. and Smith, G. P. (1990) *Science* 249: 386). The utility of phage display lies in the fact that large libraries of selectively randomized protein variants (or randomly cloned cDNAs) can be rapidly and efficiently sorted for those sequences that bind to a target molecule with high affinity. Display of peptide (Cwirla, S. E. et al. (1990) *Proc. Natl. Acad. Sci.*

WO 2004/030615

PCT/US2003/028547

USA, 87:6378) or protein (Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363) libraries on phage have been used for screening millions of polypeptides or oligopeptides for ones with specific binding properties (Smith, G. P. (1991) Current Opin. Biotechnol., 2:668). Sorting phage libraries of random mutants requires a strategy for constructing and propagating a large number of variants, a procedure for affinity purification using the target receptor, and a means of evaluating the results of binding enrichments. U.S. Patent Nos. 5,223,409, 5,403,484, 5,571,689, and 5,663,143.

Although most phage display methods have used filamentous phage, lambdoid phage display systems (WO 95/34683; U.S. 5,627,024), T4 phage display systems (Ren, Z-J. et al. (1998) Gene 215:439; Zhu, Z. (1997) CAN 33:534; Jiang, J. et al. (1997) can 128:44380; Ren, Z-J. et al. (1997) CAN 127:215644; Ren, Z-J. (1996) Protein Sci. 5:1833; Efimov, V. P. et al. (1995) Virus Genes 10:173) and T7 phage display systems (Smith, G. P. and Scott, J.K. (1993) Methods in Enzymology, 217, 228-257; U.S. 5,766,905) are also known.

Many other improvements and variations of the basic phage display concept have now been developed. These improvements enhance the ability of display systems to screen peptide libraries for binding to selected target molecules and to display functional proteins with the potential of screening these proteins for desired properties. Combinatorial reaction devices for phage display reactions have been developed (WO 98/14277) and phage display libraries have been used to analyze and control bimolecular interactions (WO 98/20169; WO 98/20159) and properties of constrained helical peptides (WO 98/20036). WO 97/35196 describes a method of isolating an affinity ligand in which a phage display library is contacted with one solution in which the ligand will bind to a target molecule and a second solution in which the affinity ligand will not bind to the target molecule, to selectively isolate binding ligands. WO 97/46251 describes a method of biopanning a random phage display library with an affinity purified antibody and then isolating binding phage, followed by a micropanning process using microplate wells to isolate high affinity binding phage. The use of *Staphylococcus aureus* protein A as an affinity tag has also been reported (Li et al. (1998) Mol Biotech., 9:187). WO 97/47314 describes the use of substrate subtraction libraries to distinguish enzyme specificities using a combinatorial library which may be a phage display library. A method for selecting enzymes suitable for use in detergents using phage display is described in WO 97/09446. Additional methods of selecting specific binding proteins are described in U.S. Patent Nos. 5,498,538, 5,432,018, and WO 98/15833.

Methods of generating peptide libraries and screening these libraries are also disclosed in U.S. Patent Nos. 5,723,286, 5,432,018, 5,580,717, 5,427,908, 5,498,530, 5,770,434, 5,734,018, 5,698,426, 5,763,192, and 5,723,323.

C. TAT Binding Organic Molecules

TAT binding organic molecules are organic molecules other than oligopeptides or antibodies as defined herein that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules

WO 2004/030615

PCT/US2003/028547

that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules may be, for example, aldehydes, ketones, oximes, hydrazones, semicarbazones, carbazides, primary amines, secondary amines, tertiary amines, N-substituted hydrazines, hydrazides, alcohols, ethers, thiols, thioethers, disulfides, carboxylic acids, esters, amides, ureas, carbamates, carbonates, ketals, thioketals, acetals, thioacetals, aryl halides, aryl sulfonates, alkyl halides, alkyl sulfonates, aromatic compounds, heterocyclic compounds, anilines, alkenes, alkynes, diols, amino alcohols, oxazolidines, oxazolines, thiazolidines, thiazolines, enamines, sulfonamides, epoxides, aziridines, isocyanates, sulfonyl chlorides, diazo compounds, acid chlorides, or the like.

D. Screening for Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT Binding Organic Molecules With the Desired Properties

Techniques for generating antibodies, oligopeptides and organic molecules that bind to TAT polypeptides have been described above. One may further select antibodies, oligopeptides or other organic molecules with certain biological characteristics, as desired.

The growth inhibitory effects of an anti-TAT antibody, oligopeptide or other organic molecule of the invention may be assessed by methods known in the art, e.g., using cells which express a TAT polypeptide either endogenously or following transfection with the TAT gene. For example, appropriate tumor cell lines and TAT-transfected cells may be treated with an anti-TAT monoclonal antibody, oligopeptide or other organic molecule of the invention at various concentrations for a few days (e.g., 2-7) days and stained with crystal violet or MTT or analyzed by some other colorimetric assay. Another method of measuring proliferation would be by comparing ³H-thymidine uptake by the cells treated in the presence or absence of an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule of the invention. After treatment, the cells are harvested and the amount of radioactivity incorporated into the DNA quantitated in a scintillation counter. Appropriate positive controls include treatment of a selected cell line with a growth inhibitory antibody known to inhibit growth of that cell line. Growth inhibition of tumor cells *in vivo* can be determined in various ways known in the art. Preferably, the tumor cell is one that overexpresses a TAT polypeptide. Preferably, the anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule will inhibit cell proliferation of a TAT-expressing tumor cell *in vitro* or *in vivo* by about 25-100% compared to the untreated tumor cell, more preferably, by about 30-100%, and even more preferably by about 50-100% or 70-100%, in one embodiment, at an antibody concentration of about 0.5 to 30 μ g/ml. Growth inhibition can be measured at an antibody concentration of about 0.5 to 30 μ g/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. The antibody is growth inhibitory *in vivo* if administration of the anti-TAT antibody at about 1 μ g/kg to about 100 mg/kg body weight results in reduction in tumor size or reduction of tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

WO 2004/030615

PCT/US2003/028547

To select for an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule which induces cell death, loss of membrane integrity as indicated by, e.g., propidium iodide (PI), trypan blue or 7AAD uptake may be assessed relative to control. A PI uptake assay can be performed in the absence of complement and immune effector cells. TAT polypeptide-expressing tumor cells are incubated with medium alone or medium containing the appropriate anti-TAT antibody (e.g., at about 10 µg/ml), TAT binding oligopeptide or TAT binding organic molecule. The cells are incubated for a 3 day time period. Following each treatment, cells are washed and aliquoted into 35 mm strainer-capped 12 x 75 tubes (1ml per tube, 3 tubes per treatment group) for removal of cell clumps. Tubes then receive PI (10 µg/ml). Samples may be analyzed using a FACSCAN® flow cytometer and FACSCONVERT® CellQuest software (Becton Dickinson). Those anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules that induce statistically significant levels of cell death as determined by PI uptake may be selected as cell death-inducing anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules.

To screen for antibodies, oligopeptides or other organic molecules which bind to an epitope on a TAT polypeptide bound by an antibody of interest, a routine cross-blocking assay such as that described in Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. This assay can be used to determine if a test antibody, oligopeptide or other organic molecule binds the same site or epitope as a known anti-TAT antibody. Alternatively, or additionally, epitope mapping can be performed by methods known in the art. For example, the antibody sequence can be mutagenized such as by alanine scanning, to identify contact residues. The mutant antibody is initially tested for binding with polyclonal antibody to ensure proper folding. In a different method, peptides corresponding to different regions of a TAT polypeptide can be used in competition assays with the test antibodies or with a test antibody and an antibody with a characterized or known epitope.

E. Antibody Dependent Enzyme Mediated Prodrug Therapy (ADEPT)

The antibodies of the present invention may also be used in ADEPT by conjugating the antibody to a prodrug-activating enzyme which converts a prodrug (e.g., a peptidyl chemotherapeutic agent, see WO81/01145) to an active anti-cancer drug. See, for example, WO 88/07378 and U.S. Patent No. 4,975,278.

The enzyme component of the immunoconjugate useful for ADEPT includes any enzyme capable of acting on a prodrug in such a way so as to convert it into its more active, cytotoxic form.

Enzymes that are useful in the method of this invention include, but are not limited to, alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic 5-fluorocytosine into the anti-cancer drug, 5-fluorouracil; proteases, such as serratia protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into free drugs; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as β-galactosidase and neuraminidase useful for converting glycosylated prodrugs into free drugs; β-lactamase useful for converting drugs derivatized with β-lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful

WO 2004/030615

PCT/US2003/028547

for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Alternatively, antibodies with enzymatic activity, also known in the art as "abzymes", can be used to convert the prodrugs of the invention into free active drugs (see, e.g., Massey, *Nature* 328:457-458 (1987)). Antibody-abzyme conjugates can be prepared as described herein for delivery of the abzyme to a tumor cell population.

5 The enzymes of this invention can be covalently bound to the anti-TAT antibodies by techniques well known in the art such as the use of the heterobifunctional crosslinking reagents discussed above. Alternatively, fusion proteins comprising at least the antigen binding region of an antibody of the invention linked to at least a functionally active portion of an enzyme of the invention can be constructed using recombinant DNA techniques well known in the art (see, e.g., Neuberger et al., *Nature* 312:604-608 (1984)).

10 F. Full-Length TAT Polypeptides

The present invention also provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as TAT polypeptides. In particular, cDNAs (partial and full-length) encoding various TAT polypeptides have been identified and isolated, as disclosed in further detail in the Examples below.

15 As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the TAT polypeptides and encoding nucleic acids described herein, in some cases, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

20 G. Anti-TAT Antibody and TAT Polypeptide Variants

In addition to the anti-TAT antibodies and full-length native sequence TAT polypeptides described herein, it is contemplated that anti-TAT antibody and TAT polypeptide variants can be prepared. Anti-TAT antibody and TAT polypeptide variants can be prepared by introducing appropriate nucleotide changes into the encoding DNA, and/or by synthesis of the desired antibody or polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the anti-TAT antibody or TAT polypeptide, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

25 Variations in the anti-TAT antibodies and TAT polypeptides described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the antibody or polypeptide that results in a change in the amino acid sequence as compared with the native sequence antibody or polypeptide. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the anti-TAT antibody or TAT polypeptide. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the anti-TAT antibody or

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WO 2004/030615

PCT/US2003/028547

TAT polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

Anti-TAT antibody and TAT polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native antibody or protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the anti-TAT antibody or TAT polypeptide.

Anti-TAT antibody and TAT polypeptide fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating antibody or polypeptide fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired antibody or polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, anti-TAT antibody and TAT polypeptide fragments share at least one biological and/or immunological activity with the native anti-TAT antibody or TAT polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

WO 2004/030615

PCT/US2003/028547

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe; norleucine	leu
15	Leu (L)	norleucine; ile; val; met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
20	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the anti-TAT antibody or TAT polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining

30 (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

35 (3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

40 Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

WO 2004/030615

PCT/US2003/028547

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the anti-TAT antibody or TAT polypeptide variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244:1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

Any cysteine residue not involved in maintaining the proper conformation of the anti-TAT antibody or TAT polypeptide also may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the anti-TAT antibody or TAT polypeptide to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e.g., a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e.g., 6-7 sites) are mutated to generate all possible amino substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e.g., binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and human TAT polypeptide. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

Nucleic acid molecules encoding amino acid sequence variants of the anti-TAT antibody are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-

WO 2004/030615

PCT/US2003/028547

mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of the anti-TAT antibody.

H. Modifications of Anti-TAT Antibodies and TAT Polypeptides

Covalent modifications of anti-TAT antibodies and TAT polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an anti-TAT antibody or TAT polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the anti-TAT antibody or TAT polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking anti-TAT antibody or TAT polypeptide to a water-insoluble support matrix or surface for use in the method for purifying anti-TAT antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the anti-TAT antibody or TAT polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the antibody or polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence anti-TAT antibody or TAT polypeptide (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence anti-TAT antibody or TAT polypeptide. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Glycosylation of antibodies and other polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-aceylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

WO 2004/030615

PCT/US2003/028547

Addition of glycosylation sites to the anti-TAT antibody or TAT polypeptide is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the sequence of the original anti-TAT antibody or TAT polypeptide (for O-linked glycosylation sites). The anti-TAT antibody or TAT polypeptide amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the anti-TAT antibody or TAT polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the anti-TAT antibody or TAT polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the anti-TAT antibody or TAT polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of anti-TAT antibody or TAT polypeptide comprises linking the antibody or polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. The antibody or polypeptide also may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

The anti-TAT antibody or TAT polypeptide of the present invention may also be modified in a way to form chimeric molecules comprising an anti-TAT antibody or TAT polypeptide fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the anti-TAT antibody or TAT polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the anti-TAT antibody or TAT polypeptide. The presence of such epitope-tagged forms of the anti-TAT antibody or TAT polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the anti-TAT

WO 2004/030615

PCT/US2003/028547

antibody or TAT polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the anti-TAT antibody or TAT polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of an anti-TAT antibody or TAT polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH₂ and CH₃, or the hinge, CH₁, CH₂ and CH₃ regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

I. Preparation of Anti-TAT Antibodies and TAT Polypeptides

The description below relates primarily to production of anti-TAT antibodies and TAT polypeptides by culturing cells transformed or transfected with a vector containing anti-TAT antibody- and TAT polypeptide-encoding nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare anti-TAT antibodies and TAT polypeptides. For instance, the appropriate amino acid sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the anti-TAT antibody or TAT polypeptide may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the desired anti-TAT antibody or TAT polypeptide.

1. Isolation of DNA Encoding Anti-TAT Antibody or TAT Polypeptide

DNA encoding anti-TAT antibody or TAT polypeptide may be obtained from a cDNA library prepared from tissue believed to possess the anti-TAT antibody or TAT polypeptide mRNA and to express it at a detectable level. Accordingly, human anti-TAT antibody or TAT polypeptide DNA can be conveniently obtained from a cDNA library prepared from human tissue. The anti-TAT antibody- or TAT polypeptide-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated

WO 2004/030615

PCT/US2003/028547

nucleic acid synthesis).

Libraries can be screened with probes (such as oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding anti-TAT antibody or TAT polypeptide is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

Techniques for screening a cDNA library are well known in the art. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl₂, CaPO₄, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology,

WO 2004/030615

PCT/US2003/028547

52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescens*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG karf*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

Full length antibody, antibody fragments, and antibody fusion proteins can be produced in bacteria, in particular when glycosylation and Fc effector function are not needed, such as when the therapeutic antibody is conjugated to a cytotoxic agent (e.g., a toxin) and the immunoconjugate by itself shows effectiveness in tumor cell destruction. Full length antibodies have greater half life in circulation. Production in *E. coli* is faster and more cost efficient. For expression of antibody fragments and polypeptides in bacteria, see, e.g., U.S. 5,648,237 (Carter et. al.), U.S. 5,789,199 (Joly et al.), and U.S. 5,840,523 (Simmons et al.) which describes translation initiation regio (TIR) and signal sequences for optimizing expression and secretion, these patents incorporated herein by reference. After expression, the antibody is isolated from the *E. coli* cell paste in a soluble fraction and can be purified through, e.g., a protein A or G column depending on the isotype. Final purification can be carried out similar to the process for purifying antibody expressed e.g., in CHO cells.

WO 2004/030615

PCT/US2003/028547

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for anti-TAT antibody- or TAT polypeptide-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolyptocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated anti-TAT antibody or TAT polypeptide are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells, such as cell cultures of cotton, corn, potato, soybean, petunia, tomato, and tobacco. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruitfly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol. 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub et al., Proc. Natl. Acad. Sci. USA 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2,

WO 2004/030615

PCT/US2003/028547

HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci. 383:44-68 (1982)); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

Host cells are transformed with the above-described expression or cloning vectors for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding anti-TAT antibody or TAT polypeptide may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The TAT may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the anti-TAT antibody- or TAT polypeptide-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification

WO 2004/030615

PCT/US2003/028547

of cells competent to take up the anti-TAT antibody- or TAT polypeptide-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the anti-TAT antibody- or TAT polypeptide-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding anti-TAT antibody or TAT polypeptide.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

Anti-TAT antibody or TAT polypeptide transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the anti-TAT antibody or TAT polypeptide by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the

WO 2004/030615

PCT/US2003/028547

late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the anti-TAT antibody or TAT polypeptide coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding anti-TAT antibody or TAT polypeptide.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of anti-TAT antibody or TAT polypeptide in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Culturing the Host Cells

The host cells used to produce the anti-TAT antibody or TAT polypeptide of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham et al Meth. Enz. 58:44 (1979), Barnes et al., Anal. Biochem. 102:255 (1980), U.S. Pat. Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Patent Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

WO 2004/030615

PCT/US2003/028547

5. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence TAT polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to TAT DNA and encoding a specific antibody epitope.

6. Purification of Anti-TAT Antibody and TAT Polypeptide

Forms of anti-TAT antibody and TAT polypeptide may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of anti-TAT antibody and TAT polypeptide can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify anti-TAT antibody and TAT polypeptide from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the anti-TAT antibody and TAT polypeptide. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular anti-TAT antibody or TAT polypeptide produced.

When using recombinant techniques, the antibody can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter et al., Bio/Technology 10:163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium

WO 2004/030615

PCT/US2003/028547

acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human $\gamma 1$, $\gamma 2$ or $\gamma 4$ heavy chains (Lindmark et al., J. Immunol. Meth. 62:1-13 (1983)). Protein G is recommended for all mouse isotypes and for human $\gamma 3$ (Guss et al., EMBO J. 5:15671575 (1986)). The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody comprises a C_H3 domain, the Bakerbond ABX™ resin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

Following any preliminary purification step(s), the mixture comprising the antibody of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, preferably performed at low salt concentrations (e.g., from about 0-0.25M salt).

J. Pharmaceutical Formulations

Therapeutic formulations of the anti-TAT antibodies, TAT binding oligopeptides, TAT binding organic molecules and/or TAT polypeptides used in accordance with the present invention are prepared for storage by mixing the antibody, polypeptide, oligopeptide or organic molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as acetate, Tris, phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine,

WO 2004/030615

PCT/US2003/028547

histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; tonicifiers such as trehalose and sodium chloride; sugars such as sucrose, mannitol, trehalose or sorbitol; surfactant such as polysorbate; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN®, PLURONICS® or polyethylene glycol (PEG). The antibody preferably comprises the antibody at a concentration of between 5-200 mg/ml, preferably between 10-100 mg/ml.

The formulations herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, in addition to an anti-TAT antibody, TAT binding oligopeptide, or TAT binding organic molecule, it may be desirable to include in the one formulation, an additional antibody, e.g., a second anti-TAT antibody which binds a different epitope on the TAT polypeptide, or an antibody to some other target such as a growth factor that affects the growth of the particular cancer. Alternatively, or additionally, the composition may further comprise a chemotherapeutic agent, cytotoxic agent, cytokine, growth inhibitory agent, anti-hormonal agent, and/or cardioprotectant. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Osol, A. Ed. (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT® (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

K. Diagnosis and Treatment with Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT Binding Organic Molecules

To determine TAT expression in the cancer, various diagnostic assays are available. In one embodiment, TAT polypeptide overexpression may be analyzed by immunohistochemistry (IHC). Paraffin embedded tissue sections from a tumor biopsy may be subjected to the IHC assay and accorded a TAT protein staining intensity criteria as follows:

WO 2004/030615

PCT/US2003/028547

Score 0 - no staining is observed or membrane staining is observed in less than 10% of tumor cells.

Score 1+ - a faint/barely perceptible membrane staining is detected in more than 10% of the tumor cells. The cells are only stained in part of their membrane.

Score 2+ - a weak to moderate complete membrane staining is observed in more than 10% of the tumor cells.

Score 3+ - a moderate to strong complete membrane staining is observed in more than 10% of the tumor cells.

Those tumors with 0 or 1+ scores for TAT polypeptide expression may be characterized as not overexpressing TAT, whereas those tumors with 2+ or 3+ scores may be characterized as overexpressing TAT.

Alternatively, or additionally, FISH assays such as the INFORM® (sold by Ventana, Arizona) or PATHVISION® (Vysis, Illinois) may be carried out on formalin-fixed, paraffin-embedded tumor tissue to determine the extent (if any) of TAT overexpression in the tumor.

TAT overexpression or amplification may be evaluated using an *in vivo* diagnostic assay, e.g., by administering a molecule (such as an antibody, oligopeptide or organic molecule) which binds the molecule to be detected and is tagged with a detectable label (e.g., a radioactive isotope or a fluorescent label) and externally scanning the patient for localization of the label.

As described above, the anti-TAT antibodies, oligopeptides and organic molecules of the invention have various non-therapeutic applications. The anti-TAT antibodies, oligopeptides and organic molecules of the present invention can be useful for diagnosis and staging of TAT polypeptide-expressing cancers (e.g., in radioimaging). The antibodies, oligopeptides and organic molecules are also useful for purification or immunoprecipitation of TAT polypeptide from cells, for detection and quantitation of TAT polypeptide *in vitro*, e.g., in an ELISA or a Western blot, to kill and eliminate TAT-expressing cells from a population of mixed cells as a step in the purification of other cells.

Currently, depending on the stage of the cancer, cancer treatment involves one or a combination of the following therapies: surgery to remove the cancerous tissue, radiation therapy, and chemotherapy. Anti-TAT antibody, oligopeptide or organic molecule therapy may be especially desirable in elderly patients who do not tolerate the toxicity and side effects of chemotherapy well and in metastatic disease where radiation therapy has limited usefulness. The tumor targeting anti-TAT antibodies, oligopeptides and organic molecules of the invention are useful to alleviate TAT-expressing cancers upon initial diagnosis of the disease or during relapse. For therapeutic applications, the anti-TAT antibody, oligopeptide or organic molecule can be used alone, or in combination therapy with, e.g., hormones, antiangiogens, or radiolabelled compounds, or with surgery, cryotherapy, and/or radiotherapy. Anti-TAT antibody, oligopeptide or organic molecule treatment can be administered in conjunction with other forms of conventional therapy, either consecutively with, pre- or post-conventional therapy. Chemotherapeutic drugs such as TAXOTERE® (docetaxel), TAXOL® (paclitaxel), estramustine and mitoxantrone are used in treating cancer, in particular, in good risk patients. In the present method of the invention for treating or alleviating cancer, the cancer patient can be administered anti-TAT

WO 2004/030615

PCT/US2003/028547

antibody, oligopeptide or organic molecule in conjunction with treatment with the one or more of the preceding chemotherapeutic agents. In particular, combination therapy with paclitaxel and modified derivatives (see, e.g., EP0600517) is contemplated. The anti-TAT antibody, oligopeptide or organic molecule will be administered with a therapeutically effective dose of the chemotherapeutic agent. In another embodiment, the anti-TAT antibody, oligopeptide or organic molecule is administered in conjunction with chemotherapy to enhance the activity and efficacy of the chemotherapeutic agent, e.g., paclitaxel. The Physicians' Desk Reference (PDR) discloses dosages of these agents that have been used in treatment of various cancers. The dosing regimen and dosages of these aforementioned chemotherapeutic drugs that are therapeutically effective will depend on the particular cancer being treated, the extent of the disease and other factors familiar to the physician of skill in the art and can be determined by the physician.

In one particular embodiment, a conjugate comprising an anti-TAT antibody, oligopeptide or organic molecule conjugated with a cytotoxic agent is administered to the patient. Preferably, the immunoconjugate bound to the TAT protein is internalized by the cell, resulting in increased therapeutic efficacy of the immunoconjugate in killing the cancer cell to which it binds. In a preferred embodiment, the cytotoxic agent targets or interferes with the nucleic acid in the cancer cell. Examples of such cytotoxic agents are described above and include maytansinoids, calicheamicins, ribonucleases and DNA endonucleases.

The anti-TAT antibodies, oligopeptides, organic molecules or toxin conjugates thereof are administered to a human patient, in accord with known methods, such as intravenous administration, e.g., as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerebrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. Intravenous or subcutaneous administration of the antibody, oligopeptide or organic molecule is preferred.

Other therapeutic regimens may be combined with the administration of the anti-TAT antibody, oligopeptide or organic molecule. The combined administration includes co-administration, using separate formulations or a single pharmaceutical formulation, and consecutive administration in either order, wherein preferably there is a time period while both (or all) active agents simultaneously exert their biological activities. Preferably such combined therapy results in a synergistic therapeutic effect.

It may also be desirable to combine administration of the anti-TAT antibody or antibodies, oligopeptides or organic molecules, with administration of an antibody directed against another tumor antigen associated with the particular cancer.

In another embodiment, the therapeutic treatment methods of the present invention involves the combined administration of an anti-TAT antibody (or antibodies), oligopeptides or organic molecules and one or more chemotherapeutic agents or growth inhibitory agents, including co-administration of cocktails of different chemotherapeutic agents. Chemotherapeutic agents include estramustine phosphate, prednimustine, cisplatin, 5-fluorouracil, melphalan, cyclophosphamide, hydroxyurea and hydroxyureataxanes (such as paclitaxel and doxorubicin) and/or anthracycline antibiotics. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in Chemotherapy

WO 2004/030615

PCT/US2003/028547

Service Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992).

The antibody, oligopeptide or organic molecule may be combined with an anti-hormonal compound; e.g., an anti-estrogen compound such as tamoxifen; an anti-progesterone such as onapristone (see, EP 616 812); or an anti-androgen such as flutamide, in dosages known for such molecules. Where the cancer to be treated is androgen independent cancer, the patient may previously have been subjected to anti-androgen therapy and, after the cancer becomes androgen independent, the anti-TAT antibody, oligopeptide or organic molecule (and optionally other agents as described herein) may be administered to the patient.

Sometimes, it may be beneficial to also co-administer a cardioprotectant (to prevent or reduce myocardial dysfunction associated with the therapy) or one or more cytokines to the patient. In addition to the above therapeutic regimes, the patient may be subjected to surgical removal of cancer cells and/or radiation therapy, before, simultaneously with, or post antibody, oligopeptide or organic molecule therapy. Suitable dosages for any of the above co-administered agents are those presently used and may be lowered due to the combined action (synergy) of the agent and anti-TAT antibody, oligopeptide or organic molecule.

For the prevention or treatment of disease, the dosage and mode of administration will be chosen by the physician according to known criteria. The appropriate dosage of antibody, oligopeptide or organic molecule will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the antibody, oligopeptide or organic molecule is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, oligopeptide or organic molecule, and the discretion of the attending physician. The antibody, oligopeptide or organic molecule is suitably administered to the patient at one time or over a series of treatments. Preferably, the antibody, oligopeptide or organic molecule is administered by intravenous infusion or by subcutaneous injections. Depending on the type and severity of the disease, about 1 µg/kg to about 50 mg/kg body weight (e.g., about 0.1-15mg/kg/dose) of antibody can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A dosing regimen can comprise administering an initial loading dose of about 4 mg/kg, followed by a weekly maintenance dose of about 2 mg/kg of the anti-TAT antibody. However, other dosage regimens may be useful. A typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. The progress of this therapy can be readily monitored by conventional methods and assays and based on criteria known to the physician or other persons of skill in the art.

Aside from administration of the antibody protein to the patient, the present application contemplates administration of the antibody by gene therapy. Such administration of nucleic acid encoding the antibody is encompassed by the expression "administering a therapeutically effective amount of an antibody". See, for example, WO96/07321 published March 14, 1996 concerning the use of gene therapy to generate intracellular antibodies.

There are two major approaches to getting the nucleic acid (optionally contained in a vector) into the patient's cells; *in vivo* and *ex vivo*. For *in vivo* delivery the nucleic acid is injected directly into the patient,

WO 2004/030615

PCT/US2003/028547

usually at the site where the antibody is required. For *ex vivo* treatment, the patient's cells are removed, the nucleic acid is introduced into these isolated cells and the modified cells are administered to the patient either directly or, for example, encapsulated within porous membranes which are implanted into the patient (see, e.g., U.S. Patent Nos. 4,892,538 and 5,283,187). There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. A commonly used vector for *ex vivo* delivery of the gene is a retroviral vector.

The currently preferred *in vivo* nucleic acid transfer techniques include transfection with viral vectors (such as adenovirus, Herpes simplex I virus, or adeno-associated virus) and lipid-based systems (useful lipids for lipid-mediated transfer of the gene are DOTMA, DOPE and DC-Chol, for example). For review of the currently known gene marking and gene therapy protocols see Anderson et al., Science 256:808-813 (1992). See also WO 93/25673 and the references cited therein.

The anti-TAT antibodies of the invention can be in the different forms encompassed by the definition of "antibody" herein. Thus, the antibodies include full length or intact antibody, antibody fragments, native sequence antibody or amino acid variants, humanized, chimeric or fusion antibodies, immunoconjugates, and functional fragments thereof. In fusion antibodies an antibody sequence is fused to a heterologous polypeptide sequence. The antibodies can be modified in the Fc region to provide desired effector functions. As discussed in more detail in the sections herein, with the appropriate Fc regions, the naked antibody bound on the cell surface can induce cytotoxicity, e.g., via antibody-dependent cellular cytotoxicity (ADCC) or by recruiting complement in complement dependent cytotoxicity, or some other mechanism. Alternatively, where it is desirable to eliminate or reduce effector function, so as to minimize side effects or therapeutic complications, certain other Fc regions may be used.

In one embodiment, the antibody competes for binding or bind substantially to, the same epitope as the antibodies of the invention. Antibodies having the biological characteristics of the present anti-TAT antibodies of the invention are also contemplated, specifically including the *in vivo* tumor targeting and any cell proliferation inhibition or cytotoxic characteristics.

Methods of producing the above antibodies are described in detail herein.

The present anti-TAT antibodies, oligopeptides and organic molecules are useful for treating a TAT-expressing cancer or alleviating one or more symptoms of the cancer in a mammal. Such a cancer includes prostate cancer, cancer of the urinary tract, lung cancer, breast cancer, colon cancer and ovarian cancer, more specifically, prostate adenocarcinoma, renal cell carcinomas, colorectal adenocarcinomas, lung adenocarcinomas, lung squamous cell carcinomas, and pleural mesothelioma. The cancers encompass metastatic cancers of any of the preceding. The antibody, oligopeptide or organic molecule is able to bind to at least a portion of the cancer cells that express TAT polypeptide in the mammal. In a preferred embodiment, the antibody, oligopeptide or organic molecule is effective to destroy or kill TAT-expressing tumor cells or inhibit

WO 2004/030615

PCT/US2003/028547

the growth of such tumor cells, *in vitro* or *in vivo*, upon binding to TAT polypeptide on the cell. Such an antibody includes a naked anti-TAT antibody (not conjugated to any agent). Naked antibodies that have cytotoxic or cell growth inhibition properties can be further harnessed with a cytotoxic agent to render them even more potent in tumor cell destruction. Cytotoxic properties can be conferred to an anti-TAT antibody by, e.g., conjugating the antibody with a cytotoxic agent, to form an immunoconjugate as described herein. The cytotoxic agent or a growth inhibitory agent is preferably a small molecule. Toxins such as calicheamicin or a maytansinoid and analogs or derivatives thereof, are preferable.

The invention provides a composition comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. For the purposes of treating cancer, compositions can be administered to the patient in need of such treatment, wherein the composition can comprise one or more anti-TAT antibodies present as an immunoconjugate or as the naked antibody. In a further embodiment, the compositions can comprise these antibodies, oligopeptides or organic molecules in combination with other therapeutic agents such as cytotoxic or growth inhibitory agents, including chemotherapeutic agents. The invention also provides formulations comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. In one embodiment, the formulation is a therapeutic formulation comprising a pharmaceutically acceptable carrier.

Another aspect of the invention is isolated nucleic acids encoding the anti-TAT antibodies. Nucleic acids encoding both the H and L chains and especially the hypervariable region residues, chains which encode the native sequence antibody as well as variants, modifications and humanized versions of the antibody, are encompassed.

The invention also provides methods useful for treating a TAT polypeptide-expressing cancer or alleviating one or more symptoms of the cancer in a mammal, comprising administering a therapeutically effective amount of an anti-TAT antibody, oligopeptide or organic molecule to the mammal. The antibody, oligopeptide or organic molecule therapeutic compositions can be administered short term (acute) or chronic, or intermittent as directed by physician. Also provided are methods of inhibiting the growth of, and killing a TAT polypeptide-expressing cell.

The invention also provides kits and articles of manufacture comprising at least one anti-TAT antibody, oligopeptide or organic molecule. Kits containing anti-TAT antibodies, oligopeptides or organic molecules find use, e.g., for TAT cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For example, for isolation and purification of TAT, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT *in vitro*, e.g., in an ELISA or a Western blot. Such antibody, oligopeptide or organic molecule useful for detection may be provided with a label such as a fluorescent or radiolabel.

L. Articles of Manufacture and Kits

Another embodiment of the invention is an article of manufacture containing materials useful for the treatment of anti-TAT expressing cancer. The article of manufacture comprises a container and a label or

WO 2004/030615

PCT/US2003/028547

package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is effective for treating the cancer condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an anti-TAT antibody, oligopeptide or organic molecule of the invention. The label or package insert indicates that the composition is used for treating cancer. The label or package insert will further comprise instructions for administering the antibody, oligopeptide or organic molecule composition to the cancer patient. Additionally, the article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

Kits are also provided that are useful for various purposes, e.g., for TAT-expressing cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For isolation and purification of TAT polypeptide, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT polypeptide *in vitro*, e.g., in an ELISA or a Western blot. As with the article of manufacture, the kit comprises a container and a label or package insert on or associated with the container. The container holds a composition comprising at least one anti-TAT antibody, oligopeptide or organic molecule of the invention. Additional containers may be included that contain, e.g., diluents and buffers, control antibodies. The label or package insert may provide a description of the composition as well as instructions for the intended *in vitro* or diagnostic use.

M. Uses for TAT Polypeptides and TAT-Polypeptide Encoding Nucleic Acids

Nucleotide sequences (or their complement) encoding TAT polypeptides have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA probes. TAT-encoding nucleic acid will also be useful for the preparation of TAT polypeptides by the recombinant techniques described herein, wherein those TAT polypeptides may find use, for example, in the preparation of anti-TAT antibodies as described herein.

The full-length native sequence TAT gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length TAT cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of TAT or TAT from other species) which have a desired sequence identity to the native TAT sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence TAT. By way of example, a screening method will comprise isolating the coding region of the TAT gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety

WO 2004/030615

PCT/US2003/028547

of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the TAT gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below. Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the TAT-encoding nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target TAT mRNA (sense) or TAT DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of TAT DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. Such methods are encompassed by the present invention. The antisense oligonucleotides thus may be used to block expression of TAT proteins, wherein those TAT proteins may play a role in the induction of cancer in mammals. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Preferred intragenic sites for antisense binding include the region incorporating the translation initiation/start codon (5'-AUG / 5'-ATG) or termination/stop codon (5'-UAA, 5'-UAG and 5'-UGA / 5'-TAA, 5'-TAG and 5'-TGA) of the open reading frame (ORF) of the gene. These regions refer to a portion of the mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation or termination codon. Other preferred regions for antisense binding include: introns; exons; intron-exon junctions; the open reading frame (ORF) or "coding region," which is the region between the translation initiation codon and the translation termination codon; the 5' cap of an mRNA which comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage and includes 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap; the 5' untranslated region (5' UTR), the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene; and the 3' untranslated region (3' UTR), the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene.

WO 2004/030615

PCT/US2003/028547

Specific examples of preferred antisense compounds useful for inhibiting expression of TAT proteins include oligonucleotides containing modified backbones or non-natural internucleoside linkages. Oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotri-esters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, selenophosphates and borano-phosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e. a single inverted nucleoside residue which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included. Representative United States patents that teach the preparation of phosphorus-containing linkages include, but are not limited to, U.S. Pat. Nos.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697 and 5,625,050, each of which is herein incorporated by reference.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH₂ component parts. Representative United States patents that teach the preparation of such oligonucleosides include, but are not limited to, U.S. Pat. Nos.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269 and 5,677,439, each of which is herein incorporated by reference.

In other preferred antisense oligonucleotides, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic

WO 2004/030615

PCT/US2003/028547

that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen et al., Science, 1991, 254, 1497-1500.

Preferred antisense oligonucleotides incorporate phosphorothioate backbones and/or heteroatom backbones, and in particular $-\text{CH}_2\text{-NH-O-CH}_2-$, $-\text{CH}_2\text{-N(CH}_3\text{)-O-CH}_2-$ [known as a methylene (methylimino) or MMI backbone], $-\text{CH}_2\text{-O-N(CH}_3\text{)-CH}_2-$, $-\text{CH}_2\text{-N(CH}_3\text{)-N(CH}_3\text{)-CH}_2-$ and $-\text{O-N(CH}_3\text{)-CH}_2\text{-CH}_2-$ [wherein the native phosphodiester backbone is represented as $-\text{O-P-O-CH}_2-$] described in the above referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above referenced U.S. Pat. No. 5,602,240. Also preferred are antisense oligonucleotides having morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-alkyl, S-alkyl, or N-alkyl; O-alkenyl, S-alkenyl, or N-alkenyl; O-alkynyl, S-alkynyl or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $\text{O}[(\text{CH}_2)_n\text{O}]_m\text{CH}_3$, $\text{O}(\text{CH}_2)_n\text{OCH}_3$, $\text{O}(\text{CH}_2)_n\text{NH}_2$, $\text{O}(\text{CH}_2)_n\text{CH}_3$, $\text{O}(\text{CH}_2)_n\text{ONH}_2$, and $\text{O}(\text{CH}_2)_n\text{ON}[(\text{CH}_2)_m\text{CH}_3]_2$, where n and m are from 1 to about 10. Other preferred antisense oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3 , OCN, Cl, Br, CN, CF_3 , OCF_3 , SOCH_3 , SO_2CH_3 , ONO_2 , NO_2 , N_3 , NH_2 , heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy ($2'\text{-O-CH}_2\text{CH}_2\text{OCH}_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., Helv. Chim. Acta, 1995, 78, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminoethoxy, i.e., a $\text{O}(\text{CH}_2)_2\text{ON}(\text{CH}_3)_2$ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., $2'\text{-O-CH}_2\text{-O-CH}_2\text{-N(CH}_3)_2$.

A further preferred modification includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring thereby forming a bicyclic sugar moiety. The linkage is preferably a methylene ($-\text{CH}_2-$)_n group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in WO 98/39352 and WO 99/14226.

Other preferred modifications include 2'-methoxy ($2'\text{-O-CH}_3$), 2'-aminopropoxy ($2'\text{-OCH}_2\text{CH}_2\text{CH}_2$

WO 2004/030615

PCT/US2003/028547

NH₂), 2'-allyl (2'-CH₂-CH=CH₂), 2'-O-allyl (2'-O-CH₂-CH=CH₂) and 2'-fluoro (2'-F). The 2'-modification may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar.

5 Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Pat. Nos.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 5,792,747; and 5,700,920, each of which is herein incorporated by reference in its entirety.

10 Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of

15 adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl (-C≡C-CH₃ or -CH₂-C≡CH) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine

20 and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified nucleobases include tricyclic pyrimidines such as phenoxazine cytidine(1H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido[5,4-b][1,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g. 9-(2-aminoethoxy)-H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), carbazole cytidine

25 (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. I., ed. John Wiley & Sons, 1990, and

30 those disclosed by Englisch et al., Angewandte Chemie, International Edition, 1991, 30, 613. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2.degree. C. (Sanghvi et al, Antisense Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are preferred base substitutions, even more

35 particularly when combined with 2'-O-methoxyethyl sugar modifications. Representative United States patents

WO 2004/030615

PCT/US2003/028547

that teach the preparation of modified nucleobases include, but are not limited to: U.S. Pat. No. 3,687,808, as well as U.S. Pat. Nos.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121; 5,596,091; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; 5,681,941 and 5,750,692, each of which is herein incorporated by reference.

5 Another modification of antisense oligonucleotides chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. The compounds of the invention can include conjugate groups covalently bound to functional groups such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of
10 oligomers. Typical conjugates groups include cholesterol, lipids, cation lipids, phospholipids, cationic phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve oligomer uptake, enhance oligomer resistance to degradation, and/or strengthen sequence-specific hybridization with RNA. Groups that enhance the pharmacokinetic properties, in the context
15 of this invention, include groups that improve oligomer uptake, distribution, metabolism or excretion. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., Bioorg. Med. Chem. Lett., 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci., 1992, 660, 306-309; Manoharan et al., Bioorg. Med. Chem. Lett., 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., Nucl.
20 Acids Res., 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J., 1991, 10, 1111-1118; Kabanov et al., FEBS Lett., 1990, 259, 327-330; Svinarchuk et al., Biochimie, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654; Shea et al., Nucl. Acids Res., 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan
25 et al., Nucleosides & Nucleotides, 1995, 14, 969-973), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety. Oligonucleotides of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone,
30 ibuprofen, suprofen, fenbufen, ketoprofen, (S)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in U.S. patent application Ser. No. 09/334,130 (filed Jun. 15, 1999) and United States patents Nos.: 4,828,979; 4,948,882; 5,218,105; 5,525,465;
35 5,541,313; 5,545,730; 5,552,538; 5,578,717; 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025;

WO 2004/030615

PCT/US2003/028547

4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241; 5,391,723; 5,416,203; 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, each of which is herein incorporated by reference.

5 It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds which are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each
10 made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular
15 endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Chimeric antisense compounds of the invention may be formed as composite structures of two or more
20 oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Preferred chimeric antisense oligonucleotides incorporate at least one 2' modified sugar (preferably 2'-O-(CH₂)₂-O-CH₃) at the 3' terminal to confer nuclease resistance and a region with at least 4 contiguous 2'-H sugars to confer RNase H activity. Such compounds have also been referred to in the art as hybrids or gapmers. Preferred gapmers have a region of 2' modified sugars (preferably 2'-O-(CH₂)₂-O-CH₃) at the 3'-terminal and
25 at the 5' terminal separated by at least one region having at least 4 contiguous 2'-H sugars and preferably incorporate phosphorothioate backbone linkages. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S. Pat. Nos. 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, each of which is herein incorporated by reference in its entirety.

30 The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives. The compounds
35 of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor targeted molecules, oral,

WO 2004/030615

PCT/US2003/028547

rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption assisting formulations include, but are not limited to, U.S. Pat. Nos. 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710,

WO 2004/030615

PCT/US2003/028547

720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related TAT coding sequences.

5 Nucleotide sequences encoding a TAT can also be used to construct hybridization probes for mapping the gene which encodes that TAT and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

10 When the coding sequences for TAT encode a protein which binds to another protein (example, where the TAT is a receptor), the TAT can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor TAT can be used to isolate correlative ligand(s).
15 Screening assays can be designed to find lead compounds that mimic the biological activity of a native TAT or a receptor for TAT. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.
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Nucleic acids which encode TAT or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding TAT. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S.
25 Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for TAT transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding TAT introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding TAT. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In
30 accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential
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WO 2004/030615

PCT/US2003/028547

therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of TAT can be used to construct a TAT "knock out" animal which has a defective or altered gene encoding TAT as a result of homologous recombination between the endogenous gene encoding TAT and altered genomic DNA encoding TAT introduced into an embryonic stem cell of the animal. For example, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques. A portion of the genomic DNA encoding TAT can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the TAT polypeptide.

Nucleic acid encoding the TAT polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau

WO 2004/030615

PCT/US2003/028547

et al., Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., J. Biol. Chem. 262, 4429-4432 (1987); and Wagner et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., Science 256, 808-813 (1992).

The nucleic acid molecules encoding the TAT polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each TAT nucleic acid molecule of the present invention can be used as a chromosome marker.

The TAT polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the TAT polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. TAT nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

This invention encompasses methods of screening compounds to identify those that mimic the TAT polypeptide (agonists) or prevent the effect of the TAT polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the TAT polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins, including e.g., inhibiting the expression of TAT polypeptide from cells. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a TAT polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the TAT polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the TAT polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the TAT polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the

WO 2004/030615

PCT/US2003/028547

immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular TAT polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, *Nature (London)*, 340:245-246 (1989); Chien et al., *Proc. Natl. Acad. Sci. USA*, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA*, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1- *lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a TAT polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the TAT polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence

WO 2004/030615

PCT/US2003/028547

of the TAT polypeptide indicates that the compound is an antagonist to the TAT polypeptide. Alternatively, antagonists may be detected by combining the TAT polypeptide and a potential antagonist with membrane-bound TAT polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The TAT polypeptide can be labeled, such as by radioactivity, such that the number of TAT polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the TAT polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the TAT polypeptide. Transfected cells that are grown on glass slides are exposed to labeled TAT polypeptide. The TAT polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled TAT polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled TAT polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with TAT polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the TAT polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the TAT polypeptide.

Another potential TAT polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature TAT polypeptides herein, is used to design an antisense

WO 2004/030615

PCT/US2003/028547

RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the TAT polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the TAT polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the TAT polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the TAT polypeptide, thereby blocking the normal biological activity of the TAT polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Ross Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Isolated TAT polypeptide-encoding nucleic acid can be used herein for recombinantly producing TAT polypeptide using techniques well known in the art and as described herein. In turn, the produced TAT polypeptides can be employed for generating anti-TAT antibodies using techniques well known in the art and as described herein.

WO 2004/030615

PCT/US2003/028547

Antibodies specifically binding a TAT polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders, including cancer, in the form of pharmaceutical compositions.

If the TAT polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993).

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Analysis of Differential TAT Polypeptide Expression by GEPIS

An expressed sequence tag (EST) DNA database (LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) was searched and interesting EST sequences were identified by GEPIS. Gene expression profiling *in silico* (GEPIS) is a bioinformatics tool developed at Genentech, Inc. that characterizes genes of interest for new cancer therapeutic targets. GEPIS takes advantage of large amounts of EST sequence and library information to determine gene expression profiles. GEPIS is capable of determining the expression profile of a gene based upon its proportional correlation with the number of its occurrences in EST databases, and it works by integrating the LIFESEQ® EST relational database and Genentech proprietary information in a stringent and statistically meaningful way. In this example, GEPIS is used to identify and cross-validate novel tumor antigens, although GEPIS can be configured to perform either very specific analyses or broad screening tasks. For the initial screen, GEPIS is used to identify EST sequences from the LIFESEQ® database that correlate

WO 2004/030615

PCT/US2003/028547

to expression in a particular tissue or tissues of interest (often a tumor tissue of interest). Then, GEPIS was employed to generate a complete tissue expression profile for the various sequences of interest. Using this type of screening bioinformatics, various TAT polypeptides (and their encoding nucleic acid molecules) were identified as being significantly overexpressed in a particular type of cancer or certain cancers as compared to other cancers and/or normal non-cancerous tissues. The rating of GEPIS hits is based upon several criteria including, for example, tissue specificity, tumor specificity and expression level in normal essential and/or normal proliferating tissues. The following is a list of molecules whose tissue expression profile as determined by GEPIS evidences significant upregulation of expression in a specific tumor or tumors as compared to other tumor(s) and/or normal tissues and optionally relatively low expression in normal essential and/or normal proliferating tissues.

Under each tissue heading shown below is a list of the cDNA sequences that are detectably overexpressed in tumor tissue of the indicated tissue type as compared to normal non-tumor tissue of the same tissue type. As such, the molecules listed below (and the polypeptides they encode) are excellent nucleic acid (and polypeptide) targets for the diagnosis and therapy of cancer in mammals.

PERIPHERAL NERVOUS SYSTEM

DNA324303	DNA324573	DNA324681	DNA325296	DNA325405	DNA325407
DNA325408	DNA325409	DNA325410	DNA325449	DNA325503	DNA326083
DNA326231	DNA188229	DNA327080	DNA327081	DNA327082	

BRAIN

DNA323721	DNA323722	DNA323723	DNA323724	DNA323726	DNA323727
DNA323728	DNA323729	DNA323731	DNA323732	DNA287173	DNA151148
DNA323740	DNA323742	DNA323743	DNA323744	DNA323751	DNA323753
DNA323755	DNA323757	DNA323759	DNA323764	DNA323765	DNA323778
DNA323781	DNA323783	DNA323785	DNA323795	DNA323796	DNA323797
DNA323805	DNA323810	DNA323811	DNA323812	DNA323814	DNA83085
DNA323817	DNA323821	DNA273060	DNA323823	DNA323824	DNA256503
DNA323825	DNA323826	DNA323828	DNA323829	DNA323830	DNA323833
DNA103214	DNA323834	DNA323837	DNA323838	DNA323839	DNA323846
DNA323856	DNA323859	DNA323863	DNA323869	DNA323871	DNA323874
DNA323882	DNA323887	DNA323888	DNA323892	DNA323893	DNA323897
DNA323898	DNA323900	DNA323901	DNA323902	DNA323908	DNA210134
DNA323912	DNA323918	DNA323921	DNA323922	DNA323923	DNA323924
DNA323925	DNA323926	DNA257916	DNA323927	DNA323931	DNA323936
DNA323937	DNA323938	DNA323939	DNA323940	DNA323942	DNA226793
DNA294794	DNA323943	DNA323944	DNA323946	DNA323947	DNA323950

WO 2004/030615

PCT/US2003/028547

	DNA323951	DNA103436	DNA323953	DNA323958	DNA323959	DNA323961
	DNA226619	DNA323962	DNA323964	DNA323969	DNA323970	DNA323973
	DNA323974	DNA323975	DNA323976	DNA323977	DNA323979	DNA323980
	DNA323991	DNA323992	DNA323994	DNA323995	DNA324000	DNA324001
	DNA324002	DNA324003	DNA227246	DNA324004	DNA324008	DNA324009
5	DNA324010	DNA324011	DNA324012	DNA196344	DNA193882	DNA324024
	DNA324034	DNA324037	DNA324042	DNA324046	DNA324047	DNA324048
	DNA324050	DNA324051	DNA324055	DNA275195	DNA324059	DNA324060
	DNA275049	DNA324063	DNA324065	DNA324066	DNA324067	DNA324071
	DNA324072	DNA324073	DNA227165	DNA324074	DNA324076	DNA324077
10	DNA324078	DNA324079	DNA324080	DNA271243	DNA324081	DNA324082
	DNA324084	DNA324088	DNA324090	DNA324091	DNA324092	DNA324099
	DNA324101	DNA324106	DNA324109	DNA324111	DNA324112	DNA324121
	DNA324122	DNA324123	DNA324128	DNA324129	DNA227795	DNA324130
	DNA324131	DNA324132	DNA324133	DNA227528	DNA324134	DNA150725
15	DNA324136	DNA324138	DNA324139	DNA324141	DNA324146	DNA324152
	DNA324153	DNA324155	DNA324159	DNA324160	DNA324161	DNA324162
	DNA194740	DNA324166	DNA324175	DNA324176	DNA272127	DNA324177
	DNA324182	DNA324184	DNA324186	DNA324188	DNA324194	DNA324197
	DNA324198	DNA324203	DNA324204	DNA324207	DNA324209	DNA324210
20	DNA324216	DNA324218	DNA324220	DNA324221	DNA324222	DNA324223
	DNA324224	DNA324227	DNA324228	DNA194827	DNA324230	DNA324231
	DNA324233	DNA324234	DNA324235	DNA324237	DNA324239	DNA254204
	DNA324240	DNA189697	DNA324243	DNA324246	DNA324251	DNA324253
	DNA150884	DNA324256	DNA324258	DNA324260	DNA324262	DNA324264
25	DNA324269	DNA324270	DNA324271	DNA324274	DNA324275	DNA269910
	DNA324279	DNA324285	DNA324286	DNA324288	DNA324290	DNA270401
	DNA226547	DNA324295	DNA324296	DNA324299	DNA324300	DNA324304
	DNA324305	DNA324308	DNA324309	DNA324310	DNA324313	DNA324314
	DNA324315	DNA324316	DNA324317	DNA103505	DNA324318	DNA324319
30	DNA324320	DNA324323	DNA324327	DNA324328	DNA324329	DNA324330
	DNA324331	DNA324333	DNA324336	DNA324338	DNA324342	DNA324343
	DNA324353	DNA88547	DNA324356	DNA324358	DNA324359	DNA324361
	DNA324363	DNA324364	DNA324365	DNA324366	DNA324367	DNA324368
	DNA324369	DNA324371	DNA324377	DNA324387	DNA324388	DNA324389
35	DNA324390	DNA324397	DNA324398	DNA324410	DNA324411	DNA324412
	DNA324413	DNA254620	DNA324415	DNA324417	DNA324418	DNA89239

WO 2004/030615

PCT/US2003/028547

	DNA324420	DNA225592	DNA324422	DNA324428	DNA324429	DNA324434
	DNA324435	DNA324437	DNA324441	DNA324442	DNA324443	DNA324448
	DNA324449	DNA324457	DNA324465	DNA324466	DNA324467	DNA324472
	DNA257511	DNA324483	DNA324485	DNA324486	DNA225919	DNA324487
	DNA324491	DNA324495	DNA324496	DNA324497	DNA324498	DNA324510
5	DNA324512	DNA324513	DNA324516	DNA324518	DNA324519	DNA324521
	DNA324524	DNA324525	DNA227575	DNA324526	DNA225920	DNA324527
	DNA225921	DNA324528	DNA324531	DNA324532	DNA324533	DNA324534
	DNA324538	DNA324540	DNA324541	DNA324542	DNA324545	DNA324546
	DNA324548	DNA324558	DNA324559	DNA324564	DNA324577	DNA324578
10	DNA288259	DNA324590	DNA324591	DNA324595	DNA324596	DNA324597
	DNA324600	DNA324604	DNA324605	DNA324613	DNA324614	DNA324615
	DNA324616	DNA324618	DNA324619	DNA324620	DNA324624	DNA324625
	DNA83020	DNA324626	DNA103380	DNA226872	DNA324632	DNA324640
	DNA324642	DNA324643	DNA324645	DNA324646	DNA324647	DNA324649
15	DNA324651	DNA324652	DNA324653	DNA150679	DNA324654	DNA324655
	DNA324656	DNA324657	DNA324658	DNA324659	DNA324660	DNA324661
	DNA324662	DNA324663	DNA324664	DNA324665	DNA324666	DNA324667
	DNA324668	DNA324669	DNA324670	DNA324671	DNA324672	DNA324673
	DNA324674	DNA324675	DNA324676	DNA324678	DNA324681	DNA324682
20	DNA324685	DNA324686	DNA324691	DNA324694	DNA324696	DNA324697
	DNA324698	DNA324700	DNA324701	DNA324702	DNA324704	DNA324705
	DNA225909	DNA274206	DNA324706	DNA324707	DNA324710	DNA324711
	DNA324714	DNA324715	DNA324716	DNA270675	DNA324717	DNA269593
	DNA324718	DNA324719	DNA324720	DNA324721	DNA272171	DNA324728
25	DNA324729	DNA304680	DNA324730	DNA324734	DNA324736	DNA324737
	DNA227204	DNA324738	DNA324740	DNA287246	DNA324743	DNA324745
	DNA304716	DNA324748	DNA324749	DNA324750	DNA324751	DNA324755
	DNA324756	DNA324757	DNA324758	DNA227442	DNA324766	DNA324767
	DNA324768	DNA324769	DNA287227	DNA324771	DNA324772	DNA324773
30	DNA324774	DNA272263	DNA287319	DNA324777	DNA324778	DNA324779
	DNA324782	DNA324784	DNA324785	DNA324786	DNA324787	DNA271040
	DNA324789	DNA324791	DNA324792	DNA324794	DNA324796	DNA324797
	DNA324798	DNA324799	DNA324803	DNA324804	DNA324805	DNA324809
	DNA324810	DNA324812	DNA324817	DNA324819	DNA324820	DNA324821
35	DNA324826	DNA324830	DNA324836	DNA324837	DNA324838	DNA324840
	DNA324841	DNA324842	DNA324844	DNA324853	DNA324866	DNA324873

WO 2004/030615

PCT/US2003/028547

	DNA324876	DNA324877	DNA324878	DNA324879	DNA324884	DNA324885
	DNA324886	DNA324889	DNA324890	DNA324891	DNA324892	DNA324894
	DNA225631	DNA274326	DNA324895	DNA324896	DNA324899	DNA324902
	DNA324903	DNA324906	DNA324907	DNA324908	DNA324916	DNA324917
	DNA324918	DNA324920	DNA324922	DNA275334	DNA324924	DNA324925
5	DNA324929	DNA273865	DNA324931	DNA324932	DNA304707	DNA324938
	DNA324944	DNA324945	DNA324947	DNA324952	DNA324953	DNA324955
	DNA324960	DNA304710	DNA324962	DNA324963	DNA324965	DNA324966
	DNA324968	DNA324969	DNA324972	DNA324973	DNA324974	DNA324977
	DNA324978	DNA324979	DNA324980	DNA324982	DNA324984	DNA272090
10	DNA324988	DNA324989	DNA324990	DNA324996	DNA324997	DNA324998
	DNA324999	DNA325002	DNA325005	DNA325006	DNA325012	DNA325013
	DNA325014	DNA325015	DNA325019	DNA325020	DNA325024	DNA325026
	DNA325027	DNA325032	DNA325033	DNA325034	DNA325035	DNA325037
	DNA325040	DNA325041	DNA325043	DNA325044	DNA325045	DNA325046
15	DNA325047	DNA325050	DNA325052	DNA325054	DNA325062	DNA325064
	DNA325065	DNA274178	DNA325069	DNA83022	DNA325070	DNA325071
	DNA325072	DNA325073	DNA225671	DNA325075	DNA325076	DNA227267
	DNA325082	DNA325083	DNA325084	DNA325085	DNA325088	DNA325102
	DNA325103	DNA325105	DNA325106	DNA325111	DNA325112	DNA325116
20	DNA325117	DNA325118	DNA325119	DNA325126	DNA325128	DNA325132
	DNA325136	DNA325137	DNA325138	DNA325139	DNA325140	DNA325141
	DNA325143	DNA325144	DNA325145	DNA325146	DNA325147	DNA325148
	DNA325150	DNA325151	DNA325152	DNA325153	DNA325155	DNA325156
	DNA325157	DNA325160	DNA325161	DNA325163	DNA325164	DNA325165
25	DNA325166	DNA325167	DNA325168	DNA325170	DNA325171	DNA226345
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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

DNA327067

PANCREAS

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WO 2004/030615

PCT/US2003/028547

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35	DNA324595	DNA324596	DNA254147	DNA324604	DNA324605	DNA324613
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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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	DNA325296	DNA325326	DNA325332	DNA325334	DNA325335	DNA325339
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	DNA97285	DNA325456	DNA226080	DNA325471	DNA325473	DNA325475
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	DNA326482	DNA326484	DNA326485	DNA326489	DNA326497	DNA326498
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WO 2004/030615

PCT/US2003/028547

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	DNA327025	DNA327027	DNA327050	DNA327052	DNA327053	DNA273254
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WO 2004/030615

PCT/US2003/028547

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	DNA323851	DNA323856	DNA323858	DNA323859	DNA323861	DNA323864
	DNA323865	DNA323866	DNA323867	DNA323869	DNA323871	DNA323872
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	DNA324213	DNA324214	DNA324218	DNA324219	DNA324229	DNA324230
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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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	DNA287234	DNA326449	DNA326450	DNA326451	DNA326452	DNA326453
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	DNA324155	DNA271608	DNA324219	DNA324259	DNA324320	DNA324351
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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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ADIPOSE

5 DNA325952 DNA325957 DNA325958

WHOLE BLOOD

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

DNA326243 DNA326554 DNA326563 DNA326747

MUSCLE

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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5

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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WO 2004/030615

PCT/US2003/028547

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	DNA270315	DNA326546	DNA326557	DNA326559	DNA326562	DNA326579
15	DNA326615	DNA326620	DNA227249	DNA326633	DNA326634	DNA326635
	DNA326651	DNA326657	DNA272347	DNA326669	DNA326686	DNA326687
	DNA326688	DNA326698	DNA326732	DNA290260	DNA326741	DNA326742
	DNA83154	DNA326756	DNA326758	DNA326759	DNA326769	DNA326777
	DNA287270	DNA326792	DNA326796	DNA326798	DNA326799	DNA326816
20	DNA194701	DNA103525	DNA326841	DNA326862	DNA326863	DNA304670
	DNA326864	DNA326866	DNA326870	DNA326885	DNA326886	DNA326903
	DNA326921	DNA326952	DNA326969	DNA326971	DNA326974	DNA326981
	DNA327016	DNA327023	DNA327025	DNA327029	DNA273992	DNA327060
	DNA327062	DNA273254	DNA327067	DNA327068	DNA327073	DNA327085
25	DNA327087	DNA327090	DNA327092	DNA276159	DNA327127	

STOMACH

	DNA287173	DNA323805	DNA323849	DNA323864	DNA323865	DNA323866
	DNA323873	DNA323884	DNA323920	DNA323925	DNA323934	DNA323990
30	DNA324028	DNA324029	DNA324039	DNA324048	DNA324065	DNA227545
	DNA227795	DNA324155	DNA324179	DNA324180	DNA324216	DNA324243
	DNA324244	DNA324294	DNA324362	DNA324364	DNA324398	DNA324417
	DNA324418	DNA324471	DNA324504	DNA324541	DNA324552	DNA324555
	DNA324556	DNA324558	DNA324624	DNA324630	DNA304680	DNA324756
35	DNA324769	DNA324790	DNA324808	DNA324850	DNA225631	DNA324906
	DNA324907	DNA324908	DNA324922	DNA304710	DNA324962	DNA324963

WO 2004/030615

PCT/US2003/028547

	DNA324972	DNA324973	DNA324982	DNA324997	DNA325033	DNA325074
	DNA325078	DNA325079	DNA325104	DNA325105	DNA325106	DNA325148
	DNA325149	DNA325156	DNA325157	DNA89242	DNA325186	DNA325191
	DNA325192	DNA325202	DNA325224	DNA325233	DNA325235	DNA325236
	DNA325251	DNA325262	DNA325268	DNA325306	DNA325316	DNA325318
5	DNA325320	DNA325368	DNA325418	DNA97285	DNA325441	DNA325442
	DNA325444	DNA325446	DNA325474	DNA325480	DNA325506	DNA325534
	DNA325535	DNA325570	DNA325601	DNA225632	DNA325642	DNA325644
	DNA325645	DNA270458	DNA227092	DNA325773	DNA325775	DNA325776
	DNA325803	DNA325804	DNA274058	DNA325843	DNA325873	DNA325941
10	DNA325986	DNA325993	DNA326019	DNA287331	DNA326043	DNA326133
	DNA326196	DNA326284	DNA326311	DNA326333	DNA326347	DNA326397
	DNA326427	DNA326517	DNA326603	DNA326641	DNA326642	DNA326698
	DNA326750	DNA326791	DNA326846	DNA326859	DNA326862	DNA326863
	DNA304670	DNA326864	DNA326865	DNA326918	DNA326961	DNA326977
15	DNA326983	DNA327040	DNA327042	DNA327055	DNA273254	DNA327099
	DNA327116	DNA327127				

BONE

	DNA323765	DNA323817	DNA323820	DNA323829	DNA323864	DNA323867
20	DNA323869	DNA323871	DNA323914	DNA323947	DNA323964	DNA324004
	DNA324009	DNA324090	DNA324091	DNA324092	DNA324111	DNA324112
	DNA324154	DNA324155	DNA324200	DNA324201	DNA324210	DNA324230
	DNA324293	DNA226547	DNA324295	DNA324326	DNA324347	DNA324390
	DNA324417	DNA324418	DNA324423	DNA324437	DNA324472	DNA324483
25	DNA324488	DNA324501	DNA324502	DNA324503	DNA324504	DNA324505
	DNA324512	DNA324521	DNA324525	DNA324541	DNA324549	DNA324550
	DNA324551	DNA324554	DNA324555	DNA324556	DNA324557	DNA324558
	DNA324575	DNA324576	DNA324579	DNA324595	DNA324596	DNA324604
	DNA324613	DNA324624	DNA324632	DNA324641	DNA324645	DNA324682
30	DNA324687	DNA324697	DNA324717	DNA324720	DNA324737	DNA324756
	DNA304661	DNA324785	DNA324796	DNA324797	DNA150772	DNA324828
	DNA324829	DNA324844	DNA324866	DNA324902	DNA324904	DNA324905
	DNA324906	DNA324926	DNA324989	DNA325015	DNA325024	DNA325026
	DNA325027	DNA325034	DNA325111	DNA325116	DNA131588	DNA325156
35	DNA325157	DNA325164	DNA325179	DNA325182	DNA325183	DNA325184
	DNA325202	DNA325206	DNA325222	DNA325229	DNA325231	DNA325232

WO 2004/030615

PCT/US2003/028547

	DNA325234	DNA325236	DNA325250	DNA325301	DNA325303	DNA325326
	DNA325339	DNA325340	DNA325347	DNA325358	DNA325395	DNA325430
	DNA325437	DNA325451	DNA325452	DNA325523	DNA325558	DNA325570
	DNA325576	DNA325601	DNA225632	DNA325633	DNA325731	DNA325733
	DNA325736	DNA325762	DNA325786	DNA302016	DNA325789	DNA325806
5	DNA325810	DNA325811	DNA325812	DNA325843	DNA325844	DNA325906
	DNA325908	DNA325913	DNA325922	DNA325935	DNA325985	DNA326002
	DNA326041	DNA326046	DNA326099	DNA326233	DNA326234	DNA326251
	DNA97300	DNA304715	DNA326286	DNA326289	DNA326381	DNA326457
	DNA326580	DNA326633	DNA326634	DNA326635	DNA326651	DNA290260
10	DNA326796	DNA326884	DNA326886	DNA326974	DNA326977	DNA327005
	DNA327025	DNA327060	DNA327062	DNA327067	DNA327114	

EXAMPLE 2: Use of TAT as a hybridization probe

15 The following method describes use of a nucleotide sequence encoding TAT as a hybridization probe for, i.e., diagnosis of the presence of a tumor in a mammal.

DNA comprising the coding sequence of full-length or mature TAT as disclosed herein can also be employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of TAT) in human tissue cDNA libraries or human tissue genomic libraries.

WO 2004/030615

PCT/US2003/028547

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled TAT-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence TAT can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of TAT in *E. coli*

This example illustrates preparation of an unglycosylated form of TAT by recombinant expression in *E. coli*.

The DNA sequence encoding TAT is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the TAT coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized TAT protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

TAT may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding TAT is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110

WO 2004/030615

PCT/US2003/028547

fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.₆₀₀ of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A₂₈₀ absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded TAT polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using

WO 2004/030615

PCT/US2003/028547

this technique(s).

EXAMPLE 4: Expression of TAT in mammalian cells

This example illustrates preparation of a potentially glycosylated form of TAT by recombinant expression in mammalian cells.

5 The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the TAT DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the TAT DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-TAT.

10 In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-TAT DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25°C. The
15 precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

 Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml ³⁵S-cysteine and 200 µCi/ml ³⁵S-methionine.
20 After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of TAT polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

 In an alternative technique, TAT may be introduced into 293 cells transiently using the dextran sulfate
25 method described by Sompariyac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-TAT DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and
30 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed TAT can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

 In another embodiment, TAT can be expressed in CHO cells. The pRK5-TAT can be transfected into CHO cells using known reagents such as CaPO₄ or DEAE-dextran. As described above, the cell cultures can
35 be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ³⁵S-methionine. After determining the presence of TAT polypeptide, the culture medium may be replaced

WO 2004/030615

PCT/US2003/028547

with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed TAT can then be concentrated and purified by any selected method.

Epitope-tagged TAT may also be expressed in host CHO cells. The TAT may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged TAT insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged TAT can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

TAT may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect[®] (Quiagen), Dosper[®] or Fugene[®] (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day

WO 2004/030615

PCT/US2003/028547

1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 µm filter. The filtrate was
5 either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional
10 equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20
15 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 µL of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

20 Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 5: Expression of TAT in Yeast

The following method describes recombinant expression of TAT in yeast.

25 First, yeast expression vectors are constructed for intracellular production or secretion of TAT from the ADH2/GAPDH promoter. DNA encoding TAT and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of TAT. For secretion, DNA encoding TAT can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native TAT signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory
30 signal/leader sequence, and linker sequences (if needed) for expression of TAT.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

35 Recombinant TAT can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The

WO 2004/030615

PCT/US2003/028547

concentrate containing TAT may further be purified using selected column chromatography resins.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 6: Expression of TAT in Baculovirus-Infected Insect Cells

5 The following method describes recombinant expression of TAT in Baculovirus-infected insect cells.

The sequence coding for TAT is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding TAT or the desired portion of the coding sequence of
10 TAT such as the sequence encoding an extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus
15 DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged TAT can then be purified, for example, by Ni²⁺-chelate affinity
20 chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm
25 filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching
30 A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₆-tagged TAT are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) TAT can be performed using known
35 chromatography techniques, including for instance, Protein A or protein G column chromatography.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using

WO 2004/030615

PCT/US2003/028547

this technique(s).

EXAMPLE 7: Preparation of Antibodies that Bind TAT

This example illustrates preparation of monoclonal antibodies which can specifically bind TAT.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified TAT, fusion proteins containing TAT, and cells expressing recombinant TAT on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the TAT immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-TAT antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of TAT. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against TAT. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against TAT is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-TAT monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8: Purification of TAT Polypeptides Using Specific Antibodies

Native or recombinant TAT polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-TAT polypeptide, mature TAT polypeptide, or pre-TAT polypeptide is purified by immunoaffinity chromatography using antibodies specific for the TAT polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-TAT polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium

WO 2004/030615

PCT/US2003/028547

sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of TAT polypeptide by preparing a fraction from cells containing TAT polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble TAT polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble TAT polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TAT polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/TAT polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and TAT polypeptide is collected.

EXAMPLE 9: *In Vitro* Tumor Cell Killing Assay

Mammalian cells expressing the TAT polypeptide of interest may be obtained using standard expression vector and cloning techniques. Alternatively, many tumor cell lines expressing TAT polypeptides of interest are publicly available, for example, through the ATCC and can be routinely identified using standard ELISA or FACS analysis. Anti-TAT polypeptide monoclonal antibodies (and toxin conjugated derivatives thereof) may then be employed in assays to determine the ability of the antibody to kill TAT polypeptide expressing cells *in vitro*.

For example, cells expressing the TAT polypeptide of interest are obtained as described above and plated into 96 well dishes. In one analysis, the antibody/toxin conjugate (or naked antibody) is included throughout the cell incubation for a period of 4 days. In a second independent analysis, the cells are incubated for 1 hour with the antibody/toxin conjugate (or naked antibody) and then washed and incubated in the absence of antibody/toxin conjugate for a period of 4 days. Cell viability is then measured using the CellTiter-Glo Luminescent Cell Viability Assay from Promega (Cat# G7571). Untreated cells serve as a negative control.

EXAMPLE 10: *In Vivo* Tumor Cell Killing Assay

To test the efficacy of conjugated or unconjugated anti-TAT polypeptide monoclonal antibodies, anti-TAT antibody is injected intraperitoneally into nude mice 24 hours prior to receiving tumor promoting cells subcutaneously in the flank. Antibody injections continue twice per week for the remainder of the study. Tumor volume is then measured twice per week.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to

WO 2004/030615**PCT/US2003/028547**

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practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WO 2004/030615

PCT/US2003/028547

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having a nucleotide sequence that has at least 80% nucleic acid sequence identity to:

(a) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

5 (b) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

10 (d) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

15 2. Isolated nucleic acid having:

(a) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

20 (c) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

25 (f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

3. Isolated nucleic acid that hybridizes to:

30 (a) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

35 (d) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

WO 2004/030615

PCT/US2003/028547

- (e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- (g) the complement of (a), (b), (c), (d), (e) or (f).
4. The nucleic acid of Claim 3, wherein the hybridization occurs under stringent conditions.
- 5 5. The nucleic acid of Claim 3 which is at least about 5 nucleotides in length.
6. An expression vector comprising the nucleic acid of Claim 1, 2 or 3.
7. The expression vector of Claim 6, wherein said nucleic acid is operably linked to control sequences recognized by a host cell transformed with the vector.
8. A host cell comprising the expression vector of Claim 7.
- 10 9. The host cell of Claim 8 which is a CHO cell, an *E. coli* cell or a yeast cell.
10. A process for producing a polypeptide comprising culturing the host cell of Claim 8 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture.
11. An isolated polypeptide having at least 80% amino acid sequence identity to:
- (a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- 15 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;
- (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- 20 (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).
- 25 12. An isolated polypeptide having:
- (a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;
- 30 (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- 35 (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

WO 2004/030615

PCT/US2003/028547

13. A chimeric polypeptide comprising the polypeptide of Claim 11 or 12 fused to a heterologous polypeptide.

14. The chimeric polypeptide of Claim 13, wherein said heterologous polypeptide is an epitope tag sequence or an Fc region of an immunoglobulin.

15. An isolated antibody that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

16. An isolated antibody that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

17. The antibody of Claim 15 or 16 which is a monoclonal antibody.

18. The antibody of Claim 15 or 16 which is an antibody fragment.

19. The antibody of Claim 15 or 16 which is a chimeric or a humanized antibody.

20. The antibody of Claim 15 or 16 which is conjugated to a growth inhibitory agent.

21. The antibody of Claim 15 or 16 which is conjugated to a cytotoxic agent.

22. The antibody of Claim 21, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

23. The antibody of Claim 21, wherein the cytotoxic agent is a toxin.

WO 2004/030615

PCT/US2003/028547

24. The antibody of Claim 23, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

25. The antibody of Claim 23, wherein the toxin is a maytansinoid.

26. The antibody of Claim 15 or 16 which is produced in bacteria.

27. The antibody of Claim 15 or 16 which is produced in CHO cells.

5 28. The antibody of Claim 15 or 16 which induces death of a cell to which it binds.

29. The antibody of Claim 15 or 16 which is detectably labeled.

30. An isolated nucleic acid having a nucleotide sequence that encodes the antibody of Claim 15 or 16.

10 31. An expression vector comprising the nucleic acid of Claim 30 operably linked to control sequences recognized by a host cell transformed with the vector.

32. A host cell comprising the expression vector of Claim 31.

33. The host cell of Claim 32 which is a CHO cell, an *E. coli* cell or a yeast cell.

34. A process for producing an antibody comprising culturing the host cell of Claim 32 under conditions suitable for expression of said antibody and recovering said antibody from the cell culture.

15 35. An isolated oligopeptide that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

20 (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

25 (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

36. An isolated oligopeptide that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

30 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

35 (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355

WO 2004/030615

PCT/US2003/028547

(SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

37. The oligopeptide of Claim 35 or 36 which is conjugated to a growth inhibitory agent.

38. The oligopeptide of Claim 35 or 36 which is conjugated to a cytotoxic agent.

5 39. The oligopeptide of Claim 38, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

40. The oligopeptide of Claim 38, wherein the cytotoxic agent is a toxin.

41. The oligopeptide of Claim 40, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

10 42. The oligopeptide of Claim 40, wherein the toxin is a maytansinoid.

43. The oligopeptide of Claim 35 or 36 which induces death of a cell to which it binds.

44. The oligopeptide of Claim 35 or 36 which is detectably labeled.

45. A TAT binding organic molecule that binds to a polypeptide having at least 80% amino acid sequence identity to:

15 (a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

20 (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

25 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

46. The organic molecule of Claim 45 that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

30 (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

35 (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown

WO 2004/030615

PCT/US2003/028547

in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

47. The organic molecule of Claim 45 or 46 which is conjugated to a growth inhibitory agent.

48. The organic molecule of Claim 45 or 46 which is conjugated to a cytotoxic agent.

49. The organic molecule of Claim 48, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

5 50. The organic molecule of Claim 48, wherein the cytotoxic agent is a toxin.

51. The organic molecule of Claim 50, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

52. The organic molecule of Claim 50, wherein the toxin is a maytansinoid.

53. The organic molecule of Claim 45 or 46 which induces death of a cell to which it binds.

10 54. The organic molecule of Claim 45 or 46 which is detectably labeled.

55. A composition of matter comprising:

(a) the polypeptide of Claim 11;

(b) the polypeptide of Claim 12;

(c) the chimeric polypeptide of Claim 13;

15 (d) the antibody of Claim 15;

(e) the antibody of Claim 16;

(f) the oligopeptide of Claim 35;

(g) the oligopeptide of Claim 36;

(h) the TAT binding organic molecule of Claim 45; or

20 (i) the TAT binding organic molecule of Claim 46; in combination with a carrier.

56. The composition of matter of Claim 55, wherein said carrier is a pharmaceutically acceptable carrier.

57. An article of manufacture comprising:

(a) a container; and

25 (b) the composition of matter of Claim 55 contained within said container.

58. The article of manufacture of Claim 57 further comprising a label affixed to said container, or a package insert included with said container, referring to the use of said composition of matter for the therapeutic treatment of or the diagnostic detection of a cancer.

30 59. A method of inhibiting the growth of a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

35 (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-

WO 2004/030615

PCT/US2003/028547

6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody, oligopeptide or organic molecule that binds to said protein, the binding of said antibody, oligopeptide or organic molecule to said protein thereby causing an inhibition of growth of said cell.

60. The method of Claim 59, wherein said antibody is a monoclonal antibody.

61. The method of Claim 59, wherein said antibody is an antibody fragment.

62. The method of Claim 59, wherein said antibody is a chimeric or a humanized antibody.

63. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

64. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

65. The method of Claim 64, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

66. The method of Claim 64, wherein the cytotoxic agent is a toxin.

67. The method of Claim 66, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

68. The method of Claim 66, wherein the toxin is a maytansinoid.

69. The method of Claim 59, wherein said antibody is produced in bacteria.

70. The method of Claim 59, wherein said antibody is produced in CHO cells.

71. The method of Claim 59, wherein said cell is a cancer cell.

72. The method of Claim 71, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

73. The method of Claim 71, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

74. The method of Claim 71, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

75. The method of Claim 59 which causes the death of said cell.

76. The method of Claim 59, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures

WO 2004/030615

PCT/US2003/028547

1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

5 (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

77. A method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

10 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

15 (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

20 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to said mammal a therapeutically effective amount of an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said mammal.

78. The method of Claim 77, wherein said antibody is a monoclonal antibody.

79. The method of Claim 77, wherein said antibody is an antibody fragment.

80. The method of Claim 77, wherein said antibody is a chimeric or a humanized antibody.

25 81. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

82. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

30 83. The method of Claim 82, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

84. The method of Claim 82, wherein the cytotoxic agent is a toxin.

85. The method of Claim 84, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

86. The method of Claim 84, wherein the toxin is a maytansinoid.

35 87. The method of Claim 77, wherein said antibody is produced in bacteria.

88. The method of Claim 77, wherein said antibody is produced in CHO cells.

WO 2004/030615

PCT/US2003/028547

89. The method of Claim 77, wherein said tumor is further exposed to radiation treatment or a chemotherapeutic agent.

90. The method of Claim 77, wherein said tumor is a breast tumor, a colorectal tumor, a lung tumor, an ovarian tumor, a central nervous system tumor, a liver tumor, a bladder tumor, a pancreatic tumor, or a cervical tumor.

5 91. The method of Claim 77, wherein said protein is more abundantly expressed by the cancerous cells of said tumor as compared to a normal cell of the same tissue origin.

92. The method of Claim 77, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

10 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

15 (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

20 93. A method of determining the presence of a protein in a sample suspected of containing said protein, wherein said protein has at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

25 (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

30 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising exposing said sample to an antibody, oligopeptide or organic molecule that binds to said protein and determining binding of said antibody, oligopeptide or organic molecule to said protein in said sample, wherein binding of the antibody, oligopeptide or organic molecule to said protein is indicative of the presence of said protein in said sample.

35 94. The method of Claim 93, wherein said sample comprises a cell suspected of expressing said protein.

WO 2004/030615

PCT/US2003/028547

95. The method of Claim 94, wherein said cell is a cancer cell.

96. The method of Claim 93, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

97. The method of Claim 93, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

5 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

10 (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

15 98. A method of diagnosing the presence of a tumor in a mammal, said method comprising determining the level of expression of a gene encoding a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

20 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

25 (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), in a test sample of tissue cells obtained from said mammal and in a control sample of known normal cells of the same tissue origin, wherein a higher level of expression of said protein in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

30 99. The method of Claim 98, wherein the step of determining the level of expression of a gene encoding said protein comprises employing an oligonucleotide in an *in situ* hybridization or RT-PCR analysis.

100. The method of Claim 98, wherein the step determining the level of expression of a gene encoding said protein comprises employing an antibody in an immunohistochemistry or Western blot analysis.

35 101. The method of Claim 98, wherein said protein has:

WO 2004/030615

PCT/US2003/028547

- (a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;
- 5 (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- 10 (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

102. A method of diagnosing the presence of a tumor in a mammal, said method comprising contacting a test sample of tissue cells obtained from said mammal with an antibody, oligopeptide or organic molecule that binds to a protein having at least 80% amino acid sequence identity to:

- (a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- 15 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;
- (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;
- 20 (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or
- (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), and detecting the formation of a complex between said antibody, oligopeptide or organic molecule and said protein in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in said mammal.
- 25

103. The method of Claim 102, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

104. The method of Claim 102, wherein said test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

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105. The method of Claim 102, wherein said protein has:
- (a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);
- (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;
- 35 (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

WO 2004/030615

PCT/US2003/028547

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

5 (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

106. A method for treating or preventing a cell proliferative disorder associated with increased expression or activity of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

10 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

15 (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to a subject in need of such treatment an effective amount of an antagonist of said protein, thereby effectively treating or preventing said cell proliferative disorder.

107. The method of Claim 106, wherein said cell proliferative disorder is cancer.

108. The method of Claim 106, wherein said antagonist is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic molecule or antisense oligonucleotide.

109. A method of binding an antibody, oligopeptide or organic molecule to a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

30 (c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

35 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody,

WO 2004/030615

PCT/US2003/028547

oligopeptide or organic molecule that binds to said protein and allowing the binding of the antibody, oligopeptide or organic molecule to said protein to occur, thereby binding said antibody, oligopeptide or organic molecule to said cell.

110. The method of Claim 109, wherein said antibody is a monoclonal antibody.

111. The method of Claim 109, wherein said antibody is an antibody fragment.

5 112. The method of Claim 109, wherein said antibody is a chimeric or a humanized antibody.

113. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

114. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

10 115. The method of Claim 114, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

116. The method of Claim 114, wherein the cytotoxic agent is a toxin.

117. The method of Claim 116, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

15 118. The method of Claim 116, wherein the toxin is a maytansinoid.

119. The method of Claim 109, wherein said antibody is produced in bacteria.

120. The method of Claim 109, wherein said antibody is produced in CHO cells.

121. The method of Claim 109, wherein said cell is a cancer cell.

20 122. The method of Claim 121, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

123. The method of Claim 121, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

25 124. The method of Claim 123, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

125. The method of Claim 109 which causes the death of said cell.

126. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

30 127. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treating a tumor.

128. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

35 129. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

130. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of

WO 2004/030615**PCT/US2003/028547**

medicament for treating a tumor.

131. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

132. Use of a host cell as claimed in any of Claims 8, 9, 32, or 33 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

5 133. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treating a tumor.

134. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

WO 2004/030615

PCT/US2003/028547

135. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

136. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treating a tumor.

5 137. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

138. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

139. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treating a tumor.

10 140. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

141. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

15 142. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treating a tumor.

143. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

144. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

20 145. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treating a tumor.

146. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

25 147. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

148. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treating a tumor.

149. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

30 150. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

151. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treating a tumor.

WO 2004/030615

PCT/US2003/028547

152. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

153. A method for inhibiting the growth of a cell, wherein the growth of said cell is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

5 (b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

10 (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

15 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, thereby inhibiting the growth of said cell.

154. The method of Claim 153, wherein said cell is a cancer cell.

155. The method of Claim 153, wherein said protein is expressed by said cell.

156. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

20 157. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein induces the death of said cell.

158. The method of Claim 153, wherein said antibody is a monoclonal antibody.

159. The method of Claim 153, wherein said antibody is an antibody fragment.

160. The method of Claim 153, wherein said antibody is a chimeric or a humanized antibody.

25 161. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

162. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

30 163. The method of Claim 162, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

164. The method of Claim 162, wherein the cytotoxic agent is a toxin.

165. The method of Claim 164, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

166. The method of Claim 164, wherein the toxin is a maytansinoid.

35 167. The method of Claim 153, wherein said antibody is produced in bacteria.

168. The method of Claim 153, wherein said antibody is produced in CHO cells.

WO 2004/030615

PCT/US2003/028547

169. The method of Claim 153, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

5 (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

10 (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

170. A method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

15 (a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

20 (d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

25 (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said tumor.

171. The method of Claim 170, wherein said protein is expressed by cells of said tumor.

172. The method of Claim 170, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

30 173. The method of Claim 170, wherein said antibody is a monoclonal antibody.

174. The method of Claim 170, wherein said antibody is an antibody fragment.

175. The method of Claim 170, wherein said antibody is a chimeric or a humanized antibody.

176. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

35 177. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

WO 2004/030615

PCT/US2003/028547

178. The method of Claim 177, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

179. The method of Claim 177, wherein the cytotoxic agent is a toxin.

180. The method of Claim 179, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

5 181. The method of Claim 179, wherein the toxin is a maytansinoid.

182. The method of Claim 170, wherein said antibody is produced in bacteria.

183. The method of Claim 170, wherein said antibody is produced in CHO cells.

184. The method of Claim 170, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

10 (b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

15 (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

WO 2004/030615

PCT/US2003/028547

1/6881
FIGURE 1

ATCACATGCCTATCATATAGTAAAACCCAGCCCATGGCCCCTAACAGGGGCCCTCTCAGCCCTCCTAATGACCTC
CGGCCTAGCCATGTGATTTCACTTCCACTCCACAACCCTCCTCATACTAGGCCTACTAACCAACACACTAACCAT
ATACCAATGATGGCGCGATGTAACACGAGAAAGCACATACCAAGGCCACCACACACCACCTGTCCAGAAAGGCGT
TCGATACGGGATAATCCTATTTATTACCTCAGAAGTTTTTTCTTCGCAGGATTTTCTGAGCCTTTTACCACTC
CAGCCTAGCTCCCACCCCACAAC TAGGGGGACACTGGCCCCAACAGGCATCACCCCGCTAAATCCCCTAGAAGT
CCCCTCCTAAACACATCCGTATTACTCGCATCAGGGGTATCAATCACCTGAGCTCACCATAGTCTAATAGTCTA
TTTTACCCTCCTACAAGCCTCAGAGTACTTCGAG

WO 2004/030615

PCT/US2003/028547

2/6881
FIGURE 2

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATTTCAGTTGCAGGAAAAACAAGCTTA
ACACGCCCACTAATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATAACCCTATGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAAAGTCTGCCTCACAGCAGATTCTTCACGCCCAGCATCTACCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCAGCCTCTGC
CTCACAGCGGACTCTC

WO 2004/030615

PCT/US2003/028547

3/6881
FIGURE 3

CAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACGTACGGCAGCCTCCGCAGATGAGCCTACTGC
CTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTT
CTCTCCAGGCTCTGAACCTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGAGTGTAGTAGTGCTATCGCAGCTGA
CTGCAGCCTCAACCTTCCAGGCTGAAGCGATCCTCCCACCTCAACCTCCCACGTGGCTGAGACTACAGGTGCTTG
CCACTATGCCCCAACTAACATTTGGAATTTTCGTATACGTGGATTCCAGAGGGGTGACAGCGAAACGTGGGACCAT
TCAGTTGCAGGAAACAAGCTTAACACGCCCACTAATTCTACATTATGCTCCTACCTCCCGGCAGCCTCTCCAGG
CCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATG

WO 2004/030615

PCT/US2003/028547

4/6881
FIGURE 4

CGTCGGCCCCCGGCCCCCAGCAGCCTCCAAAGCCCTGTGACTCACAGCCCTGCTTCCACGGGGGGACCTGCCAG
GACTGGGCATTGGGCGGGGGCTTCACCTGCAGCTGCCCGGCAGGCAGGGGAGGCGCCGTCTGTGAGAAGGTGCTT
GGCGCCCCCTGTGCCGGCCTTCGAGGGCCGCTCCTTCCTGGCCTTCCCCACTCTCCGCGCCTACCACACGCTGCGC
CTGGCACTGGAATTCCGGGCGCTGGAGCCTCAGGGGCTGCTGCTGTACAATGGCAACGCCCGGGGCAAGGACTTC
CTGGCATTGGGCGCTGCTAGATGGCCGCGTGCAGCTCAGGTTTGACACAGGTTTCGGGGCCGGCGGTGCTGACCAGT
GCCGTGCCGGTAGAGCCGGGCCAGTGGCACCGCCTGGAGCTGTCCCGGCCTGGCGCCGGGGCACCCCTCTCGGTG
GATGGTGAGACCCCTGTTCTGGGCGAGAGTCCAGTGGCACCGACGGCCTCAACCTGGACACAGACCTCTTTGTG
GGCGGCGTACCCGAGGACCAGGCTGCCGTGGCGCTGGAGCGGACCTTCGTGGGCGCCGGCCTGAGGGGGTGCATC
CGTTTGCTGGACGTCAACAACCAGCGCCTGGAGCTTGGCATTGGGCGGGGGCTGCCACCCGAGGCTCTGGCGTG
GGCAAGTGCGGGGACCACCCCTGCCTGCCCAACCCCTGCCATGGCGGGGGCCCCATGCCAGAACCTGGAGGCTGGA
AGGTTCCATTGCCAGTGCCCGCCCGGCCGCTCGGACCAACCTGTGCCGATGAGAAGAGCCCTGCCAGCCCCAAC
CCCTGCCATGGGGCGGCGCCCTGCCGTGTGCTGCCCGAGGGTGGTGCTCAGTGCGAGTGCCCCCTGGGGCGTGAG
GGCACCTTCTGCCAGACAGCCTCGGGGCGAGGACGGCTCTGGGCCCTTCTGGCTGACTTCAACGGCTTCTCCAC
CTGGAGCTGAGAGGCTGCACACCTTTGCACGGGACCTGGGGGAGAAGATGGCGCTGGAGGTCTGTCTCTGGCA
CGAGGCCCCAGCGCCTCCTGCTCTACAACGGGCGAGAAGACGGACGGCAAGGGGGACTTCGTGTGCTGGCACTG
CGGGACCGCCGCTGGAGTTCCGCTACGACCTGGGCAAGGGGCGAGCGGTCTATCAGGAGCAGGGAGCCAGTCACC
CTGGGAGCCTGGACCAGGGTCTCACTGGAGCGAAACGGCCGCAAGGGTGCCCTGCGTGTGGGCGACGGCCCCCGT
GTGTTGGGGAGTCCCGGTTCCGCACACCGTCTCAACCTGAAGGAGCCGCTCTACGTAGGGGGCGCTCCCGAC
TTCAGCAAGCTGGCCCGTGTGCTGCCGTGTCTCTGGCTTCGACGGTGCCATCCAGCTGGTCTCCCTCGGAGGC
CGCCAGCTGCTGACCCCGGAGCACGTGTGCGGCAGGTGGACGTACGTCTTTGCAGGTACCCCTGCACCCGG
GCCTCAGGCCACCCCTGCCTCAATGGGGCTCCTGCGTCCCGAGGGAGGCTGCCTATGTGTGCTGTGTCCCGG
GGATTCTCAGGACCGCACTGCGAGAAGGGGCTGGTGAGAAAGTCAGCGGGGGACGTGGATACCTTGGCCTTTGAC
GGGCGGACCTTTGTGAGTACCTCAACGCTGTGACCGAGAGCGAGAAGGCACTGCAGAGCAACCACTTTGAACTG
AGCCTGCGCACTGAGGCCACGACGGGGCTGGTGCTCTGGAGTGGCAAGGCCACGGAGCGGGCAGACTATGTGGCA
CTGGCCATTGTGGACGGGCACCTGCAACTGAGCTACAACCTGGGCTCCAGCCCGTGGTGCTGCGTTCCACCGTG
CCGTCAACACCAACCGTGTTGCGGGTCTGGGCACATAGGGAGCAGAGGGAAGGTTCCCTGCAGGTGGGCAAT
GAGGCCCTGTGACCGGCTCCTCCCCGCTGGGCGCCACGCAGCTGGACACTGATGGAGCCCTGTGGCTTGGGGG
CTGCCGGAGCTGCCCGTGGGCCCAGCACTGCCAAGGCCTACGGCACAGGCTTTGTGGGCTGCTTGGGGACGCTG
GTGTTGGGCGGCAACCGCTGCACCTGTGGAGACGCGGTACCAAGCCAGAGCTGCGGCCCTGCCCCACCCCA
TGAGCTGGCACCAAGAGCCCCGCGCCCGCTGTAATTTATTTCTATTTTGTAAACTTGTGCTTTTGTATATGATT
TTCTTGCTGAGTGTGGCCGGAGGGACTGCTGGCCCCGGCCTCCCTTCCGTCCAGGCAGCCGTGCTGCAGACAGA
CCTAGTGCCGAGGGATGGACAGGCGAGGTGGCAGCGTGGAGGGCTCGGCGTGGATGGCAGCCTCAGGACACACAC
CCCTGCCTCAAGGTGCTGAGCCCCCGCCTTGCACTGCGCCTGCCCCACGGTGTCCCGCCGGGAAGCAGCCCCGG
CTCCTGAATCACCCCTCGCTCCGTACGGCGGGACTCGTGTCCAGAGAGGAAGGGGCTGCTGAGGTCTGATGGGGC
CCTTCTCCGGGTGACCCACAGGGCCTTTTCAAGCCCCCATTTGAGCTGCTCCTTCTGTGTGTGCTCTGGGCC
CTGCCTCGGCCTCTGCGCCAATACTGTGACTTCCAAACAATGTTACTGCTGGGCACAGCTCTGCGTTGCTCCCG
TGCTGCCTGCGCCAGCCCCAGGCTGTGAGGAGCAGAGGCCAGACCAGGGCCGATCTGGGTGTCTGACCCTCAG
CTGGCCCTGCCAGCCACCCCTGGACATGACCGTATCCCTCTGCCACACCCAGGCCCTGCGAGGGGGCTATCGAGA
GGAGCTCACTGTGGGATGGGGTTGACCTCTGCGCGCTGCCTGGGTATCTGGGCTGGCCATGGCTGTGTTCTTCA
TGTGTTGATTTTATTTGACCCCTGGAGTGGTGGGTCTCATCTTTCCATCTCGCCTGAGAGCGGCTGAGGGCTGC
CTCACTGCAAATCCTCCCCACAGCGTCAGTGAAAGTCGTCTTGTCTCAGAATGACCAGGGGGCCAGCCAGTGTCT
GACCAAGGTCAAGGGGCGAGGTGCAGAGGTGGCAGGGATGGCTCCGAAGCCAGAAATGCCTTAACTGCAACGTCC
CGTCCCTTCCCCACCCCATCCCATCCCCACCCCGAGCCCGAGCCAGTCTCTAGGAGCAGGACCCGATGAAG
CGGGCGGCGGTGGGGCTGGGTGCCGTGTTACTAACTCTAGTATGTTTCTGTGTCAATCGCTGTGAAATAAAGTCT
GAAAACCTT

WO 2004/030615

PCT/US2003/028547

5/6881
FIGURE 5

MLNSSLMRITLRNLEEVEFCVEDKPGTHFTVPPTPPDACRGMLCGFGAVCEPNAEGPGRASCVCCKSPCPSVVA
PVCGS DASTYSNECELQRAQCSQQRRI RLLSRGPGCSRDPCSNVTC SFGSTCARSADGLTASCLCPATCRGAPEG
TVCGSDGADYPGECQLLRACARQENVFKFDGPCDPCQ GALPDP SRSCRVNPRTRRPEMLLRPESCPARQAPVC
GDDGVITYENDCVMGRSGAARGLLLQKVRSGQCQGRDQCPEPCRFNAVCLSRGRPRCSCDRVTC DGAYRPVCAQD
GRTYSDSDCWRRQAECRQORAI P SKHQGPCDQAPSPCLGVQCAFGATCAVKNGQAACECLQACSSLYDPVCGSDGV
TYGSACELEATACTLGREIQVARKGPCDRCGQCRFGALCEAETGRCVCP SECVALAQPVCGSDGHTYPTSECM LHV
HACTHQI SLHVASAGPCE TCGDAVCAFGAVCSAGQVCPCPCEHPPPGPVCGSDGV TYGSACELEAACLQQTQIE
EARAGPCEQAECGSGSGSGSGEDGDCEQELCRQRGGIWDDESEDGPCVCD FSCQSVPGSPVCGSDGV TYSTEC ELK
KARCESQRGLYVAAQGACRGPTFAPLP PVAPLHCAQTPYGCCQDNIT AARGVGLAGCPSACQCNP HGSYGGTCDF
ATGQCSCRPGVGGRLRCDRCEPGFWNFRGIVTDGRSGCTPCSCDPQGA VRDDCEQMTGLCSCKPGVAGPKCGQCPD
GRALGPAGCEADASAPATCAEMRCEFGARCVEESGSAHVC PMLTCPEANATKVC GSDGV TYGNECQLKTIACRQ
GLQISIQLGPCQEAVAPSTHPTSASVTVTTPGLLLSQALPAPP GALPLAPSSTAHSQTTPPPSSRPRTTASVPR
TTVWPVLTVPPTAPSPAPSLVASAFGESGSTDGSSDEELSGDQEASGGGSGGLEPLEGSSVATPGPPVERASCYN
SALGCCSDGKTPSLDAEGSNCPATKVFQGVLELEGVGEQELFYTP EMADPKSELFGETARSIESTLDDLFRNSDV
KKDFRSVRLRDLGPGKSVRAIVDVHFDPTTA FRAPDVARALLRQIQVSRRRSLGVRRLQEHVRFMDFDWFFAFI
TGATSGAIAAGATARATTASRLPSSAVTPRAPHPSHTSQPVAKTTAAP TTRRPPTAPSRVPGRPPAPQQPPKP
CDSQPCFHGGTCQDWALGGGFTCSCPAGRGGAVCEKVLGAPVPAFEGRSFLAFTL RAYHTLRLLALEFRALEPQG
LLLYNGNARGKDFLALALLDGRVQLRFDTGSGPAVLTSAPVPEPGQWHRLELSRHWRRGTLSDGETPVLGESPS
GTDGLNLDTDLFVGGVPEDQAAVALERTFVGAGLRGCI RLLDVNNQRLELGI GPGAATRGSGVGKCGDHPCLPNP
CHGGAPCQNLEAGRFHCQCPPGRVGPTCADEKSPCQPNPCHGAAPCRVLPEGGAQCECPLGREGTFCQTASGQDG
SGPFLADFNGFSHLELRGLHTFARDLGEKMALEVFLARGPSGLLLYNGQKT DGKGD FVSLALRDRRLEFRYDLG
KGA AVIRSREPVTLGAWTRVSLERNRKGALRVGDGPRVLGESPVPH TVLNLKEPLYVGGAPDFSKLARA AAVSS
GFDGAIQLVSLGGRQLLTPEHVL RQVDVTSFAGHPCTRASGHPC LINGASCVPREAA YVCLCPGGFSGPHCEKGLV
EKSAGD VDTLAFDGRTFVEYLN AVTESEKALQSNHFELSLRTEATQGLVLWSGKATERADYVALAIVDGH LQLSY
NLGSQPVVLRSTVPVNTNRWLRVVAHREQREGSLQVGNEAPVTGSSPLGATQLD TDGALWLGGLPPELPVGPALPK
AYGTGFVGCLRDVVGRHPLHLLEDAVTKPELRPCPTP

WO 2004/030615

PCT/US2003/028547

6/6881
FIGURE 6

ACAGAGACCCCGAGTTCTACAAGTTCTGTCAGGAGAATGACCAGAGCCTGCTAAACTTCAGCGACTCGGACAGCT
CTGAGGAGGAAGAGGGGCCGTTCCACTCCCTGCCAGATGTGCTGGAGGAAGCCAGTGAGGAGGAGGATGGAGCGG
AGGAAGGAGAAGATGGGGACAGAGTCCCCAGAGGGCTGAAGGGGAAGAAGAATTCTGTTCCTGTGACCGTCGCCA
TGGTTGAGAGATGGAAGCAGGCAGCAAAAGCAACGCCTCACTCCAAAGCTGTTCCATGAAGTGGTACAGGCCTTCC
GAGCAGCTGTGGCCACCACCCGAGGGGACCAGGAAAGTGCTGAGGCCAACAAATTCAGGTACAGGACAGTGCTG
CATTCAATGCTCTGGTTACCTTCTGCATCAGAGACCTCATTGGCTGTCTCCAGAAGCTGCTGTTTGAAAGGTGG
CAAAGGATAGCAGCAGGATGCTGCAGCCGTCCAGCAGCCCGCTCTGGGGGAAGCTTCGTGTGGACATCAAGGCTT
ACCTGGGCTCGGCCATACAGCTGGTGTCTGTCTGTCGGAGACGACGGTGTGGCGGCCGTGCTGCGGCACATCA
GCGTGCTGGTGCCCTGCTTCTGACCTTCCCCAAGCAGTGCCGCATGCTGCTCAAGAGAATGGTGATCGTATGGA
GCACTGGGGAAGAGTCTCTGCGGGTGCTGGCTTTCCTGGTCTCAGCAGAGTCTGCCGGCACAAGAAGGACACTT
TCCTTGGCCCCGTCTCAAGCAAATGTACATCACGTATGTGAGGAAGTCAAGTTACCTCGCCTGGTGCCCTCC
CCTTCATCAGTTTCATGCAGTGGACCTTGACGGAGCTGCTGGCCCTGGAGCCGGGTGTGGCCTACCAGCACGCCT
TCCTCTACATCCGCCAGCTCGCCATACCTGCGCAACGCCATGACCACTCGCAAGAAGGAAACATACCAGTCTG
TGTAACACTGGCAGTATGTGCACTGCCTCTTCTGTGGTGCCGGGTCTGAGCACTGCGGGCCCCAGCGAAGCCC
TCCAGCCCTTGGTCTACCCCTTGCCCAAGTCATCATTGGCTGTATCAAGCTCATCCCCACTGCCCGCTTCTACC
CGCTGCGAATGCACTGCATCCGTGCCCTGACGCTGCTCTCGGGGAGCTCGGGGGCCTTCATCCCGGTGCTGCCTT
TCATCCTGGAGATGTTCCAGCAGGTGCACTTCAACAGGAAGCCAGGGCGCATGAGCTCCAAGCCCATCAACTTCT
CCGTGATCCTGAAGCTGTCCAATGTCAACCTGCAGGAGAAGGCGTACCGGGACGGCCTGGTGGAGCAGCTGTACG
ACCTCACCTGGAGTACCTGCACAGCCAGGCACACTGCATCGGCTTCCCGGAGCTGGTGCTGCCTGTGGTCTCTGC
AGCTGAAGTCGTTCCCTCCGGGAGTGCAAGGTGGCCAACCTACTGCCGGCAGGTGCAGCAGCTGCTTGGGAAGGTT
AGGAGAACTCGGCATACATCTGCAGCCGCCGCCAGAGGGTTTCTTCCGGCGTCTCTGAGCAGCAGGCAGTGGAAG
CCTGGGAGAAGCTGACCCGGAAGAGGGGACACCCCTGACCTTGTAACAGCCACTGGCGCAAGCTGCGTGACC
GGGAGATCCAGCTGGAGATCAGTGGCAAAGAGCGGCTGGAAGACCTGAACTTCCCTGAGATCAAACGAAGGAAGA
TGGCTGACAGGAAGGATGAGGACAGGAAGCAATTTAAAGACCTCTTTGACCTGAACAGCTCTGAAGAGGACGACA
CCGAGGGATTCTCGGAGAGAGGGATACTGAGGCCCCCTGAGCACTCGGCATGGGGTGAAGACGATGAAGAGGACG
AGGAGGAGGGCGAGGAGGACAGCAGCAACTCGGAGGATGGAGACCCAGACGCAGAGGCGGGGCTGGCCCTGGGG
AGCTGCAGCAGCTGGCCCAGGGGCCGAGGACGAGCTGGAGGATCTGCAGCTCTCAGAGGACGACTGAGGCAGCC
CATCTGGGGGGCCTGTAGGGGCTGCCGGGCTGGTGGCCAGTGTTCACCTCCCTGGCAGTCAGGCCTAGAGGCT
GGCGTCTGTGCACTTGGGGGAGGCAGTAGACAGGGACAGGCTTTATTATTATTTTTCAGCATGAAAGACCAAA
CGTATCGAGAGCTGGGCTGGGCTGGGCTGGTGTGGCTGTGAAGCCCCACAGCTGTGGGCTGTGAAGTCAGCTC
CGCGGGGGAGCTGACCCTGACGTGAGCAGACCGAGACCAGTCCAGTTCCAGGGGAGGCCTGCAGGCCCTGGC
CCCTTCCACCACCTCTGCCCTCCGTCTGCAGACCTCGTCCATCTGCACCAGGCTCTGCCTTCACTCCCCCAAGTC
TTTGAAAATTGTTCCTTTCCTTTGAAGTCACATTTTCTTTTAAATTTTTTGTGTTTGCATCCGAAACCGAAAGA
AATAAAGCGGTGGGAGGCAGGGCCATTGTGTTG

WO 2004/030615

PCT/US2003/028547

7/6881
FIGURE 7

MAAAGSRKRRLAELTVDEF LASGFDSESESESESEN SPQAETREAREAARSPDKPGGSPSASRRKGRASEHKDQLSR
LKDRDPEFYKFLQENDQSLLNFS DSDSSEEEEGPFHSLPDVLEEASEEEDGAEEGEDGDRVPRGLKGKKNSVPVT
VAMVERWKQAAKQRLTPKLFHEVVQAFRAAVATTRGDQESAEANKFQVTD SAAFNALVTFCIRD LIGCLQKLLFG
KVAKDSSRMLQPSSSPLWGKLRVDIKAYLGSAIQLV SCLSETTVLAAVLRHISVLVPCFLTFFPKQCRMLLKRMVI
VWSTGEESLRVLAFLVLSRVCRHKKDTFLGPVLKQMYITYVRNCKFTSPGALPFI SFMQWTLTELLALEPGVAYQ
HAFLYIRQLAIHLRNAMTTRKKETYQSVYNWQYVHCLFLWCRVLSTAGPSEALQPLVYPLAQVIIGCIKLIPTAR
FYPLRMHCIRALTLLSGSSGAFIPVLEFIFILEMFQQVDFNRKPGRMSSKPINFSVILKLSNVNLQEKAYRDGLVEQ
LYDLTLEYLHSQAHCIGFPELVLPVVLQ LKSFLRECKVANYCRQVQQLLGKVQENSAYICSRQRVSFGVSEQQA
VEAWEKLTREEGTPLTLYYSHWRKLRDREIQLEISGKERLEDLNFPEIKRRKMADRKDEDRKQFKDLFDLNSSEE
DDTEGFSERGILRPLSTRHGVEDDEEDEEEGEEDSSNSE DGPD AEAGLAPGELQQLAQGPEDLEDLQLSEDD

WO 2004/030615

PCT/US2003/028547

8/6881
FIGURE 8

GTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAGCTGAGCCCATGAGCTC
CCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTGCGGTAGTCCCCATCCTGGAGGGGCAGGCTCT
GCGCATCTGCTCCTGGCATGGCGCTGCGGCACCTCGCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGT
CCATGGAGAACACGGCCCAGCTGCCCCAGTGTCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAA
GTCTGTGTGGTCCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGAA
CCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCCATGAACAGAAGCT
CAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCTCCCTCTTCCTGGGCACGTTCTTCATTA
GCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTACCTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACA
GAAGAAACAAGCTCCGGCCCTGCAGCCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCCTCAGTACGGA
AGCCGCGCTACGTAGGCGGGAGCGGCCCTGGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTA
TCAGCAATGTCTTGACCTGGAGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGC
GGGAACCAGCACAAAGTGTGGCATCGCCCGCGCCCGGGACAGTCCTGGGCACAGCCTCGGCTCTGGGTCCCTC
CGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCTGAGGCTCCTCCCCACCACAGCCATCTCGTTTATCG
GACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGCCTTGGGGGGTCCGGGCCCCCCCAGGAAAC
ACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGGCACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCA
GGGGCTCTGCTGCCGTGCCCTCCAGAGCCACAGCGGGCAGGACTCCTCCAGCACCACCACCCAGTGGCCCGA
GACCCCTCTGAGAACAGTGAGGCTGGTCCCTCGTGCCGTTCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGCCT
AGGAACCAGCTGCCTGAGACCAGGGTGCTCTGGGCTGTCTCCTCCCGCTGGCGGAGACCCCAAGCACGCAGCCAC
CCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAGCAGAAATTCATTGTGCTGAAAAGTC
CTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACCCCCATGCCTGGCTGATCCCTGCCACGTGGGGCAGGC
CCACATCTAACCCCCACAAGTCACTGCCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCT
CCCGGAGTTCTTGGGAGAAAAGCGCCGCTCGTGGCCGCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCA
GACGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCCTTCGGGGTCC
CCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTGGGCCAGCGGGAACGTGGGGGCA
CTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

9/6881
FIGURE 9

MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGSASCVRCGNGTLPAYN
GSECRSFAGPGAPFFPMNRSSGTPGRPHPGAPRVAASLFLGTFFISSGLILSVAGFFYLKRSSKLPRACYRRNKAP
ALQPGEEAAAMIPPPQSSVRKPRYVRRERPLDRATDPAAFPGEARI SNV

WO 2004/030615

PCT/US2003/028547

10/6881
FIGURE 10

AAAAAAAAAAAAAAAAACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCGCGAGTCAGACTCGGGTGGGGG
TCCCGGCGGCGGTAGCGGCGGCGGCGGTGCGAGCATGTCGTGGCTCTTCGGCATTAAACAAGGGCCCCAAGGGTGA
AGGCGCGGGGCGCCGCCCGCTTTGCCGCGCGCGCAGCCCGGGGCCGAGGGCGGCGGGGACCGCGGCTTGGGAGA
CCGGCCGGCGCCCAAGGACAAATGGAGCAACTTCGACCCACCGGCCTGGAGCGCGCCGCCAAGGCGGCGCGCGA
GCTGGAGCACTCGCGTTATGCCAAGGACGCCCTGAATCTGGCACAGATGCAGGAGCAGACGCTGCAGTTGGAGCA
ACAGTCCAAGCTCAAAGAGTATGAGGCCGCCGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGA
GAGGAGGAAGACCCCTGAGCGAGGAGACCCGGCAGCACCCAGGCCAGGGCCCAGTATCAAGACAAGCTGGCCCCGGCA
GCGCTACGAGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCA
GAAGCAGGAAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGT
GGAGGCCGAGGCCCGGGCGCGCGCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAA
GGCGGCCGAGCACCGTCAGACCGTCTTGGAGTCCATCAGGACGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGC
CTTTGTGACAGACTGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTTGGGGTCTACTCAGC
CAAGAATGCCACGCTTGTCGCGGCCGCTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTC
CCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAGGTACGCCGCGGCTCCTCAGTCGACCCACGAGCGC
GCTGGAGGGTGTGTGCTCAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACAAGGAACACCAA
GAAGAACCGCAGCCTGTACAGGAACATCCTGATGTACGGGCCACAGGCACCGGGAAGACGCTGTTTGCCAAGAA
ACTCGCCCTGCACTCAGGCATGGACTACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGT
GACCGCCATGCACAAGCTCTTTGACTGGGCCAATACCAGCCGGCGCGGCCTCCTGCTCTTTGTGGATGAAGCGGA
CGCCTTCCTTCGGAAGCGAGCCACCGAGAAGATAAGCGAGGACCTCAGGGCCACACTGAACGCCTTCCTGTACCG
CACGGGCCAGCACAGCAACAAGTTTCATGCTGGTCCTGGCCAGCAACCAACCAGAGCAGTTCGACTGGGCCATCAA
TGACCGCATCAATGAGATGGTCCACTTCGACCTGCCAGGGCAGGAGGAACGGGAGCGCCTGGTGAGAATGTATTT
TGACAAGTATGTTCTTAAGCCGGCCACAGAAGGAAAGCAGCGCCTGAAGCTGGCCCACTTTGACTACGGGAGGAA
GTGCTCGGAGGTGCTCGGCTGACGGAGGGCATGTCGGGCCGGGAGATCGCTCAGCTGGCCGTGTCCTGGCAGGC
CACGGCGTATGCCTCCGAGGACGGGGTCTGACCGAGGCCATGATGGACACCCGCGTGCAAGATGCTGTCCAGCA
GCACCAGCAGAAGATGTGCTGGCTGAAGGCGGAAGGGCCTGGGCGTGGGACGAGCCTTCCCCATCCTGAGTCCA
CAGGGAGATCCACAGCTCACGGAGCCTGGCCGCGGACCCCTCCACCCCTGCCTTGCCGGCCCCCTGCACATTTAG
GATATGCTCCTGGGTGGGACTGGGCTGTGCCCAGGGCCTCTGTCCCCAGGATGTCTTGTTGGTGCGGGTCCGGCC
GTTCTGCCCCCAGGGCACCCCTGTTGTAGGCACTGGCTAGGGAGGGGCAGGCCTCCTTCTGCCCCTCGAGAC
ACTCTTGGGAGATGCATTTTCCGTCTGGCTCACAGGGGAGGGTGAGGCTTTGCACCCAGCCCCTGCCAGGCC
ACTGTGAGGGTGGGTGCTGGCTGACCCCCGGGGCAGCAGGAGCCAGGCAGGTGATGCTTTGTTCTCGGCTCCC
ACAGCAGAGCCAGGTGAGGGGGCGCCTGCCAGGGCCAGACCCAGGTGGGGCAGCCTGAACCCCTGCTTCCCCCTGT
GGCCGGCATGCCCCGATCTTTACACACTGGTGACCTGAGAGAGGAGGGAGGAGGGAACCTGGCGGGGGTGTCT
GAGGCCGCACTGTGAGCTGGCCGGTCCAAGCCTGTGGCTGGAGCTGGGGTCTGTTTACCTAATAAAGTCCCACAG
GTGCCTCATT

WO 2004/030615

PCT/US2003/028547

11/6881
FIGURE 11

MSWLF GINKGPKGEGAGPPPP LPPAQP GAEGGGDRGLGDRPAPKDKWSNFDPTGLERA AKAARELEHSRYAKDAL
NLAQM QEQT LQLEQQSKLKEYEAAVEQLKSEQIRAQAEERRKTLSEETRQHQAQAQYQDKLARQRYEDQLKQQQL
LNEENLRKQEE SVQKQEAMRRATVEREMELRHKNEMLRVEAEARARAKAERENADI IREQIRLKAAEHRQTVLES
IRTAGTLFGEGFRAFVTDWDKVTATVAGLTLLAVGVYSAKNATLVAGR FIEARLGKPSLVRETSRITVLEALRHP
IQVSRRLLSRPQDALEGVVLSPSLEARVRDIAIATRNTKKNRSLYRNILMYGPPGTGKTLFAKKLALHSGMDYAI
MTGGDVAPMGREGVTAMHKLFDWANTSRRGLLLFVDEADAF LRKRATEKISED LRATLNAFLYRTGQHSNKFMLV
LASNQPEQFDWAINDRINEMVHFDLPGQEERERLVRMYFDKYVLKPATEGKQRLKLAQFDYGRKCSEVARLTEGM
SGREIAQLAVSWQATAYASEDGVLTEAMMDTRVQDAVQHQQKMCWLKAEGPGRGDEPSPS

WO 2004/030615

PCT/US2003/028547

12/6881
FIGURE 12

ATCAGTTCTCGCCCGTCTGGGCGTGGGCGTGGCCGGCGTGGCTGCTCGGGACCACCCGAACCCGCGGGCCATGGCC
CCGGCCGCCGCCAGCCCCCGGAGGTGATCCGCGCGGGCGCAGAAGGACGAGTACTACCGCGGTGGGCTGCGGAGC
GCGGCGGGCGGGCGCCCTGCACAGCCTGGCGGGTGCAGGAAGTGGCTGGAGTGGAGGAAGGAGGTTGAGCTGCTC
TCAGATGTGGCCTACTTTGGCCTCACACACTTGCAGGCTACCAGACCCTGGGGGAGGAGTACGTACGATCATC
CAGGTGGACCCATCGCGGATACATGTGCCCTCCTCGCTGCGCCGTGGCGTGCTGGTGACGCTGCATGCCGTCCCTG
CCCTACCTGCTGGACAAGGCCCTGCTCCCCCTGGAGCAGGAGCTGCAGGCTGACCCCGACAGTGGGCGACCCCTG
CAGGGGAGCCTGGGGCCAGGTGGGCGTGGCTGCTCAGGGGCGCGGCGCTGGATGCGTCACCACACGGCCACCCTG
ACTGAGCAGCAGAGGAGGGCGCTGCTGCGGGCGGTCTTCGTCTCAGACAGGGCCTCGCCTGCCTCCAGCGGCTA
CATGTTGCTGGTTTTACATCCACGGTGTCTTACCACCTGGCCAAGAGGCTCACGGGGATCACGTACCTCCGT
GTCCGAGCCTGCCCGGAGAGGACCTGAGGGCCCGTGTAGCTACAGGCTGCTGGGGGTCACTCACTGCTGCAC
CTGGTGCTGTCCATGGGGCTGCAGCTGTACGGTTTCAGGCAGCGGCAGCGAGCCAGGAAGGAGTGGAGGCTGCAC
CGCGGCCTGTCTACCGCAGGGCCTCCTTGGAGGAGAGAGCCGTTTCCAGAAACCCCTGTGCACCTGTGCCTG
GAGGAGCGCAGGCACCCAACAGCCACGCCCTGCGGCCACCTGTTCTGCTGGGAGTGCATCACCGCGTGGTGACG
AGCAAGGCGGAGTGTCCCTCTGCGGGGAGAAGTTCCTCCCCAGAAGCTCATCTACCTTCGGCACTACCGCTGGA

GCCGGCGCCCGGGTGGGCCTGGACACAGATGACCTCTACGGGAGTCTGAACGCCAAGATTTAGTCTCAGGATTAA
CCTTGCTTGACAGAAGTTAGAACACTCTCAGTTTTTGTGTCATGTAAGATACTAACCTAGCCACCCTGGGAGAGA
ACAGAAAGCTGTCCCTGGCTGCGCTTCTCAGCCCTGGGAGGGGCGCCTGAACCCAGAACATTTCCCTAACCCCA
ACCTGGTAGGACTCAGCCACTTCTTCAGGAATTTCACTTATTTGGACGGGATTTTAGGTTTCCCTCCCTTCCCCA
AACCATACAGTTGAGAAGTAATTCAGAAGTAGGCCAGAAGACACTTTATTCGTTTATATTGTGAGAAAACAGCCC
CATCAGGCTTGTGTTAAGGCAATGGACTGAATGAGTGCCTGCTGGTGGGTGGGGCACGGAGGCTGGCGGGTTG
CTTCAGCCAGTGCAAGTGAAGACAGCAGCCCCACGGCCCATGGGAGGCGGCGCTGCTCTCCCGAGGGCGGCTGG
GCAGAGCACATCCCCAGGACTTGATGACCACACGGGGCAGAGAGAAACCAACCAAGGCCAGCACCTCCGTCCGA
AGCATTTGGCACACACACCTTCAATACACGTCAAGGTCGCTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGC
CTGAGACGCACAGAGAGGTCTCTCCTGACCCAGACGCACTCACGAGCCAGGTCCTGGGGGTATGGGGGCTGCCA
GGGGCGCCGAGCCCTCTCCTGGGGGGCCTGCTGGGCAGGCGACCTGCTGACCCACGGTCACTGCTGTGTTACAGC
CCCTCAGCTCGGCCCCAGCCTATTTCCCGCCTCCATTTGATGTTTCCAGGTTTTCAAACCTGCATTTAACCTGCG
CCAGAGAGTTACCGTAGGCATCTTTAATAAACTAACTCCAGCAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

13/6881
FIGURE 13

MAPAAASPPEVIRAAQKDEYYRGGLRSAAGGALHSLAGARKWLEWRKEVELLSDVAYFGLTTLAGYQTLGEEYVS
IIQVDPRIHVPSLRRGVLVTLHAVLPYLLDKALLPLEQELQADPDSSGRPLQGSLGPGGRGCSGARRWMRHHTA
TLTEQQRALLRAVFVLRQGLACLQRLHVAWFYIHGVFYHLAKRLTGITYLRVRSPLGEDLRARVSYRLLGVISL
LHLVLSMGLQLYGFRQQRARKEWRLHRGLSHRRASLEERAVSRNPLCTLCLEERRHPTATPCGHLFCWECITAW
CSSKAECPLCREKFPPQKLIYLRHYR

WO 2004/030615

PCT/US2003/028547

14/6881
FIGURE 14

GGGCGGCGAGTGGGGAGCGGGGCCGGGAGTGGAGCAGCCGCCGCGGGGACTGGACCGAGCCTCGCCGGCGCGC
ACCTGCCCCGAGCGCCCCGCGGAGCGCGCAGCGCGGCCCGAGCGCGACGACCTGCCGAGCGGGCGGCCGAGGCGCG
GTGTGGGCGCGTCAGGCCGCGACGAGGGCGCTGAGACAAATTTACATGTATTGGAGACCAGACCAGAAGCCCTTC
TGAATTAAGATCTCACATTCTTGAAGGTGGCATTGAAGAGCACTAAGATCGGAAGATGAGTGTGAGCTTGACCAGTT
ACGGCAGGAGGCCGAGCAACTTAAGAACCAGATTGAGACGCCAGGAAAGCATGTGCAGATGCAACTCTCTCTCA
GATCACAACAACATCGACCCAGTGGGAAGAATCCAAATGCGCACGAGGAGGACACTGCGGGGGCACCTGGCCAA
GATCTACGCCATGCACTGGGGCACAGACTCCAGGCTTCTCGTCAGTGCCTCGCAGGATGGTAAACTTATCATCTG
GGACAGCTACACCACCAACAAGGTCCACGCCATCCCTCTGCGCTCCTCCTGGGTATGACCTGTGCATATGCCCC
TTCTGGGAACTATGTGGCCTGCGGTGGCTGGATAACATTTGCTCCATTTACAATCTGAAAACCTCGTGAGGGGAA
CGTGCGCGTGAGTCGTGAGCTGGCAGGACACACAGGTTACCTGTCTGCTGCTGCCGATTCTGGATGACAATCAGAT
CGTACCAGCTCTGGAGACACCACGTGTGCCCTGTGGGACATCGAGACCGGCCAGCAGACGACCACGTTTACCGG
ACACACTGGAGATGTCATGAGCCTTTCTCTGTCTGACACCAGACTGTTCTGTCTCTGGTGCTTGTGATGCTTC
AGCCAACTCTGGGATGTGCGAGAAGGCATGTGCCGCGCAGACCTTCACTGGCCACGAGTCTGACATCAATGCCAT
TTGCTTCTTTCCAAATGGCAATGCATTTGCCACTGGCTCAGACGCGCCACCTGCAGGCTGTTTGACCTTCTGTG
TGACCAGGAGCTCATGACTTACTCCCATGACAACATCATCTGCGGGATCACCTCTGTCTCCTTCTCCAAGAGCGG
GCGCCTCCTCCTTGCTGGGTACGACGACTTCAACTGCAACGTCTGGGATGCACTCAAAGCCGACCGGGCAGGTGT
CTTGGCTGGGCATGACAACCGCGTCAGCTGCCTGGGCGTGACTGACGATGGCATGGCTGTGGCGACAGGGTCTG
GGATAGCTTCTCAAGATCTGGAACAAACGCCAGTAGCATGTGGATGCCATGGAGACTGGAAGACCATTCCAAC
TGGACGCGTTACCATGAGAGCATATCCTATCCAACCGTACTAACGTGGACAACCTACACCTCCCTCAGAACTTC
AAAAGGGCAAGATCTTTTTCTTCACTTATTTGCTGAAACCAAGAGCACAATTTCCATTGAGAGAAAGATCTCTG
TGCTGTAACTAAACAAATTTGTGCATTCCTTCCGGGGCCATCGTCTTTGTTTTCTTTTTGTCTTGAATGAATT
TAAAAGGAAATATATAATAAATAATGTTAACCAAGGTAACCTTGTAGTGAATTGTGACACAGACACACTTTTC
CACCAGTGATTTTGAATTTTAGACCAAGTACCTGTTTTGTGGCATTGATGCAAAACATGCTGAGGGCTTTGTTC
ATCTGGTCATCGTGTCCAAATTTTCACTCATGTTTGTAGCAAGATTTTGAAGCATTATATTTCTTTTTAAAT
GTATTCCTTTGTGTTCAACAGTTAATCAAAACCAGAGAGTCTAGGGCAGCCTCTCTGATGTTGTCAATGATGTA
ATTCACTCCCTGGTTTTTAATTTTCTGTCTGATGTCACAGATCATTGTTGCACACAAACGTGGCATAGAAAAGAA
CATGTTTCAAGCCATGGGGCCAAAGCACATGCGGGGACGGTCTCAATGCGTGATCAGAGAATCCTTCACCTTTG
CTGAAAAGTGAGCTCAGATCCAGCACCATGTTCCCTCCTGACCCATCCTGTCTATCTTCTCAGTTGAGTTTTAAT
CTCACTTTGGGTTTTCTTGTGAAGTTGGAGGGAAGTTATAATAGCCTAACACTACCCACCCCACTAGGAGG
AACCTCTGTTTTCAAGAGAGATGCCGTGCTGTGCTTGGATAGTCAGTCAATTATTTGTGTATGAAACAATGTAC
AAATCAATGTTTTGAAAATAATGATCTCAGACTTTCTAAGTTAAATTTTAAAAATTTTGATTGTTTGCCATATTG
GGTGGGTTTACTCTTAGAATCGCATGCTGTAGAAATGCTCAAAAGTGATATGGGACTCAGTCTTAGGTGTTCT
TTTTCTTTTAAAGAAATAACCTCTTACAGTTGTAACCATGCGGCTCTGTCCACTTCTCGTTGCTGCTCTGTGGCA
CATATCGGAAGCAGTACAGCGCGCGGCTCTACACGCTGGGTAGCGGGATAAGTCACTGTTTTCTTTATTTCTTT
AAAAAAGGAAAGTTCTGTGCAACGACTGCTGTGGATTCTGAGGGTGGGAGGGAGAGAGAGGGAGGGAGAG
GGAGTGAAGAGCCTGCCCTCCTATATGGATTCTTCAGGGCCCTCCACATCTGAGGTGGCTCATTCCCATCACACA
CAGATTGCTCTGGTGTTCATTTCAAGGCCAGTGTTCAGCAGCAGCGTTTGAAAGCAGGTTCTGTGGGACCCCCC
GCCCCGCCCCCGCACTCCTTCATAGCAGCAGTAGTGCTTCTCCATCCTGTTTTCTGCAACATTCTATACAAAA
CTGTGCTGTGACCTTGGGTAGGCTGGATCTGGCAAAGAGAATACAAAATGAAACCCCTTCTTTCTCTTTCCGTC
CAACAACTCTGTAGAGCTCTCTGCACCCTTACCCCTTCCACCTTTTGTATTTAATTTTAAAGTCAGTGTACTGC
AAGGAAGCTGGATGCAAGATAGATACTATATTAACCTGTACTGTTATTTAAGATGTAATAAAGCAGTTTGACATG

WO 2004/030615

PCT/US2003/028547

15/6881
FIGURE 15

ATCAAACCACCCAGCAAAATGTCTCGGAAAGAAAAAGTTCATCACAGAAAAGATGAAAAGAGAAAAGAAAAATGT
AGGCATCATAGCCATTCAGCAGAAGGGGGGAAGCATGCTAGAGTGAAAGAAAGAGAGCACGAACGTCGGAAACGA
CATCGAGAAGAACAGGATAAAGCTCGCCGGGAATGGGAAAGACAGAAGAGAAGGGAAATGGCAAGGGAGCATTC
AGGAGAGAAAGGGACCGCTTGGAGCAGTTAGAAAGGAAGCGGGAGCGGGAGCGCAAGATGCGGGAGCAGCAGAAG
GAGCAGCAGTCAAGAAGATGACCTTCAGCGAGCACCCCTACAACAACCTCCGCAAGCGCTTCGGGGCTCTGCTCT
CAGACCAGGGCTTCGACCTCATGAACAAGTTCCTGACCTACTTCCCCGGGAGGAGGATCAGCGCTGAGGACGGCC
TCAAGCATGAGTATTTCCGCGAGACCCCCCTCCCCATCGACCCCTCCATGTTCCCCACGTGGCCCGCCAAGAGCG
AGCAGCAGCGTGTGAAGCGGGGCACCAGCCCGAGGCCCCCTGAGGGAGGCCTGGGCTACAGCCAGCTGGGTGACG
ACGACCTGAAGGAGACGGGCTTCCACCTTACCACCACGAACCAGGGGGCCTCTGCCGCGGGCCCCGGCTTCAGCC
TCAAGTTCTTGAAGGTCAGAGTGGACCCCGTCATGGGG

WO 2004/030615

PCT/US2003/028547

16/6881
FIGURE 16

MGKTEEKGNKGAFQERKGPLGAVRKEAGAGAQDAGAAEGAAVKKMTFSEHPYNNLRKRFGALLSDQGF DLMNKF
LTYFPGRRISAEDGLKHEYFRETPLPIDPSMFPTWPAKSEQQRVKRGTSRPPEGGLGYSQLGDDDLKETGFHLT
TTNQGASAAGPGFSLKF

WO 2004/030615

PCT/US2003/028547

17/6881
FIGURE 17

TCGCGCGGAAGCCGCGGTAGGGTGGGAACCCAAGCGGGAGAGCCGCGGGATTTGCGGCCGCCGCCATGCCGTCGT
CCCCGCTGCGGGTGGCGGTGGTGTGCTCGAGCAACCAGAACCGGAGCATGGAGGCGCACAAACATCCTCAGCAAAC
GGGGATTCAGCGTCCGATCCTTTGGAACAGGGACTCACGTGAAGCTTCCAGGACCAGCTCCCGACAAGCCCAATG
TTTATGATTTCAAAACCACATATGACCAGATGTACAATGATCTTCTTAGGAAAGACAAAGAAGCTCTATACACAGA
ATGGGATTTTACATATGCTGGACAGAAATAAGAGAATCAAGCCCCGGCCAGAAAGATTCCAGAAGTCAAAGACC
TGTTTGATCTGATCCTCACTTGCGAAGAGAGAGTGTATGACCAGGTGGTGGAAAGATCTGAATTCCAGAGAACAGG
AGACCTGCCAGCCCGTGACGTGGTCAATGTGGACATCCAGGACAACCACGAGGAGGCCACCCTGGGGGCGTTTC
TCATCTGTGAGCTCTGCCAGTGTATCCAGCACACGGAAGACATGGAGAACGAGATCGACGAGCTGCTGCAGGAGT
TCGAGGAGAAGAGTGGCCGACCTTTCTGCACACCGTCTGCTTCTACTAGAGCCAGCGCCCGCATGGAGCCGCCT
CTGGAGCTTCCTGTTGTTTCATACTTTTTTCCTTCCTGACATTTGTTTTTACTTACAGGTGTTCTGCTGGTGACGGT
AGCATTACCCAAATAAACTGTGCATATGAAATGGGAGAGGAGATGCCAAAACGCCAGATGAAAGCAATCAAGTTT
CTTCTTTTCCACTTTTACTTATGAGCGGGATATTGATTACAAAGTTTTTCTTCTTTAACCAAAAAGGAAAGACAA
CGGTTTGTGTGCACTTCCCGACATACCTGTGTCTTCGTGTGCCTGCCTTCCCTCCCTCCTCCCCACCGGGCCGGA
CTGTACAGAGCCCTGCTGCGGCGTGTTAGGAATGACCTGGAATTGTCAATAAACAGATGCTGCTGTCAAAAAAAA
AAAAAAA

WO 2004/030615

PCT/US2003/028547

18/6881
FIGURE 18

MPSSPLRVAVVCSSNQNRSM EAHNILSKRGFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDKEL
YTQNGILHMLDRNKRIKPRPERFQNC KDLFDLILTCEERVYDQVVEDLNSREQETCQPVHVNVNDIQDNHEEATL
GAFLICELCQCIQHTEDMENEIDELLQEFEEKSGRTFLHTVCFY

WO 2004/030615

PCT/US2003/028547

19/6881
FIGURE 19

CCTGGCCACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCCCGAGTCAGACTCGGGTGGGGGTCCC GGCG
GCGGTAGCGGCGGCGGCGGTGCGAGCATGTCGTGGCTCTTCGGCGTTAACAAGGGCCCCAAGGGTGAAGGCGCGG
GGCCGCCCGCCCTTTGCCGCGCGCAGCCCGGGGCGAGGGCGGCGGGGACCGCGGTTTGGGAGACCGGCGCGG
CGCCCAAGGACAAATGGAGCAACTTCGACCCACCGGCCTGGAGCGCGCCGCCAAGGCGGCGCGGAGCTGGAGC
ACTCGCGTTACGCCAAGGAGGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCA
AGCTCAAAGAGTATGAGGCCGCGGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGAGAGGAGGA
AGACCCTGAGCGAGGAGACCCGGCAGCACCAGGCCAGGGCCAGTATCAAGACAAGCTGGCCCGGCAGCGCTACG
AGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCAGG
AAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGTGGAGACCG
AGGCCCGGGCGCGCGCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAAGGCGTCCG
AGCACCGTCAGACCGTCTTGGAGTCCATCAGGACGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGCCCTTTGTGA
CAGACCGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTCGGGGTCTACTCAGCCAAGAATG
CGACAGCCGTCACTGGCCGCTTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTCCCGCATCA
CGGTGCTGGAGGCGCTGCGGCACCCATCCAGGTACCGCGCGGCTCCTCAGTCGACCCAGGACGTGCTGGAGG
GTGTTGTGCTTAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACCAGGAACACCAAGAAGAACC
GGGGCCTGTACAGGCACATCCTGCTGTATGGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAACTCGCCC
TGCACTCAGGCATGGACTACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGTGACCGCCA
TGCACAAGCTCTTTGACTGGGCCAATACCAGCCGCGCGGCCCTCCTGCTCTTCATGGATGAAGCAGACGCCTTCC
TTCGGAAGCGAGCCACTGAGGAGATAAGCAAGGACCTCAGAGCCACACTGAACGCCTTCCTGTACCACATGGGCC
AACACAGCAACAAATTCATGTGGTCTGGCCAGCAATCTGCCTGAGCAGTTCGACTGTGCCATCAACAGCCGCA
TTGACGTGATGGTCCACTTCGACCTGCCGCGAGCAGGAGGAGCGGGAGCGCCTGGTGAGACTGCATTTTGACAACT
GTGTTCTTAAGCCGGCCACAGAAGGAAAACGGCGCCTGAAGCTGGCCCAGTTTGACTACGGGAGGAAGTGCTCGG
AGGTGCTCGGCTGACGGAGGGCATGTGCGGCCGGGAGATCGCTCAGCTGGCCGTGTCTGGCAGGCCACGGCAT
ATGCCTCCAAGGACGGGGTCTCCTACTGAGGCCATGATGGACGCTGTGTGCAAGATGCTGTCCAGCAGTACCGAC
AGAAGATGCGCTGGCTGAAGGCGGAGGGGCTGGGCGCGGGGTGAGCACCCCTATCCGGAGTCCAAGGCGAGA
CCCTCACCTCATGGAGCCTGGCCACGGACCCCTCCTACCCCTGCCTTGCCGGCCCCCTGCACATTTAGGATATGCT
CCTGGATGGGGACTGGGCTGTGCCAGGGCCTCTGTCCCCAGGATGTCTTGTGGTGGCGGTGGGCCGTTCTGCC
CCCCAGGGCACCCCTGTTGTAGGCACTGGCTAGGGAGGGGAGGCCCTCCTTCTGCCCCCTCGAGACACTCTTGG
GAGATGCATTTTCCGTCTGGCTCACAGGGGAGGGTGAGGCTTTGTACCCAGCCCCCTGCCAGGCCACTGTGAG
GGTGGGTGCTGGCTGAGCCCTGGGGCAGAAGGAGTGGGGCAGGCGGGGTCTTTGTTCTCGGCTCCACAGCAGA
GCCAGGTGAGGGGGGGCCTGCCAGGACTAGACAGAAGTGGGGCGGC

WO 2004/030615

PCT/US2003/028547

20/6881
FIGURE 20

ATGAGGCTGCAGAGTGATGTGGGGGCCAGCGGTGACTTCATGACCACACTGCGCCCAGGTGTAAGAGGGGCACGCT
TCTGCCCAGGCATCGTCCATGGAAGACACGCAGTCGGCCACTGCAGCCTCGGTCTTGGGTGCCCTGGGGCTGGGT
CACTGGGGGGCCACAGGCCACACTGAGAGACCACAGTCCTGGCATGCCATGCAGCTCCCTGTCCCCAGAGGCCATG
TCAAAGGACGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCAAGCTCAAACAA
CTTGTC AATGAGGATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCACCATCAGACCTTCTTGGAGTCCATCAGG
GCGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGCCTTTGTGACAGACCGGGACAAAGTGACAGCCACGGTGGCT
GGGCTGACGCTGCTGGCTGTGCGGGTCTACTCAGCCAAGAATGCGACAGCCGTCCTGAGCCGCTACATCGAGGCT
CGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTCCCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAG
CAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGTGCTGGAGGGTGTTGTGCTTAGTCCCAGCCTGGAAGCA
CGGGTGCGCGACATCGCCATAATGACAAGGAACATCAAGAAGAACCGGGGCCTGTACAGGCACATCCTGCTGTAC
GGGCCACCAAGCACCGGGAAGACGCTGTTTGCCAAGAACTCGCCCTGCACTCAGGCATGGACTACGCCATCATG
ACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGTGACCGCCATGCACAAGCTCTTTGACTGGGCCAATACC
AGCCGGCGCGGCCTCCTGCTCTTTGTGGATGAAGCGGACGCCTTCCTTCGGAAGCGAGCCACTGAGAAGATAAGC
GAGGACCTCAGGGCCACACTGAACGCCTTCTGTACCGCACGGGCCAGCACAGCAACAAATTCATGCTGATCCTG
GCCAGCTGCCACCCCGAGCAGTTCGACTGGGCCATCAATGCCTGCATCGACGTGATGGTCCACTTCGACCTGCCA
GGGCAGGAGGAGCGGGCGCGCCTGGGATTGGAGGGAGAGGCTCCTCATGAGACCCCATGTGCGGACTAGAGGGA
GAGGCTCCTCATGGTCCACTGCTGGCTTCTGGCCTGGCCTCCCTGCAGCTGCCACACCCGGCCCTGGAGCCTCGT
GGTGTGGGGCGCGGCTCTTGCTTCTGCTGCACATGTGCCTTGAGGCTGTCAGGCTCCCTGTTGCTGGCGGGCCC
CGGTTTCTGAGTCCTTCTGTGCACCTGACCCAAATCCCTGCTGTGCCCAGTGACGACAAAAGCTGCTCTGTTCCA
AAGAGAGCCTGGTTCTCCCCTGCCGACCCCTCCACTGCCGCCTGCTCCATGCTAGACCAGCTTCCGGGCGTCTG
AAGCTGGCCAGTTTGACTACGGGAGGAAGTGCTTAGAGATCGCTCGGCTGACAGAGGGCATGTCATGCCGGAAG
ATCGCACAGCTGGCCGTGTCCTGGCAGGCCACGGCGTATGCCTCCAAGGACGGGGTCTTGACCGAGGCCATGATG
GACGCCTGCGTGCAAGACTTTGTCCAGCAGCACCAGCAGATGATGCGCTGGCTGAAGGGGGAGAGGCCTGGGCCC
GAGGACGAGCAACCCCTCATCCTGA

WO 2004/030615

PCT/US2003/028547

21/6881
FIGURE 21

MRLQSDVGASGDFMTTLRPGVRGHASQAASSMEDTQSATAASVLGALGLGHWGPQATLRDHSPGMPCCSSLSPEAM
SKDALNLAQMQEQTLEQQSKLKQLVNEDLRKQEEVQKHHQTFLESIRAAGTLFGEGFRAFVTDRDKVTATVA
GLTLLAVGVYSAKNATAVTGRYIEARLGKPSLVRETSRITVLEALRHPIQQVSRRLLSRPQDVLEGVVLSPSLEA
RVRDIAIMTRNIKKNRGLYRHILLYGPPGTGKTLFAKKLALHSGMDYAIMTGGDVAPMGREGVTAMHKLFDWANT
SRRGLLLFVDEADAFLRKRATEKISEDLRATLNAFLYRTGQHSNKFMLILASCHPEQFDWAINACIDVMVHFDLP
GQEERARLGLEGEAPHETPMGSGLEGEAPHGPELLASGLASLQLPHPALEPRGVGRGSCFLLHMCLEAVRLPVAGGP
RFLSPSVHLTQIPAVASDDKSCSVPKRAWFSPADPSTAACSMLDQLSGRLKLAQFDYGRKCLEIARLTEGMSCRK
IAQLAVSWQATAYASKDGVLTEAMMDACVQDFVQQHQMMRWLKERPGPEDEQPSS

WO 2004/030615

PCT/US2003/028547

22/6881
FIGURE 22

AAGTGCCCGAGGGCGGCCGCAGAACGGTCAATTTGAGCCGCGTCGAGCTCCCCTGGGACCTGTGGCCGCGCCCA
CAGACCATGCTCCTGGGGCGCCTGACTTCCCAGCTGTTGAGGGCCGTTTCCTTGGGCAGGCGGCCGCCGCCTTGG
CCCGTCTCTGGAGTGCTGGGCAGCCGGGTCTGCGGGCCCCTTTACAGCACATCGCCGGCCGGCCCAGGTAGGGCG
GCCTCTCTCCCTCGCAAGGGGGGCCAGCTGGAGCTGGAGGAGATGCTGGTCCCCAGGAAGATGTCCGTCAGCCCC
CTGGAGAGCTGGCTCACGGCCCCGCTGCTTCTGCCCAGACTGGATACCGGGACCGCAGGGACTGTGGCTCCACCG
CAATCCTACCAGTGTCGCCCCAGCCAGATAGGGGAAGGGGCCGAGCAGGGGGATGAAGGCGTCGCGGATGCGCCT
CAAATTCAGTGCAAAAACGTGCTGAAGATCCGCCGGCGGAAGATGAACCACCACAAGTACCGGAAGCTGGTGAAG
AAGACGCGGTTCTGCGGAGGAAGGTCCAGGAGGGACGCCTGAGACGCAAGCAGATCAAGTTCGAGAAAGACCTG
AGGCGCATCTGGCTGAAGGCGGGGCTAAAGGAAGCCCCGAAGGCTGGCAGACCCCCAAGATCTACCTGCGGGGC
AAATGAGTCTGGCGCCGCCCTTCCCGCCCGTTGCTGCTGTGATCCGTAGTAATAAATTCTCAGAGGACTCAGCCT
TTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

23/6881
FIGURE 23

MLLGRLTSQLLRAVPWAGGRPPWPFVSGVLGSRVCGPLYSTSPAGPGRAASLPRKGAQLELEEMLVPRKMSVSPLE
SWLTARCFLPRLDTGTAGTVAPPQSYQCPPSQIGEGAEQGDEGVADAPQIQCKNVLKIRRRKMNHKKYRKLVKKT
RFLRRKVQEGRLRRKQIKFEKDLRRIWLKAGLKEAPEGWQTPKIYLRGK

WO 2004/030615

PCT/US2003/028547

24/6881
FIGURE 24

GCGGTGCGGGCCGGGCGGGGCGCAGGCGGGCGGGCGGGTAGCGCCCCGCGTCCGAGCCCCGGGCGGGCCCTGAG
CGCGCGGGCTCCGCGCCCGCCGCGGCCATGGCGGAGACCAAGATTATCTACCACATGGACGAGGAGGAGACGCC
GTACCTGGTCAAGCTGCCCGTGGCCCCCGAGCGCGTACGCTGGCCGACTTCAAGAACGTGCTCAGCAACCGGCC
CGTGACAGCCTACAAATTCTTCTTTAAGTCCATGGACCAGGACTTCGGGGTGGTGAAGGAGGAGATCTTTGATGA
CAATGCCAAGCTTCCTTGCTTCAACGGCCGCGTGGTCTCCTGGCTGGTCTGGCTGAGGGTGCTCACTCGGATGC
GGGGTCCCAGGGCAGGCACAGCCACACAGACCTGCCCCCGCTCTTGAGCGGACAGGCGGCATCGGGGACTCCCG
GCCCCCTCTTCCACCCAAATGTGGCCAGCAGCCGTGACGGGATGGACAACGAGACAGGCACGGAGTCCATGGT
CAGTCACCGGCGGGAGCGTGCCCGACGCCGGAACCGCGAGGAGGCCCGCCCGGACCAATGGGCACCCAAGGGGAGA
CCGACGGCGGGATGTGGGGCTGCCCCAGACAGCGCGTCCACCGCCCTCAGCAGCGAGCTTGAGTCCAGCAGCTT
TGTGGACTCGGACGAGGATGGCAGCACGAGCAGGCTCAGCAGCTCCACGGAGCAGAGCACCTCATCCAGACTCAT
CCGGAAGCACAAACGCCGGCGGAGGAAGCAGCGCCTTCGGCAGGCGGACCGGGCCCTCCTCCTTCAGCAGCATAAC
CGACTCCACCATGTCCCTCAACATCGTCACTGTACGCTCAACATGGAAAGACATCACTTTCTGGGCATCAGCAT
CGTGGGGCAGAGCAACGACCGTGGAGACGGCGGCATCTACATTGGCTCCATCATGAAGGGCGGGGCTGTGGCCGC
TGACGGCCGCATCGAGCCCGGCGACATGTTGCTGCAGGTGAATGACGTGAACCTTTGAGAACATGAGCAATGACGA
TGCCGTGCGGGTGTGCGGGAGATCGTTTCCCAGACGGGGCCCATCAGCCTCACTGTGGCCAGTGTGGGACCC
AACGCCCCGAAGCTACTTCACCGTCCACGGGCTGACCCGGTGCGGCCCATCGACCCCGCCCTGGCTGTCCCA
CACGGCGGCACTGACAGGAGCCCTGCCCCGCTACGAGCTGGAAGAGGCGCCGCTGACGGTGAAGAGTGACATGAG
CGCCGTGCTCCGGGTATGACAGCTGCCAGACTCGGGACTGGAGATCCGCGACCGCATGTGGCTCAAGATCACCAT
CGCCATGCCGTATCGGGGCGGACGTGGTGGACTGGCTGTACACACACGTGGAGGGCTTCAAGGAGCGGCGGGA
GGCCCCGAAGTACGCCAGCAGCTTGTGAAGCACGGCTTCCTGCGGCACACGGTCAACAAGATCACCTTCTCCGA
GCAGTGCTACTAGTCTTCGGGGATCTCTGCAGCAATCTCGCCACCCTGAACCTCAACAGTGGCTCCAGTGGGAC
TTCGGATCAGGACACGCTGGCCCCGCTGCCCCACCGGCTGCCCCCTGGCCTTAGCTATGGCAGCGGCAGCACCGG
GTACCCGGGACCCCCACCTGTCTCCCGCTGCCTACCAGGACCCGGGCTTTAGCTATGGCAGCGGCAGCACCGG
GAGTCAGCAGAGTGAAGGGAGCAAAAGCAGTGGGTCCACCCGGAGCAGCCGCCGGGGCCCCGGGCCGTGAGAAGGA
GCGTCGGGCGGCGGGAGCTGGGGGAGTGGCAGTGAATCGGATCACACGGCACCGAGTGGGGTGGGGAGCAGCTG
GCGAGAGCGTCCGGCCGGCCAGCTCAGCCGTGGCAGCAGCCACGCAGTCAGGCCTCGGCTACCGCCCCGGGGCT
CCCCCGCCCCACCCACGACCAAGGCCATACAGTGGTGGGGGGGCCACCCGGGGGACCCCCCTGTCCGGGAGCT
GGCTGCCGTCCCCCGGAATTGACAGGCAGCCGCCAGTCCCTCCAGAAGGCTATGGGGAACCCCTGCGAGTTCTT
CGTGACATCATGTGACTCGTGGCGCATGCCCCAGCCCTGCCTGAGGTGGGGAGCTGGCGGTCTGCCGCATGCA
GAGCTCGCGTGGGCTTGCTTTCGTGGGGGCCAGGACGGGAGGCAGGGTGGGGGGCAGGCTGGACCACCACATCT
GCCCTGGCAGCCTGGCTGCTCCAGCTCCTGACAGCACCTGTGTCTGAGCAGCCGTGTTGGGGGCGCTCCCTCTCT
GCCCCCAGCAGAGACCTCGGACCTCCCAACCCCTTGTGTCTGGTGGGGATCCCTCCTGGGATGAGGAAGACCCC
CTCGGGCTCTCGGCTGACCCCCACCTCCTGCACAGCTGTGCCAGGCCCCCAGGGTGGTCCATGCGGGGCAACCC
CCTGCGGTGCACAGGCCCCCTGTCTGGAGTAGGGATCTAATTTATTTATTTATTTGCTGGCCGGTGAATCGGGG
AGGAGGCGACCTGTCTATCTGTCCACCTGTGTGCTGCCCTTGGAGCAGCCTGCACCTTCTCTCTCCCATCCGG
CAACAGTCTGAAAGTACGTGGAGGACGGGACCGGAAGACGAGAGAGGGCTGGACATCCTGCCACCGTGTCCAG
CCAGGGCAGGGAGGGACCATGGCCCGCAGGGTCAAGGGGCCCCGATGTGCACAGCTGCCACAGGGAGGGAGGTCT
TGGGGAGATGGGCAGTCAAGTGGCCCGTCTTGGTGGTGCACACACTGCGCGCACACATCGCGGCCCTTCTGGC
TTCTCTGGCCCCACGTGTCTGTGCTGTAGATACTGTATCAAAGTCCCAGCGTTTAGATGGTTAACATAGAGCTG
CTTCTGTGTAAATGCTGCTTATTTTAAACACTAAAAAGCGTTTAAATTTTATGGG

WO 2004/030615

PCT/US2003/028547

25/6881

FIGURE 25

MAETKIIYHMDEEETPYLVKLPVAPERVTLADFKNVLSNRPVHAYKFFFKSMDQDFGVVKEEIFDDNAKLPCFNG
RVVSWLVLAEGAHS DAGSQGTDSHTDLPPPLERTGGIGDSRPPSFHPNVASSRDGMDNETGTESMVSHRRERARR
RNREEAARTINGHPRGDRRRDVGLPPDSASTALSSELESSSFVDSDEDGSTSRLSSSTEQSTSSRLIRKHKRRRRK
QRLRQADRASSFSITDSTMSLNIVTVTLNMERHHFLGISIVGQSNDRGDGGIYIGSIMKGGAVAADGRIEPGDM
LLQVNDVNFENMSNDDAVRVLREIVSQTGPISLTVAKCWDPTPRSFTVPRADPVRPIDPAAWLSHTAALTGALP
RYELEEAPLTVKSDMSAVVRVMQLPDSGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARKYASSLL
KHGFLRHTV NKITFSEQCYVFGDLCSNLATLNLNSGSSGTS DQDTLAPLPHPAAPWPLGQGYPYQYPGPPPCFP
PAYQDPGFSYSGSGSTGSQQSEGSKSSGSTRSSRRAPGREKERRAAGAGSGSESDHTAPSGVGSSWRERPAGQLS
RGSSPRSQASATAPGLPPPHTTKAYTVVGGPPGPPVRELAAVPPELTGSRQSFQKAMGNPCEFFVDIM

WO 2004/030615

PCT/US2003/028547

26/6881
FIGURE 26

GCACCGCCCCCGCCGCAAGAAAGATGGCAGTGGCCTGATCCGGGCCCCTTGGCGGGCGTCACTGACGCTTCGCTC
CGGTCCCTCGGATCCCGAGCGCGGGGAGGCAGACCGACTGTGAGCTGCTTGTCCCATCCTGCGGGCGTCCTGGGG
ACACAGAGCCCTCCGTGGTGCCCGGGGATTGGATTGGAGCCAGGACCTCACTTCCTCCTCTGCCCTGCCCTGC
CCCTCCCAAGCACCTGGCCACACCCCTGCAGCCCGCCCCATGGCTTGGCCCTGGGTGGCGATGGCGTCCAGGTGGG
GTCCCTCATTGGCCTGGCTCCGTGCTGCCTCTGGCTCCTGGGGGAGTCCTTCTGATGGACGCGTCTGCACGGC
CTGCCAACCACCTCGTCCACTCGAGAGAGAGTAGCCAACAGGGAGGAGAATGAGATCCTGCCCCAGACCACCTGA
ACGGGGTGAAGCTGGAGATGGACGGGCACCTCAATCGCGGCTTCCACCAGGAGGTCTTCTAGGCAAGGACCTGG
GTGGCTTTGATGAGGACGCGGAGCCGCGGGAGCCGGAGGAAGCTGATGGTCATCTTTTCCAAGGTGGATGTGA
ACACTGACCGGAAGATCAGTGCCAAGGAGATGCAGCGCTGGATCATGGAGAAGACGGCCGAGCACTTCCAGGAGG
CCATGGAGGAGAGCAAGACACACTTCCGCGCCGTGGACCCTGACGGGGACGGTCACGTGTCTTGGGACGAGTATA
AGGTGAAGTTTTTGGCGAGTAAAGGCCATAGCGAGAAGGAGGTTGCCGACGCCATCAGGCTCAACGAGGAACCTCA
AAGTGGACGAGGAAACACAGGAAGTCCTGGAGAACCTGAAGGACCGCTGGTACCAGGCGGACAGCCCCCTGCAG
ACCTGCTGCTGACGGAGGAGGAGTTCCTGTCTCCTCCACCCCGAGCACAGCCGGGGAATGCTCAGGTTTATGG
TGAAGGAGATCGTCCGGGACCTGGACCAGGACGGTGACAAGCAGCTCTCTGTGCCCAGTTTCTCTCCCTGCCCCG
TGGGCACCGTGGAGAACCAGCAGGGCCAGGACATTGACGACAACCTGGGTGAAAGACAGAAAAAAGGAGTTTGAGG
AGCTCATTGACTCCAACCACGACGGCATCGTGACCGCCGAGGAGCTGGAGAGCTACATGGACCCCATGAACGAGT
ACAACGCGCTGAACGAGGCCAAGCAGATGATCGCCGTGCGCGACGAGAACCAGAACCACCTGGAGCCCGAGG
AGGTGCTCAAGTACAGCGAGTTCTTACGGGCAGCAAGCTGGTGGACTACGCGCGCAGCGTGCACGAGGAGTTTT
GAGCGCCCGGCCGCGCCCCGCGCCCCCACGCAACCACGGGGCGGCCTCGCGGGTGACTCCGGGCTCCGTGG
CTGTCCCGGACCCCACTCTTCCCTGCCGCCGCCACCGGCCGACCGACCGCGGCTGCCCCAGTTGATGAGCGGC
GTGTCCCTCTGCAGCGCGCACCCCGCGGGGCTTTGGCTGTGACGCGGTGCGGGCGCGGGGCTGGGCTGTGGCC
CCGCGGCGCCGCTCCTCCTGGTCCCTCGAAATCGTGGCATCTCACTTCTGAGAACGAAATCTCGCTTCAGTCA
CTCTGCCGAAGGCGCTGACGGCATCGCGGCCGGAACCTCTGGGCCCGGCCCTCCAGGGCGCGCTCCGTGGG
AAAAACAGCTCCTCCATTTCTTTGAAAACCTGAACGATTATTAATAATAGATTAACTTCGCTGGAAATGAGTAG
CCAGGAAGTTCAGGGGAGGGTGCCGGGTCTTCCCGGGCTGGCGTGTGCGAGCCACCCAGGTCCCGCAGCTGCC
GCTGAGAAAAATGCAAAATATTTGTTGTGACAAGAATCACATACATTTACTTTAAATATAGTTGCCTTTTTTGGTCA
GCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

27/6881
FIGURE 27

MVWPWVAMASRWGPLIGLAPCCLWLLGAVLLMDASARPANHSSTRERVANREENEILPPDHLNGVKLEMDGHLNR
GFHQEVFLGKDLGGFDEDAEPRRSRRKLMVIFSKVDVNTDRKISAKEMQRWIMEKTAEHFQEAMEESKTHFRAVD
PDGDGHVSWDEYKVKFLASKGHSEKEVADAIRLNEELKVDEETQEVLENLKDRWYQADSPPADLLLTEEEFLSFL
HPEHSRGMLRFMVKEIVRDLDQDGDKQLSVPEFISLPVGTVENQQGQDIDDNWVKDRKKEFEELIDSNHDGIVTA
EELESYMDPMNEYNALNEAKQMIAVADENQNHLEPEEVLKYSEFFTGSKLVDYARSVHEEF

WO 2004/030615

PCT/US2003/028547

28/6881
FIGURE 28

AAGGGGCCAAAAGGTCCACCTGATGAACCTGTTGCACGCGAAAAGTTCAGAACCACTGCTGCCAAGATGCTGACA
GAAGCCTTGAGAAGCACCTGCTGCGGGAAAAGACGTGCAGGCCTCACAGGTGCAGTGCGGTCTTCAGCGCGCTTG
AAAGCACGAAGTTGTTTCGGCAGCCAGGTTGGCCTCTGCCCAGGAAGTTGCTGGTTCCACGTCTGCCAAGACAGCA
TGTCTGACCCGGGCCCTGATCCTAGCACCCGCCCACCCGTGTACTTCCTCATCCCACAAAGCCACAGACACGCGA
ACGTCCAAGAAGTTCAAATGTGACAAAGGACATCTTGTGAAGTCAGAATTACAGAAGCTTGTCCCTAAGAATGAC
AGCGCTTCTTTGCCAAAAGTGACACCTGAGACCCCTTGTGAAAATGAGTTTGCTGAAGGCAGTGCCTTGCTTCCA
GGCAGCGAGGCTGGCGTTTCTGTGCAGCAGGGGGCTGCAAGTCTTCCTCTCGGTGGCTGCAGAGTTGTGAGTGAC
TCTCGCTTAGCAAAGACTAGAGATGGCCTGTCCGTGCCAAAACACAGTGCCGGGTCCGGAGCAGAAGAATCCAAC
AGCAGCTCCACTGTGCAGAAGCAGAATGAGCCAGGGCTACAGACAGAGGATGTGCAGAAGCCACCACTTCAGATG
GACAACAGCGTCTTTCTAGATGACGACAGCAATCAGCCAATGCCCGTGAGCCGGTTCTTTGGAAACGTTGAGCTC
ATGCAGGCCATAGAGAGGTCCGTGTGCAGCTGCCTGACGAGAACTGCATTCCCCAGCCCCAGCGGCGTCAGGGAG
CACCTCACCGTGTGTTCTCGCCCAGGGCAGTGGAGACAAGCCATTGGGAGTGCTCTCTCCATGGCCTCTTCCTGC
CGCCACCTGCACATAGAAGCTGAGTGGAACCAACCAGGAGCAAGCTGGGGTCCCCGGGTGA

WO 2004/030615

PCT/US2003/028547

29/6881
FIGURE 29

AGAGGCGAGAACGACCCCGGGACCGACCAAAGCCCGCGCGCCGCGCATCCCGCGTACAGCACCTACATCCCGCC
ACCGTCACCGCCACCACCATGCCCCAAGAGAAAGGCTGAAGGGGATGCTAAAGGAGGTAAAGCCAAGGTGAAGGAC
GAACCACAGAGAAGGTCTGCAAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCAAGCCTAAAAAGACC
CCTGCAAAGAAGGCAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCCCAGGAGGAGGGATTCCCTGAC
TTTGACACACATGGCCACCTTGGCACAAAAGCCTTGTGGTGTGGAAAAACAAATTTGTTTTATGTCCTCTTCTC
CCTTTCCATCTTTCAGCATAGACTTAACTCCTTTAATCCAGGCATCTGTTGGGACCTGACCCCTAGTCATTGGT
TACCAGTGTGTCAGGCAATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAAGAGCAGTGGTTCCA
TTTCTAGATTGTGGATCTTCAGATAAATTCTGCCATTTTCATTTCCTGAAAGTCAGAGTCGGCTTGTGAA
AAGTTGTTAAACAACATGCTAAATGTGAAATGTCAACCCTCACTCTAACTTTCCCTGTTTCAGAGCATGAGATGA
AGACTTCTTTGGGTTTTATAGCGGCTTTCTGATTTTTTCGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTA
TACTGTTAACAATTGTCTGCCCATGTCCTGCCTGAAATACCA

WO 2004/030615

PCT/US2003/028547

30/6881
FIGURE 30

MPKRKAEGDAKGGKAKVKDEPQRRSARLSAKPAPPKPEPKPKKTPAKKAEEKVPKGKKGKADVDTHGHLGTKALWC
GKTNLF₁LCPLLPFHLSA

WO 2004/030615

PCT/US2003/028547

31/6881
FIGURE 31

TAGCTAGGCAGGAAGTCGGCGCGGGCGGCGGGACAGTATCTGTGGGTACCCGGAGCACGGAGATCTCGCCGGCT
TTACGTTACCTCGGTGTCTGCAGCACCTCCGCTTCCTCTCCTAGGCGACGAGACCCAGTGGCTAGAAAGTTCAC
CATGTCTATTCTCAAGATCCATGCCAGGGAGATCTTTGACTCTCGCGGGAATCCCACTGTTGAGGTTGATCTCTT
CACCTCAAAAGGTCTCTTCAGAGCTGCTGTGCCAGTGGTGCTTCAACTGGTATCTATGAGGCCCTAGAGCTCCG
GGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGGCTGTTGAGCACATCAATAAAACTATTGCGCC
TGCCCTGGTTAGCAAGAACTGAACGTCACAGAACAAGAGAAGATTGACAACTGATGATCGAGATGGATGGAAC
AGAAAATAAACTAAGTTTGGTGCGAACGCCATTCTGGGGGTGTCCCTTGCCGTCTGCAAAGCTGGTGCCGTTGA
GAAGGGGGTCCCCCTGTACCGCCACATCGCTGACTTGGCTGGCAACTCTGAAGTCATCCTGCCAGTCCCGGCGTT
CAATGTCATCAATGGCGGTTCTCATGCTGGCAACAAGCTGGCCATGCAGGAGTTCATGATCCTCCCAGTCCGTGC
AGCAAACCTTCAGGGAAGCCATGCGCATTGGAGCAGAGGTTTACCACAACCTGAAGAATGTCATCAAGGAGAAATA
TGGGAAAGATGCCACCAATGTGGGGGATGAAGGCGGGTTTGCTCCCAACATCCTGGAGAATAAAGAAGGCCTGGA
GCTGCTGAAGACTGCTATTGGGAAAGCTGGCTACACTGATAAGGTGGTTCATCGGCATGGACGTAGCGGCCTCCGA
GTTCTTCAGGTCGGAAGTATGACCTGGACTTCAAGTCTCCCGATGACCCAGCAGGTACATCTCGCCTGACCA
GCTGGCTGACCTGTACAAGTCCTTCATCAAGGACTACCCAGTGGTGTCTATCGAAGATCCCTTTGACCAGGATGA
CTGGGGAGCTTGGCAGAAGTTCACAGCCAGTGCAGGAATCCAGGTAGTGGGGGATGATCTCACAGTGACCAACCC
AAAGAGGATCGCCAAGGCCGTGAACGAGAAGTCCTGCAACTGCCTCCTGCTCAAAGTCAACCAGATTGGCTCCGT
GACCGAGTCTCTTCAGGCGTGCAAGCTGGCCCAGGCCAATGGTTGGGGCGTCATGGTGTCTCATCGTTCCGGGGGA
GACTGAAGATACCTTCATCGCTGACCTGGTTGTGGGGCTGTGCACTGGGCAGATCAAGACTGGTGCCCTTGCCG
ATCTGAGCGCTTGGCCAAGTACAACCAGCTCCTCAGAATTGAAGAGGAGCTGGGCAGCAAGGCTAAGTTTGCCGG
CAGGAACCTCAGAAACCCCTTGCCAAG**TAA**GCTGTGGGCAGGCAAGCCCTTCGGTCACCTGTTGGCTACACAGA
CCCCTCCCCTCGTGTGAGCTCAGGCAGCTCGAGGCCCCGACCAACACTTGCAGGGGTCCCTGCTAGTTAGCGCC
CCACCGCCGTGGAGTTCGTACCGCTTCCTTAGAAGTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAGCT
CTAGCTTTGCAGTCGTGTAATTGGCCCAAGTCATTGTTTTCTCGCCTCACTTCCACCAAGTGTCTAGAGTCAT
GTGAGCCTCGTGTCTATCTCCGGGGTGGCCACAGGCTAGATCCCCGGTGGTTTTGTGCTCAAATAAAAAGCCTCA
GTGACCCATGAG

WO 2004/030615

PCT/US2003/028547

32/6881
FIGURE 32

MSILKIHAREIFDSRGNPTVEVDLFTSKGLFRAAVPSGASTGIYEALERDNDKTRYMGKGVSKAVEHINKTIAP
ALVSKKLVTEQEKIDKLMIEMDGTENKSKFGANAILGVSLAVCKAGAVEKGVPLYRHIADLAGNSEVILPVPF
NVIINGGSHAGNKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIEKEYGKDATNVGDEGGFAPNILENKEGLE
LLKTAIGKAGYTDKVVIGMDVAASEFFRSGKYDLDFKSPDDPSRYISPDQLADLYKSFIDYPVVSIEDPFDQDD
WGAWQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLAQANGWGMVSHRSGE
TEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEEELGSKAKFAGRNFRNPLAK

WO 2004/030615

PCT/US2003/028547

33/6881
FIGURE 33

TGGTCCCAAGGCGCGTGCTTTGCAGCAGATGTGTGACCTGGCGTTCCCCTGAGTGCTCGGAAAATGGCCTTGTCT
CCGGTCGTTCCCGTTTCAGGAGCAGAATTTTCCCACTGTAAAAAACCGAGCAAGTCTGGATAAGTGAGGCTGGCTC
CATGTATCCAGAATCAACGACGGGCTCCCCGGCTCGGCTCTCGCTGCGGCAGACGGGCTCCCCGGGATGATCTA
CAGTACTCGGTATGGGAGTCCCAAAAAGACAGCTCCAGTTTTACAGGAACCTGGGCAAGTCTGGCCTGCGGGTCTC
CTGCCTGGGACTTGGAAACATGGGTGACCTTCGGAGGCCAGATCACCGATGAGATGGCAGAGCTCATGACCTT
GGCCTATGATAATGGCATCAACCTCTTCGATACAGCAGAAGTCTACGCAGCCGGCAAGGCTGAAGTGGTACTGGG
AAACATCATTAGAAGAAAGGATGGAGGCGGTCCAGCCTCGTCATCACCAAGATCTTCTGGGGCGGAAAGGC
GGAGACGGAGCGGGGCTGTCCAGGAAGCACATAATCGAAGGTCTGAAAGCTTCCCTGGAGCGACTGCAGCTGGA
GTACGTGGATGTGGTGTTCGCAACCGCCCGGACCCCAACACCCCGATGGAAGAGACCGTCCGCGCCATGACCCA
CGTCATCAACCAGGGGATGGCCATGTACTGGGGCACGTACGCTGGAGCTCCATGGAGATCATGGAGGCTACTC
CGTGGCCCGGACAGTTCAACCTGACCCCGCCCATCTGCGAGCAGGCTGAGTACCACATGTTCCAGCGTGAGAAAGT
GGAGGTGCAGCTGCCGGAGCTGTTCCACAAGATAGGAGTGGGCGCCATGACCTGGTCCCTCTGGCCTGTGGCAT
TGTTTCTGGCAAGTACGACAGTGGCATCCCACCCTACTCAAGAGCCTCCTTGAAGGGCTACCAGTGGCTGAAGGA
CAAGATCCTCAGTGAGGAGGGCGGGCGCCAGCAAGCCAAGCTGAAGGAGCTGCAGGCCATCGCCGAGCGCCTGGG
CTGCACCTTGCCCCAGCTGGCCATAGCCTGGTGCCTGAGGAATGAGGGAGTCAGCTCCGTGCTCCTGGGGGCTC
CAATGCGGACCAGCTCATGGAGAACATTGGGGCAATACAGGTCTTCCGAAACTGTCTATCTTCCATTATCCACGA
GATTGATAGTATTTTGGGCAATAAACCTACAGCAAAAAGGACTACAGATCCTAAGCCGCCCCCGCCCGCTGCT
CGGACAGTTTCCGTTCCTCTCTAGTCTCTGTTCGCTCGCTTAAGCTGTTTGAAGCCAAGTGAAGAGTGTGGTTT
GCATCCAAGAGAAAACACCACACTGTGATGTCTCGGAAATGATCTCCCAAGTCGCTGCCAGACACCACCACT
GCTTCGCCGGACAATGTCTGAAGTCCAGTCTGTGCCGGGAAGGCACCTGTTTCTCCAGCCACAGCCAAGATTCCCAAAGTC
CCCAAGCCTGTACCTCTGCTCATCTTCAAGACCACCCAGCTTTCTCCAGCCACAGCCAAGATTCCCAAAGTC
AAGGCCCAAAGATTTCCAAGGTTCCCAAAGTCAAGGCCAGGCCAAGGCCTGGTTGGGTCTTGGGGCGGGCAGGG
CCAGCCTCTCCTCTGCTGAGAATCCCCACTTGGTGTAGGGGGAGAGGGGAAAGGGGTCTGGCCCATCGAGGGGCC
CCTTCTGCCAGGGCCTTGGTTGCTGGGGCAGGGCCTCCCCACTGGGGGTCTTCTCCACCTCCCCTTTCCAAGG
GCTCCAGGAATCTGGGGCCTGACCACAGATTCTCTCCCATCCTTTTCTGCTCCAACCTGCCCCACTGGGTCCCCG
GCAGGGGCCATGCCTACCAAGCTCGAGCTGGCCCTTGACCCCAACCCACCCCTTGCTGGCAGGGGCAGGG
ACCCAGGGGGATTGACTCTGCAAGTTTGGGAGCCACAAAAGCGTAGCGGTGTGATTTCTAGCTCAGCCTCCAC
CGTCTTCTCTACACACCAATGATGAGCCTCATGCCAGTGAGGCCCGGAGCGCTTGGGAGGGGTCCCAGTGGGG
CAGGCCCTCTGTCTGGCCACCCCTCTGTCTGGCCCCGGAAGGCCCTGTGGTCATGTGCTCCTAGCTGCACGGT
GGCTGCTGGCCACACCACGGCAAGTGGCAGCAGGGGCCGGCCCTGTGCACAAGGATGCACTCCTCTCGGCCCTG
TAGACTTTCTCTAAAGCCGCCCGCCAGCCAGGCCGCTGCTCTGCACCGAGCTGGTGGGCTTGGGTTTGTGGAG
CGCATGCTTGGACCCTTTCAGTAAGGAAGGGTCTTGGGGTTTTCTGTGCCCATGACTTGGGGGCTGCACCCCA
CAGCACCCCAACAATGTAGGAAAAGACCTCAGGGAACCTCTCCCTGGAAAGACGGGCAGGGCTGGTTAGCCCTC
CCACTGCCTGACACCTGGGACAGGCTGGGCAGAGGGGAGAGAGGGCAGGACAGGCCAGAGTGACGCCCCCGTGCA
GCTTGGGCCGGAGGGCAAGGGATGCCAGTAAGTCTGCAGGTGCGGGGTGCCACCTACAGGCCAGGCCCTGTGTCC
CAAGCAGTACCCAGGCTTTGACAGACCACGCGGGGACGGGCTCCACTGAAGCCACCCCAACCCCTCGCCAGCTAGC
TCCATAGGGAAGCCTGTGTCTCCTGCCCCAGGGCGCACCTCAGTGCAGGCACCTCTGTTCCTGCTTGGCCCT
GGAGGAGCCACTATTCCAGAAGGCTCCACCCTGCCGTCTGCGGGAGCCTGCTGTCCAGTCTTGGCCGGGCCAAG
GCCTGGGAAACTGTGAAAGTCAGAAAGGCCAGCGGGGAGAGGCTGGGGCGAGGGGAGGAGGGGGATCAGCTTCTG
CTATTACCGACCCCTTTCATGCTGCCCCGCGCCTAGAACCCTTGCCCTCCTCATAGACCAAGTCCCGGGGG
TCTCCACTCAGTCTGCTGCTGCTTACCAGAAGCAGCCCTGTGAGTGTGGGGTGGGGAAGTCCCTTCCCAACG
GAGGTCCAGCCTATGGCCCTGGGCCCAGGTGGGGTGCCTGCTTCTTCCCGACAGGCTCTGCA

WO 2004/030615

PCT/US2003/028547

34/6881
FIGURE 34

CCTTTCTAACTCCGCTGCCGCCATGGCTCCTGTGAAAAAGCTTGTGGTGAAGGGGGGCAAAAAAGAAGCAAGT
TCTGAAGTTCACCTCTTGATTGCACCCACCCTGTAGAAGATGGAATCATGGATGCTGCCAATTTGAGCAGTTTTT
GCAAGAAAGGATCAAAGTGAACGGAAAAGCTGGGAACCTTGGTGGAGGGGTGGTGACCATCGAAAGGAGCAAGAG
CAAGATCACCGTGACATCCGAGGTGCCTTTCTCCAAAAGGTATTTGAAATATCTCACCAAAAAATATTTGAAGAA
GAATAATCTACGTGACTGGTTGCGCGTAGTTGCTAACAGCAAAGAGAGTTACGAATTACGTTACTTCCAGATTAA
CCAGGACGAAGAAGAGGAGGAAGACGAGGATTAAATTTTCAATTTATCTGGAAAATTTGTATGAGTTCTTGAATAA
AACTTGGGAACCAAAATGGTGGTTTATCCTTGTATCTCTGCAGTGTGGATTGAACAGAAAATTGGAATCATAGT
CAAAGGGCTTCCCTTGGTTCGCCACTCATTTATTTGTAACCTTGACTTCT

WO 2004/030615

PCT/US2003/028547

35/6881
FIGURE 35

MAPVKKLVVKGKKKKQVLKFTLDCTHPVEDGIMDAANFEQFLQERIKVNGKAGNLGGGVVTIERSKSKITVTSE
VPFSKRYLKYLTKKYLKKNNLRDWLRVVANSKESYELRYFQINQDEEEEEDED

WO 2004/030615

PCT/US2003/028547

36/6881
FIGURE 36A

CGCGCTCGCGGGGGGCGGTGGCGCCCGGCACAGAGGGGTTAAGGGGGCGGTGCAGACGTCTCCCCGCCCATCCCCG
CCCCCTCGAGAGCCGCGGGCGCCCCGCCCTATTTATAGCAGCGGTGCCTAGCGCGCCGCGTCTCTCCGCAGGCCCG
GCCGCGGCGTCTCGACAACCTATCGAAGGCGCCATGGAGCGACCGGGCGCCCTGGCCGTGCTTCCCTTCTCGGA
CCCCGCGCACGCCCTGAGCCTGCTGCGCGGCCTGAGCCAGCTGCGCGCCGAGCGCAAGTTCTTGACGTGACCCCT
GGAGGCGGGCGGGCGGGCGGACTTCCGGGCGCACCGTGCCTGCTGGCCGCCGCCAGCCCTACTTCCGCGCCAT
GTTGCGGGGGCAGCTGCGCGAGAGCCGCGCCGAGCGGGTGCCTGCACGGAGTGCCTCCCGACATGCTGCAGCT
GCTGCTGGACTTCAGCTACACGGGCCGCGTGGCGGTAAGCGGCACAACGCTGAGCCGCTGCTGCGCGCCGCCGA
CCTGCTGCAGTTCCCGGCCGCTGAAGGAGGCGTGCGGGGCCTTCTGTCAGCAGCAGCTCGACCTGGCCAAC TGCCCT
GGACATGCAGGACTTCGCTGAGGCCTTCAGCTGCTCGGGACTGGCGAGCGCGGCGCAGCGGTTCAITCTGCGCCA
CGTGGGCGAGCTGGGCGCCGAGCAGCTGGAGCGGCTGCCACTGGCGCGCCTGCTGCGCTACCTGCGGGACGACGG
GCTGTGTGTGCCCAAGGAGGAGGCCGCTACCAGCTGGCGCTGCGCTGGGTCCGCGCTGACCCGCCGCGCCGCGC
CGCGCACTGGCCGAGCTGCTGGAGGCCGCTGCGCCTGCCCTTCGTGCGCCGCTTCTACCTGTTGGCGCACGTCGA
GGCCGAGCCGCTGGTGGCGCGCTGCCACCCTGCCTGCGCCTGCTGCGCGAGGCGCGCGACTTCCAGGCGGCGCG
CTACGACCGCCACGACCGCGGGGCCCTGTCCCCGAATGCGTCTCGCCCGTCCACCGGTCTCGCCGAGATCCTCGT
GCTCGTGGGCGGCTGCGACCGAGCTGTGACGAGCTGGTCACTGTCGACTGCTACAACCCGAGACGGGTCACTG
GCGCTACCTGGCCGAGTTCCAGACCACCTGGGCGGAGGCTACAGCATCGTGGCGCTGGGCAATGACATCTACGT
GACGGGTGGGTCCGATGGCTCCCGGCTCTATGACTGCGTGTGGAGGTACAACCTCAAGCGTGAATGAGTGGGCGGA
GGTGGCGCCCATGCTGAAGGCCCGCGAGTACCACAGCTCCTCTGTGCTGGACGGACTGCTGTACGTGGTGGCCGC
CGACAGCACCGAGCGCTATGACCACACCCTGACTCCTGGGAGGCCCTGCAGCCCATGACCTACCCCATGGACAA
CTGCTCCACCCTGCGTGGCGTGGCCGGCTCTATGCCATCGGCTCCCTGGCTGGCAAGGAGACCATGGTGATGCA
GTGCTACGACCCGGACACCGACCTGTGGTTCGCTGGTGGACTGCGGCCAGCTCCCGCCCTGGTCCCTTCGCCCCAA
GACTGCGACTCTAAACGGACTCATGTACTTTGTGAGGGATGACTCCGCTGAGGTGGACGTGTACAACCCGAGCAG
GAACGAATGGGACAAGATCCCGTCCATGAATCAGGTAAATTTTCAGGCGGGCCAGCATTGGAAGCACAGGCTGGT
CCTGATTTTGAACCCAAGTGTATCGTATGAGTGTGGGATCCACAGCCATGATGGATGGGTCTCATCTCAA
TTAATAGAAGGCTGCTCTTACCCTTATTTTGCACCTAAGGCTCACTGAGACACAGATGTTAAGTAATACCCTATG
ATTACACAGCTTAGTACACATTTGAGCAGTGTATTAGTATCTGCTGTGAGCCAGAGAGCAGAAGGAAGTGAG
GGAGCAAGGCATACAGTCATCTGGGGACACCTGTTCCAGAGAGGGACAGCAGGTACAGAGGCCCTGCAGCAGGGC
ACCCTGGCGTGTCTTAGATACACAGCAGCCCATGTGGCCGGAGCAGAGTCAGCATGAGGTCTGTGACCTACCT
TTTTTATTTTGTAGACAGGGTCTTGCTCTGTCAACCCAGGCTGGAGTGCAGTGGTACAATCATGGCTCACTGCAGC
CTCCACCTCCTTGACTCGCAGTCCCTCCACCGCACCTTCTGAATAGCTGAGACTACAGGCGTGTGCCACCACAC
CCAGTAATTTTTTTCTCATATGTAGATACAAAAGGATATTCTTAAATTTTTATAGAGACAGGGTCTTGCTGTG
TTACCCAGGCTGGTCTCACACTCCTGGCCTCAAGTGACCTCCTGTCTCAGCCTCCCAAAGTGCTAGGATTATAG
GCGTGAACCACCACGCCAGCTGGTTCCTGAGGAAGTCAGTGTGGGAATACTTTTTTTTTTTTATACGGAGTCT
CGCTCTGTCAACCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAAGCTCCATCTCCAGGTTTACGCCA
TTCTCCGGCCTCAACCTCCCGAGTAGCTGGGACTACAGGTACCCACCACACGCCAGCTAATTTTGTGTTGTGTA
TTTTTAGTAGAGACGGGATTTCACTGTGTTAGCCAGGATGGTCTGGATCTCTGACCTTGTGATCTGCCTGGCTC
AGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCATGCCAGCCCACTGTGGGAATACTTGTGTTGAGCAC
TTGCTGTGTGTTCTGAATAGGACAACCAGGGTCCACCCCTTCTCTCTGGGCTTGTGAGAAGAGGGGTGCCCAGC
CTGACAGTGATGGGACAGGGAGGCTTCAGTGCCATTTGGCCATGTGAGCAGTGTTAGTCTGAGGTACACATCATA
TTGCCATACAGCCTTCTTTCCTGTGTGCTGTTAACATTTCCAAACCTACACTCCGTGACATCCAGCCTCACAGCT
TACATCACAGCTTAATGTCTGGCATTAAAGAGACCCAGCGTTCTGTTTTCCCCGAGTAAGCTGCACATAGTCA
TAGCGAATTTGGGAAAGATGGAAGGAATCATCCAGCCTCGCGGTTTCAGAGCCAGCTCTGCCACTGTGAGCCATG
CAAGCCTCAGTTTTCCCATCTGTAACATGGGGAGAACAGCACTGCTCAGCCCAGAGGGCCACTGCAGAGATTCTG
AGAGAGAACGTAGGAAGCGCTGCTCGGCACGACCTGCACACGGGGAGGCGCTGGCGCTGCAGCGGGCACCCCTCATC
ACCATAGGGAAGGCCAGCTGCCTCCGGGGAGGCCCGTTCTCCTAGGCAGGGTGTGGAAAGGGGTGGCCTCTC
TGCTGCTTTCTGGGAGAGCCAAGGCCACCCCTCTGGGGTACTGACAGGGCATGCCTTGTCTCCAGTGGTTCCCCA
GGTGGGGCCCTGCCCTACCCCTCTCTGACCTCCACTCACTCATCCCTTTGGCCACAGGTACATGTGGGGGGC
AGCCTGGCCGCTCTTGGGGGAAGCTGTACGTCTCTGGGGGATACGACAATACATTTGAACTCTCGGACGTGGTA

WO 2004/030615

PCT/US2003/028547

37/6881
FIGURE 36B

GAGGCCTATGACCCAGAGACTCGCGCGTGGAGCGTGGTGGGGCGGGCTCCCAGAACCCACCTTCTGGCATGGCAGT
GTCAGCATCTTCCGCCAGTTTCATGCCCCAGACCTTCTCGGGTGGGCGTGGCTTCGAGTTGGACAGTGGCAGCGAT
GACATGGACCCAGGCCGACCCCGGCCGCGCGGGACCCCGATGAGCTGCACTAGCCCCAGTCTGGCCCCGGCACGG
GCCTCGGTGTCAGGTAACCTGGCACCTCTGCGGGGCGAGTGGCCCACTCCTTTGTGCACAAGGACACGTGGGGCTCAC
AGGAGGAGCACAGGCTCTTGGGTGGCGAAGCCAGCCAGGATCCATTACCTGGAAGGTTTCTGTACCTTGAGAGC
CTGAATCAGAGGCCGTCGGGAACGCCCTCCCTGCAGTTGAGGAAGAGCCACTTTCCTGCCAGCACATGTTTCTGG
GTCTTGGAGGTACCCCCACCCCGCGGATCACAGCTCACCCACGCGGCGCACACCCCTCCTGCCGTTGTCATCTG
CACCTACTTGTTCACCTTGGGAGAGGACGATGACTTGGGAGGGACGCGTGAAGGGAGAAGGGGTCTCCCATG
AGGCTGAGGATGGCCTGAACCTGGAGCAGCGGACCAGGCAGACGGGCTGAAGTGGGGTCCCAAATTCCATGTCCA
GAGGTGTGGGGAGCCTGCCTCCCTAGCTCCTGGCCCCCTGCCAGGGGCTTACATCAAAACACCTCAGAGGGCTGCC
CTCCAGAGGCTGCACCCAGAACAGTGGGACATGAGCAGGGGTGTGGGCTTGGAGGGTGAAGAGGATGTGGTCTTA
TCAGATGCTGGGCCTCCTCAGCCATAGCCCCCTGCTCCTACCCCTGACTGGCTCTTGCGTCTCACCTCTCACC
CTCTCCTTCCCGGGAGGCCCTGGGAGGTGATCATTGACACCCAGCCAAGCAGACAGCTGCGGGTGGCCAGGCCCT
TGCTGGGCCTGCGCGTGAGGAGTCCCACTGCTTCTAAAGGAAGTCTGGGCAGGAGGTGGCTTTGGTGGTTGGTT
CCAAAGTTGAAATGCTTGACGTTTGACCTTAGAAGAAGTGGGAAGAAGAAGGAGCTCTACAGGGTCAGCTTTGT
TTGATTTGTCCAGTCTAAGAAGTCCCATTTGCCAAAGCTTCTGCAGGAGGGTGAATGCCGAGCTTGGCAGCCCC
TGGGTTTCTCTTGGAAATGGTCAGTTTCCCTCAAAGTACCCAAAGTAGCCTTGGCTTGAGTTTTTGTCTTGCC
TCCTTTTTAGAGAAGAGGGCATTTAGACTGCATTTTCTGGTTAAAGAAGGTTAAAGCAAATGTTTATTGCCTTT
TCTAGTGAATAACTCGTAGAGATGTTCTCAGCAGGAAGACAGTCTTAGCACTGTCACTTAGCAGATTGCACCTTA
AGTCCCTTGTGCTGGCCAGATGGCGTGGCTGGTTGCCTTAATATGTCCCAGGACCCCTGACAGGGCTGCCTGGCC
TCTCCCTCGTGCTCCTCAAGAGCCCAGTCCATACACTGTGGATGTCTGCTGTGCGGTTAGGAAGTCTTGTCTT
AGAACGCCCTGGCTGGTATGACCACAGTTTCATGGCGGCTCTTCTCGCTTGGGTGATGGTTCATCTTCCAGCACCTG
CTGTGCTGGGAAGGCCGAGGATGGGGGCCCCAGCACTGTCCAGGCTGCTGGGGCCTGGCTGGGAGTCTGTGGGC
AGCATGGAACATGCAGCTGGGCTTCTGTGACCAAGCACCCTCTGGCACTGTTGCTTGGCCTGTGCCCTGGACCT
TTTCTGCCCCTTCTCCTTCTCTGCTCCCTTGGGGCTACCCCTTGGCCCCCTCCTGGTCTGTGCAAACCTCCCTCAG
GGAGCCCCCTGCCCTGTAGCTCTCGCTTAACCTTCTAGGGGCTGCTGAGCCACCCAGAGGTTGTTGGAGTTCA
GCGGGGCAGCTTGTCTCCCTTGTGACAGGGGCGTAAGGGCTGGGTTTGGCCATACAAGGTTGGCTACGCCCTCA
ATCCCTGACCGTTCCAGGCACTGAGCTGGGCACCCACGGAAGGACATGCTGTCCAGACTGTGATGACTGCCAGCA
CAGGGCATCTCGGGCTTGGCTGGTCTGCGAGGCCTTGGCCCTGTGGAACCTCTGGGTTCTGTTTTCTCAGTCTTT
TTTGGGCTTTGCTGTGGTTGGCAGCTGCCGTAAGGCTTGTGTCGGCCACTCAGATGAGGGCTGTGGTGGC
AGCCAGTGACAGGAGAGCTGCGCTTGGGATTGTGCCCTCTCCTGTGTCTGTCTCCGGACCTACCCAGGTCTCCAC
CATCAGGACCTGTCTTTGGGTTTAGAAGACCAAGTATGGGGAAAACCAGGCACCAGCCTCTGCAGCAATGGGTC
CCTCTAGCCTGTGGACACCAGCTGGGGGATCCAGGGTCAGGCCCCCTCCTCTCCCCAGTTTCCCTCTGCTGTGGG
TTCTGGGCTGTGATGTCTCCACCACTTAAGGATGTCTTTACACTGACTTCAGGATAGATGTTGGGATGCCTGGGC
ATGGCCACATGTTACATGTACAGAACTTTGTCTACAGCACAAATTAAGTTATATAAACACAGTGAAGTATTTA
ATGCTGATCTACTATAAGGTATTCTATATTTATATGACTTCAGAGACGCGTATGTAATAAAGGACGCCCTCCCTC
CAGTGTCCACATCCAGTTACCCCGAGGGTCGGGCAGGTTGACATATTTATTTTTGTCTATTCTGTAGGCTTCC
ATGTCCAGAATCCTGCTTAAGGTTTTAGGGTACCTTCAGTACTTTTTGCAATAAAAGTATTTCTATCCATTGG

WO 2004/030615

PCT/US2003/028547

38/6881
FIGURE 37

MERPAPLAVLPFSDPAHALSLLRGLSQLRAERKFLDVTLEAAGGRDFPAHRAVLAAASPYFRAMFAGQLRESRAE
RVRLHGVPPDMLQQLLLDFSYTGRVAVSGDNAEP LLRAADLLQFPAVKEACGAFLQQQLDLANCLDMQDFAEAFSC
SGLASAAQRFILRHVGELGAEQLERLPLARLLRYLRDDGLCVPKEEAAYQLALRWVRADPPRRAHWPQLLEAVR
LPFVRRFYLLAHVEAEPLVARCPPCLRLLREARDFQAARYDRHDRGPCPRMRPRPSTGLAEILVLVGGCDQDCDE
LVTVDCYNPQTGWRYLAEFPDHLGGGYSIVALGNDIYVTGGSDGSRLYDCVWRYNSSVNEWAEVAPMLKAREYH
SSSVLDGLLYVVAADSTERYDHTTDSWEALQPMTYPM DNCSTTACRGRLYAIGSLAGKETMVMQCYDPDIDLWSL
VDCGQLPPWSFAPKTATLNGLMYFVRDDSAEVDVYNPTRNEWDKIPSMNQVNFQAGQHWKHLVLILQPKCHRDE
CLGSTAMMDGSHLN

PCT/US2003/028547

CCCGCGGCCGAGCCGGCGCGGGCCCCCGACCTCCCCCGCTCGCGGGCCTCGAGTCCAGAAGACCCGCCCTCCAC
ACACCGGGGCCGCCGCCGCGGAGCCTCATGGGGGTGGAGTCCCCAAGGTTTCCTTTGTGCGCAGTATTGGCGGG
GCCTTGGACTACCACTCCACAAGGCACCGCGCCGCTCCCCGCGCCACGCCCCCTCGCCGCTGGCTTCCAGTCG
CCACCCAGACTACATTTCCCAGACAGGCCTCCCGGCTCTCCCGCCCTCCCTCCCGAGACACGAGCCGAACCTGGGCG
TCAGGTTCGGGGAGCCGGTTCGGGTTCGCCGCTACCGCGCGCCGCCGCCGCCCTCGCAGCCACTCTCCCGCCTCTAC
CGCCGCGGGAGCTGCATCGTCCACTCCGGTTCGGCGGTGGAACCGCCAGTCCGGGGTTCACAGAGCTTGAGAAGCGA
CGCGCTGAGCCCCCATACCTCCAGCCCCGGCGACCCCTCCCGGGTCCGCCCTCGCCCTGCGCAGCCGCCCGAG
CCCCAGCCCCGGAGCGCCCCGCTCCAGCATCCAGCTCCTGCACTCTCGCAGCCGCCGCCGCCGCCCGCCCGGA
ACATGAGCTCTGACTCTTGCGCGCGCCGCTTCCACCCGGAGGAATACTCCCCAGTTGCAAGAGGCGCAGGACCC
TGGAAGACTTCAACAAATTTCTGCACCTTTGTCTTGCCCTATGCTGGCTACATCCCTTATCCGAAGGAGGAACCTCC
CTTTAAGGAGCAGCCCCAGCCCTGCTAACAGCACTGCTGGTACCATTGACAGCGACGGCTGGGACGCGGGTTTCT
CAGACATCGCGTCCCTCAGTGCCCTTGCCAGTCTCTGACCGCTGCTTTAGCCACCTGCAGCCTACTCTCTTGACG
GAGCCAAGCCAGTAACCTTCTGCTGGACAGAAAGAAAACGGACAAGCTGAAGAAGAAGAAGAAGAGGAAGCGCA
GGGACAGTGATGCGCCTGGGAAAGAGGGGTACAGGGGGGGCTTGCTGAAGCTGGAAGCCGCTGACCCCTACGTGG
AGACCCCCACGAGTCCCACCTTGCAAGGATATCCCCAGGCTCCCAGCGACCCCTGCTCGGGCTGGGACTCCGATA
CTCCCTCGAGTGGAATCTTGCGCCACTGTGTACCTGATCAGGTCAAAGAAATAAAAAGCTGAAGGCAAAACGGACTA
TCGTCCGGCAGGGAAAGCAGGTGGTGTTCGAGATGAGGACAGCACTGGCAATGATGAGGACATCATGGTGGACT
CAGATGACGATTCTGGGACCTCGTGACCTGCTTCTGCATGAAGCCATTTGCCGGCCGCCCATGATCGAGTGTA
ATGAGTGCCACACCTGGATTACCTGTCTGTGCGAAAATCCGGAAATCCAATGTTCCAGAAAGTGTGTTGTCTGCC
AAAAGTGCCGGGACTCCAAGTTTGACATCCGCCGTTCACACCGCTCGCGGACGGGCTCCCGGAAGCTGTTCTCTGG
ACTGACTGCTGGCTGGCGAGGAGGCTGCGAGCGTGGAATCGGAAGCGACCGCGGGCTTTTTTGCCCTTCTCTTAG
TTGAGCACAGAACCTCAGCTCTGGTGCGGGCAGATCCCTGCCATTTAGGTGCCTAAGCAAAAGGACAGGCTGTC
CAAGGTAGAAACTGTACATAGCCGGTGACCGAATGCGACCTTTGCCAGCCAGAGCTGCTGCCAGAGCTGCGTTCC
CTGCAGTGGAGGTGGACTGGACACCCACGTGCAGCGGGTTTGGCTCATTGAAAATGAGGGTCCGTGGTAGCTGT
GCGTTTTGCTATCATTGCTAAGAGATTCCCGCTGATTGGGCTCAGTGCCAGCTGTTATTCTGCTTCCACTGTGT
GGGGAGAGGTGTTTCGGTTTTCCCAGCCTGTTAATGAACAGCCATACGTGTAAGCTTTTTCTTGAGTGTTAAGTCT
TTTACCAAAAGTGTCTGTACAGCAGCCATCCAAGTTGCCCTTACTTAGTGGCTTGCCCTCTGCCTGCCCTCAGCTG
CTGCCTGACCGGCTGGGGGAGGCACCTGGCGGGAGGCCTCGGGCTCCCCTGGAAGGGCGCTGGGCTGGCGGGTCA
CTGGTGGTTCTTAGGTTTCTTCTGTTTGTAAAAGGGACAATGTGGCCACTTCTCTGTGGAAGGGAGTTGGTT
GGGGGGTTGAGATGGCCCGTGTTCATAACTCAGTTTCTGTTTTTGACAGATGTAAAACCCCTGTCTTTTGCACG
ATACAGCCAAAAGTATTGGCTGATTCTTGCTGAGTGCCCTCTTAGTTGGTGTGTGAGGTCTTGGTGGGCTCAGG
CCAGCTGTTTGCGAGTGTGGGAACTCATAGGTTCTGTCTTTGTCTCTTCCCTTACCTCATTCTGGTAGCAGCAT
AAAGGTTAGGCAATCACTGGGACCCGCATGGTGTTCCTCCAAAGAATAGGGTAAAGGAGAGCTGGGAGGGAGCCC
TCTCCGTTGGGTGACTCTTGTTGTGCCCTTTAGACAGGCTGGCTGCCGGTTCACAGGGTACAGTTAGGACTTGA
GTCTTTCTTTTTCTGTTTTGAGTTGGTGAGTGAGTGATAGGGTAACATGGGCCTTCAGGATGACCCCTTGAACCT
GTGCCGAGTTCCCTTAAATCTCAGCTGGGATCCTGGACCTGGGAGGCCCTGTGAGGGCCAGCTCTGGA AAAACCT
GGGAGTTGATGCCGGAGGCTGTGGAAGAACTCTGCTCGAGGGCAGGGTGCCCTGGAACACTGGTAGTTCTGGGGC
TGGGAGGGAGAGGGGCTCCGGCTTCTCTGAAATGAACACTGCTCTCAGCAGTTCAAGTACTTGTCTCAAAAC
ATTTTCTAATTGATTGGTAGGTTTTCATAGCATTGTTTCTTTAAGGCATGGAAGGGAAGAATGCTCAAGCAAG
TCATGTTTGTTTTCAGTGGGATGGGCGCGCTTCTACTGCTGGGGGCTTCCCCTTCATGTGGCACCTTTGTGCC
AGGCCACCAGGCAGACTCTTCCCACCTTCTCCCAGTGAAGCAGCAAGGGGCTTGAACCGTAATTTGGCTAATCAG
AGGCATTTTTTTGTCTAGTATCTTACACTTGTCCAACCGTCTTATTTTTTTAAAAGTTCTGTGCTTGTAT
TAACACGAACTAGAGAGAAATAGTTTCTGAAGCCAGTTTATTGTGAAGATCCCCAAGGGGGAGGTTCCGGTAGAG
AAAAATAGTAAGCTGGTTTAGAAACTGACGAGGGCAACAGCCAGGACGCATTGGAGAGGAATTTGCCAAAGATC
TACCTTGAGATAACGCCCTGTCCAGTGTCTTACCACGTGAATAACCAGCGCTCCAAAGTGTTTTTCTGCTTTGAA
AAAAAAAATTCACAAAGCTTTTTAAAGGTGCATTTAAGAATCCATGTGACTTTAGAATGGAAGTCCGGGCCCTGG
CAACTGTACAGTGTGCTAGAAGGTTTCATGCCTTGGAATGCATGTGATACTCATCTCCATTTGTTTCTTGAT
TGCATTTTTGTTCTTTTTAGCAGATCTGTCCCTGTGGGTGGTGTCTAAGAAGTCGGACACCTTGGTTTTTGTGTTA

WO 2004/030615

PCT/US2003/028547

40/6881

FIGURE 38B

GATTGAGCTGGGCAGCTGCAATCAGCTTCTTTATATGCAAATTAGGCACGACCCATCTGTGGTTCCTGGTTGGTG
GCTAATGAAGTGAGGGGAGGGAGGGATGTCACCCCAAAAGTAGGCCCTCCCATTTGGCTTTGGCCAGGCCAGACAC
TTCACATCGTTTACATGGTTCTGTGTAATTTTAAAGTTTATGTGTATAAAGCGAAGCTGTTTCTGTGAAACTGTA
TATTTTGTAATAAATATATTGCTACTTTGAGGTTTCATGATTCAAGGTTTCAGGCGATTGCGTTCTGTGCTGAAGG
A

WO 2004/030615

PCT/US2003/028547

41/6881
FIGURE 39

MDSDSCAAAFHPEEYSPSCKRRRTVEDFNKFCTFVLAYAGYIPYPKEELPLRSSPSANSTAGTIDSDGWDAGFS
DIASSVPLPVSDRCFSLQPTLLQRAKPSNFLDRKKTDKLKKKKKKRRRSDAPGKEGYRGGLLKLEAADPYVE
TPTSPTLQDIPQAPSDPCSGWSDTPSSGSCATVSPDQVKEIKTEGKRTIVRQKQVVFREDEDSTGNDEDIMVDS
DDSDWDLVTFCMKPFAGRPMIECNECHTWIHLSCAKIRKSNVPEVFVCQKCRDSKFDIRRSNRSRTGSRKLF LD

WO 2004/030615

PCT/US2003/028547

42/6881
FIGURE 40

GACGGCTCCGGGCCGCCAGGGGCCGCTGTGGCGCAGCCGGGCTGGCCCGCGCTGTCCCTGACGCGGATCACTGGC
CCCTCTTGAGCACGGCCTTGCCGGTTTGGCGGGGTGAAAAGTTGCGAAGATGGCGACGGCCTTGAGCGAGGAGGA
GCTGGACAATGAAGACTATTACTCGTTGCTGAACGTGCGCAGGGAGGCTCTTCTGAAGAGCTGAAAGCTGCCTA
CCGGAGGCTCTGTATGCTCTACCATCCAGACAAGCACAGAGACCCAGAGCTCAAGTCACAGGCGGAACGACTGTT
TAACCTTGTTTACCAGGCTTATGAAGTGCTTAGTGACCCCCAAACCAGGGCCATCTATGATATATATGGGAAGAG
AGGACTGGAATGGAAGGATGGGAGGTTGTGGAAAGGAGGAGAACCCCTGCTGAAATTCGAGAGGAGTTTGAGCG
GCTGCAGAGAGAGAGAGAAGAGAGGAGATTGCAGCAGCGAACAATCCCAAGGGAACGATCAGCGTTGGAGTAGA
TGCCACCGACCTTTTTGATCGCTATGATGAGGAGTATGAAGATGTGTCCGGCAGTAGCTTTCCGCAGATTGAAAT
TAATAAAATGCACATATCCCAGTCCATTGAGGCACCCCTTGACAGCGACAGACACAGCCATCCTCTCTGGAAGCCT
CTCAACCCAGAATGGAAATGGAGGAGGTTCCATTAACTTTGCGCTCAGACGAGTAACCTTCGGCAAAGGGATGGGG
AGAGTTGGAATTTGGAGCTGGAGACCTACAGGGGCCTTTGTTCCGTCTCAAGCTGTTCCGTAATCTCACACCAAG
ATGCTTTGTGACAACAACTGTGCTCTGCAGTTTTTCATCCCGTGGAATCCGACCCGGCCTGACCACTGTCTTAGC
TCGGAACCTAGACAAGAACACCGTGGGCTACCTGCAGTGCGGATGGGGTATCCAGTCAGCCATGAACACTAGCAT
CGTCCGAGACACTAAAACCAGCCACTTCACTGTGGCCCTGCAGCTGGGAATCCCTCACTCCTTTGCACTGATCAG
CTATCAGCACAAATTCAGATGACGATCAGACTCGTGTGAAAGGATCCCTCAAAGCAGGCTTCTTTGGGACGGT
GGTGGAGTACGGAGCTGAGAGGAAGATCTCCAGGCACAGCGTTTGGGTGCAGCTGTGAGCGTTGGAGTTCCACA
GGGTGTTTCTCTCAAAGTCAAGCTCAACAGGGCCAGTCAGACATACTTCTTCCCTATTCACTTGACGGACCACT
TCTGCCCAGCGCCATGTTCTATGCCACCGTGGGGCCTCTAGTGGTCTACTTTGCCATGCACCGTCTGATCATCAA
ACCATACCTCAGGGCTCAGAAAGAGAAGGAATTGGAGAAGCAGAGGGAAAGCGCCGCCACCGATGTGCTGCAGAA
GAAGCAAGAGGCGGAGTCCGCTGTCCGGCTGATGCAGGAATCTGTCCGAAGGATAATTGAGGCAGAAGAGTCCAG
AATGGGCCCTCATCATCGTCAATGCCTGGTACGGGAAGTTTGTAATGACAAGAGCAGGAAGAGCGAGAAGGTGAA
GGTGATTGACGTGACTGTGCCCTGCAGTGCTGGTGAAGGACTCGAAGCTCATCCTCACGGAGGCCTCCAAGGC
TGGGCTGCCGTGGCTTTTATGACCCGTGTGTGGGGGAAGAGAAGAACCTGAAAGTGCTCTATCAGTTCCGGGCGT
CCTGCATCAGGTGATGGTGCTGGACAGTGAGGCCCTCCGGATACCAAAGCAGTCCCACAGGATCGATACAGATGG
ATAAACTGCCAAGAACCAGATTTTTAAAGGCCGCAAAAATCTTTTCTGGGAGTCTACAAATTTGGAATGAA
AAAACCCAGACATCAGATGTTTTATTTATATTATTATAGAAAGGTGGTACCATTATCAATTAATGTGAAGGG
ACATGCAGACACCCAGCTTTTGAGGGTGCTGGGGGTAGGACTGAGGCAGCCCCACTGGGAACAGACTGCAGCC
TGGCCCATGGCTGTTTTCCCAAGGATCAGTTCCTGGAGGGAAGGGCTCTGGCCCTGACTCCGCTGTGTCCCGAGC
ACACGTGCTGACCGCAGCCCGCCGCCCTGTAGTTCCTGGCTGGGTCTGGAGGTGTCTGTGGAGCACCCCTGCCCTC
ACCACAGGAGCGTGAGCCACTTCTGCAGTCCACGCTGAACATGGGAAACAACCTGAAAAGCAGGCAGGCCTCCCG
GTCAGGGAGCCTCTGCTGTGCTGGCTTCCCATGACCACCTCCTCTTGCTGAAATATTACTGCTTGAATCTGGAGC
AGATTGCGGGTTTATAAACTGCTTTTTATCTGAGAACAACCGGGTTTGGAAATTAGTCGTCTTTTTTCCCCACT
CCAGAGCTGCTCAAGTCATTCCACCGGCCCTCCGGCTTGGGACAGGGTAGTGTAACCTCCCGATCCAGGGCCT
AGCCCTGACACAGGTGGCTTCCCGTATCCCGGTGGGAAAACGCCCTGCCACCAGCGGGCTTGAGCTGGCCTGTGT
CCCTCCACCGCTGCACCACCCACCTCCAGAGTGAGTGCTGGGCAAGGGCAGCTCAAGAGGACAGGACCAGGCG
CTTGGCAAGACATCAGACACACCCAAACCCAAAGGCGTGGACCCAGGCCCGGCCGCTGGTACCCAGCAGGTGGCA
CTGCAGCTCCCCGCTCCTGCAGGTCCAGCGTCTCACAGGAACACCAGGGCCTGTGCTCCGGAGCCTTCCTTCAG
ACCCTTCCCTCCACGTGCCCACTTGGGATGCAGAATGCAGCGGAGCTAGGACCCCTCCACGGCCTGGACCTCGGC
TGCAGTAAAGTTACGTGAGGCCTGTCTCTCGGGCCTGGAAGTGGCAGCCATCAGTTGCTCTTGCTGACCCCTCG
GAGCAAGCGCCGCACAGGTGGTGGCTGAGACAGCTGGCGCGGGGGGCCCCAAGCTGCGCCGGCCTCCAGCCCACC
CACAGCTGTTGCTGAAGTCAGGCCTCCCTCCCCAGCACTGGTATCTGAGTAACGGCTAAGAACCTCCTTCTCTG
GTTTTGAAAAGCAGTTTCGGGTTGTCCAATTCTGTAACTTTCATCTCCATTTTTTAAAAAGGTTTCTCTGACGGCC
CCACGGCCCCGAGCCGCGGTGAGCGTCGTGTTGCATGAGCCTGGGCCCCGGGCTTCCCGTGCCTCTGCGCGAGG
TGCTTCTGGGCACCCATCCTCTGCGTTTCATTTGCAGTCGACTGTACAGAAGGCACTCACCACAATAAACCTTTC
CTGAAAGC

WO 2004/030615

PCT/US2003/028547

43/6881
FIGURE 41

TGCGAGGCAGAGTGCTAGCGGGAGCGCGAGCCAGCAAGAGGCGCCTGCGCGATGTCCGGGCCCCCTGAGCCCCGGG
CGCTGAGCCAGCCGGGACGGACATGCGCGGGAGGGCGCCGCGGGGCGAGCCGCCGCTCCTCCGGGGGAATGAAAGC
TACTGGTTGATTTTAAAGTGCCTGGGCCTCACAGGTTTGGAGATGTCCAGAAATAAGGCACAATGTCAATAGCAG
GAGTTGCTGCTCAGGAGATCAGAGTCCCATTAATAAACTGGATTTCTACATAATGGCCGAGCCATGGGGAAATATGA
GGAAGACCTACTGGAGCAGTGCAGTGAGTTTAAAAACAACCTTTTTAAATATTGACCCGATAACCATGGCCTACA
GTCTGAACCTCTTCTGCTCAGGAGCGCCTAATACCCTTGGGCATGCTTCCAAATCTGCTCCGATGAATGGCCACT
GCTTTGCAGAAAATGGTCCATCTCAAAAGTCCAGCTTGCCCCCTCTTCTTATCCCCCAAGTGAAAACCTTGGGAC
CACATGAAGAGGATCAAGTTGTATGTGGTTTTAAGAACTCACAGTGAATGGGGTTTGTGCTTCCACCCCTCCAC
TGACACCCATAAAAACTCCCCCTTCCCTTTTCCCTGTGCCCCCTCTTGTGAACGGGGTTCTAGGCCTCTTCCAC
CGTTGCCAATCTCTGAAGCCCTCTCTCTGGATGACACAGACTGTGAGGTGGAATTCCTAACTAGCTCAGATACAG
ACTTCCTTTTAGAAGACTCTACACTTTCTGATTTCAAATATGATGTTCTTGGCAGGCGAAGCTTCCGTGGGTGTG
GACAAATCAACTATGCATATTTTGATACCCAGCTGTTTCTGCAGCAGATCTCAGCTATGTGTCTGACCAAAATG
GAGGTGTCCAGATCCAAATCCTCCTCCACCTCAGACCCACCGAAGATTAAGAAGGTCTCATTCCGGGACCAGCTG
GCTCCTTTAACAAGCCAGCCATAAGGATATCCAAGTGTGTATACACAGAGCTTCTCCTAACTCCGATGAAGACA
AACCTGAGGTTCCCCCAGAGTTCCCATACCTCCTAGACCAGTAAAGCCAGATTATAGAAGATGGTCAGCAGAAG
TTACTTCGAGCACCTATAGTGATGAAGACAGGCCTCCCAAAGTACCGCCAAGAGAACCTTTGTACCGAGTAACT
CGCGCACACCGAGTCCCAAAAGCCTTCCGTCTTACCTCAATGGGGTCATGCCCCGACACAGAGCTTTGCCCTG
ATCCCAAGTATGTCAGCAGCAAAGCACTGCAAAGACAGAACAGCGAAGGATCTGCCAGTAAGGTTCCCTTGCAATC
TGCCCCATTATTGAAAATGGGAAGAAGGTTAGTTCAACACATTATTACCTACTACCTGAACGACCACCATGCTGG
ACAAATATGAAAAATTTTTTAGGGAAGCAGAAGAAACAAATGGAGGCGCCCAATCCAGCCATTACCTGCTGACT
GCGGTATATCTTCAGCCACAGAAAAGCCAGACTCAAAAACAAAAATGGATCTGGGTGGCCACGTGAAGCGTAAAC
ATTTATCCTATGTGGTTTCTCCTTAGACCTTGGGGTCATGGTTGAGCAGAGGTTACATAGGAGCAAAATGGTTCTC
AATTTTCCAGTTTGATTGAAGTGCAGAGAAAATCCCTTAGATTGCAAAATAAAATAGTTGAACCTCTCTGTCTTC
ATGTGGAAGGTTTAGAGCAGTTGTGAGATGCTGTTATGCTGAGAAACCCTGACTTTGTTAGTGTGGAAAAAGT
CTTACAAGTCTATAATTTAAGATGTGATGGTGGGGAGGGGAGGATGGGAAGCTTTTTATATATGCATACATTA
CATACCTATATATAAACTTGTGGTATAACCATAGACCATAGCTGCAGGTTAACCAATTAGTTACTATCGTAGAGT
AATATATATTGAGAATAATAAACTCAAGCTGGAGAAATGAGTCTGATAGACTGAAAATTGAGCAAAATGGAAGAA
GATACAGTATTGTTTAGATCAGAATCATTAAAAAATATTTTTGTTTAGTAAGTTTGAAGATTTCTGGCTTTTAGG
CCTTTTCTATTTTGTTCATTTATTTTTGCAGGCAATCTTTTCCATGGAGGGCAGGGTATCCATTCTTTACCATG
GGTGTACCTGCTTAGGTTAAAAATCATACCAAGGCCTCATACTTCCAGGTTTTCATGTTGCGTCTTGTGAGGGAG
GGAGAGCAGGTTACTTGGCAACCATATTGTACCTGTACCTGTACACATCTTGAAAAATAAACGATAATAGAA
CTAGTGACTAATTTTCCCTTACAGTTTCTGCTTGGTCCCACCCACTGAAGTAGCTCATCGTAGTGCGGGCCGTAT
TAGAAGCAGTGGGGTACGTTAGACTCAGATGGAAAAGTATTCTAGGTGCCAGTGTTAGGATGTCAGTTTTACAAA
ATAATGAAGCAATTAGCTATGTGATTGAGAGTTATTGTTTGGGGATGTGTGTTGTGGTTTTGCTTTTTTTTTTTT
AGACTGTATTAATAAACATACACACAAGCTGGCCTTGTGTTGCTGGTTCTATTACAGTATTTCTGGGGATTGT
TTGCTTTTTAAGTAAACACTTCTGACCCATAGCTCAGTATGTCTGAATTCCAGAGGTCACATCAGCATCTTTCT
GCTTTGAAAACCTCTCACAGCTGTGGCTGCTTCACTTAGATGCAGTGAGACACATAGTTGGTGTTCGATTTTCAC
ATCCTTCCATGTATTTATCTTGAAGAGATAAGCACAGAAGAGAAGGTGCTCACTAACAGAGGTACATTACTGCAA
TGTTCTCTTAACAGTTAAACAAGCTGTTTACAGTTTAACTGCTGAATATTATTTGAGCTATTTAAAGCTTATTA
TATTTTAGTATGAACATAAAGGTTAAACATGCTTAAGAAAAATGCACTGATTTCTGCATTATGTGTACAGT
ATTGGACAAAGGATTTTATTCATTTTGTGCTATTATTTGAATATTGTCTTTTCATTTTAATAAAGTTATAATAC
TTAAAAA

WO 2004/030615

PCT/US2003/028547

44/6881
FIGURE 42

GAATTCGGCACGAGATAAAAATGGCTTCCAAAAGAGCTCTGGTCATCCTGGCTAAAGGAGCAGAGGAAATGGAGA
CGGTCATCCCTGTAGATGTCATGAGGCGAGCTGGGATTAAGGTCACCGTTGCAGGCCTGGCTGGAAAAGACCCAG
TACAGTGTAGCCGTGATGTGGTCATTTGTCCTGATGCCAGCCTTGAAGATGCAAAAAAGAGGGACCATATGATG
TGGTGGTTCTACCAGGAGGTAATCTGGGCGCACAGAATTTATCTGAGTCTGCTGCTGTGAAGGAGATACTGAAGG
AGCAGGAAAACCGGAAGGGCCTGATAGCCGCCATCTGTGCAGGTCCTACTGCTCTGTTGGCTCATGAAATAGGTT
GTGGAAGTAAAGTTACAACACACCCCTCTTGCTAAAGACAAAATGATGAATGGAGGTCATTACACCTACTCTGAGA
ATCGTGTGAAAAAGACGGCCTGATTCTTACAAGCCGGGGGGCCTGGGACCAGCTTCGAGTTTGCGCTTGCAATTG
TTGAAGCCCTGAATGGCAAGGAGGTGGCGGCTCAAGTGAAGGCTCCACTTGTTCTTAAAGACTAGAGCAGCGAAC
TGCGACGATCACTTAGAGAAACAGGCCGTTAGGAATCCATTCTCACTGTGTTTCGCTCTAAACAAAACAGTGGTAG
GTTAATGTGTTCAGAAGTCGCTGTCTTACTACTTTTGCGGAAGTATGGAAGTCACAACTACACAGAGATTTCTC
AGCCTACAAATTGTGTCTATACATTTCTAAGCCTTGTTTGCAGAATAAACAGGGCATTTAGCAAATAAAAAAA
AAAAAAAAAACTCGAG

WO 2004/030615

PCT/US2003/028547

45/6881
FIGURE 43

MASKRALVILAKGAEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVVICPDASLED
AKKEGPYDVVVLPGG
NLGAQNLSESAVKEILKEQENRKGLIAAICAGPTALLAHEIGCGSKVTTHPLAKDKMMNGG
HYTYSEN RVEKDG
LILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLV LKD

WO 2004/030615

PCT/US2003/028547

46/6881
FIGURE 44

CTCTAAAGCGCCGCGAGCTGCCAAAATGTCTACAGGTCCAACCTGCTGCCACTGGCAGTAATCGAAGACTTCAGCAG
ACACAAAATCAAGTAGATGAGGTGGTGGACATAATGCGAGTTAACGTGGACAAGGTTCTGGAAAGAGACCAGAAG
CTCTCTGAGTTAGACGACCGTGCAGACGCACTGCAGGCAGGCGCTTCTCAATTTGAAACGAGCGCAGCCAAGTTG
AAGAGGAAATATTGGTGGGAAGATTGCAAGATGTGGGCAATCGGGATTACTGTTCTGGTTATCTTCATCATCATC
ATCATCGTGTGGGTTGTCTCTTCATGAGAACCAGCGGAACCTCAAACTGCTGTTCAAGAAACCTCTTCAAGACT
TTTGACTTAGAACCTGCTATATTATCAAGCTTACCTACTGTTATCTCTAAAATTTTTTTTGTGTTAATGTAAAGT
TGAATTTCTAGGAAACGTGCCTTTGTTTTTAAATATGCACTCCAAATTAGAAGGCCGGCCCCGTCCACATTTTGC
ACAGTGCCTTTACAGATTTACGTATGGGCTGATGAAGAGGCCTTCTTAAGTTCCAGAGTGCTATAATCTAGATGT
AATGTTGTCACTAATTAATTGCCATTACTCCCCTTTAG

WO 2004/030615

PCT/US2003/028547

47/6881
FIGURE 45

MSTGPTAATGSNRRRLQQTQNQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN
CKMWAIGITVLVIFIIIIIVWVSS

WO 2004/030615

PCT/US2003/028547

48/6881
FIGURE 46

GCTGCGGGTCTTTCCCTCACTCGTCTCCGCGCGTCGCCGCTCTTCGGTTCTGCTCTGTCCGCCGCCATGGCCCA
AGCTGACATCGCGCTGAICGGATTGGCCGTCATGGGCCAGAACTTAATTCTGAACATGAATGACCACGGCTTTGT
GGTCTGTGCTTTTAATAGGACTGTCTCCAAAGTTGATGATTCTTGGCCAATGAGGCAAAGGGAACCAAAGTGGT
GGGTGCCCAGTCCCTGAAAGAGATGGTCTCCAAGCTGAAGAAGCCCCGGCGGATCATCTCTGGTGAAGGCTGG
GCAAGCTGTGGATGATTTTCATCGAGAAATTGGTACCATTGTTGGATACTGGTGACATCATCATTGACGGAGGAAA
TTCTGAATATAGGGACACCACAAGACGGTGCCGAGACCTCAAGGCCAAGGGAATTTTATTTGTGGGGAGCGGAGT
CAGTGGTGGAGAGGAAGGGGGCCCGGTATGGCCCATCGCTCATGCCAGGAGGGGAACAAAGAAGCGTGGCCCCACAT
CAAGACCATCTTCCAAGGCATTGCTGCAAAAGTGGGAACCTGGAGAACCCTGCTGTGACTGGGTGGGAGATGAGGG
AGCAGGCCACTTCGTGAAGATGGTGCACAACGGGATAGAGTATGGGGACATGCAGCTGATCTGTGAGGCATACCA
CCTGATGAAAGACGTGCTGGGCATGGCGCAGGACGAGATGGCCAGGCCTTTGAGGATTGGAATAAGACAGAGCT
AGACTCATTTCCTGATTGAAATCACAGCCAATATTCTCAAGTTCCAAGACACCGATGGCAAACACCTGCTGCCAAA
GATCAGGGACAGCGCGGGGCAGAAGGGCACAGGGAAGTGGACCGCCATCTCCGCCCTGGAATACGGCGTACCCGT
CACCTCATTTGGAGAAGCTGTCTTTGCTCGGTGCTTATCATCTCTGAAGGATGAGAGAATTCAAGCTAGCAAAA
GCTGAAGGGTCCCCAGAAGTTCCAGTTTGATGGTGATAAGAAATCATTCCTGGAGGACATTCGGAAGGCACTCTA
CGCTTCCAAGATCATCTCTTACGCTCAAGGCTTTATGCTGCTAAGGCAGGCAGCCACCGAGTTTGGCTGGACTCT
CAATTATGGTGGCATCGCCCTGATGTGGAGAGGGGGCTGCATCATTAGAAGTGATTCTTAGGAAAGATAAAGGA
TGCATTTGATCGAAACCCGGAACCTCAGAACCCTCTACTGGACGACTTCTTTAAGTCAGCTGTTGAAAACCTGCCA
GGACTCCTGGCGGGCGGAGTCAGCACTGGGGTCCAGGCTGGCATTCCCATGCCCTGTTTTACCACTGCCCTCTC
CTTCTATGACGGGTACAGACATGAGATGCTTCCAGCCAGCCTCATCCAGGCTCAGCGGGATTACTTCGGGGCTCA
CACCTATGAACTCTTGGCCAAACCAGGGCAGTTTATCCACACCAACTGGACAGGCCATGGTGGCACCGTGTCTATC
CTCGTCATACAATGCCTGATCATGCTGCTCCTGTCAACCCTCCACGATTCCACAGACCAGGACATTCCATGTGCCT
CATGGCACTGCCACCTGGCCCTTTGCCCTATTTTCTGTTTCAGTTTTTTAAAAGTGTTGTAAGAGACTCCTGAGGA
AGACACACAGTTTATTTGTAAAGTAGCTCTGTGAGAGCCACCATGCCCTCTGCCCTTGCCCTCTTGGGACTGACCA
GSAGCTGCTCATGTGCGTGAGAGTGGGAACCATCTCCTTGCGGCAGTGGCTTCCGCGTGCCCCGTGTGCTGGTGC
GGTTCCTCATCAGCAGACAGGAAGGGTGTGTCGCACTCTGATCAACTGGAACCTCTGTATCATGCGGCTGAATT
CCCTTTTTCCTTTACTCAATAAAAGCTACATCAGACTG

WO 2004/030615

PCT/US2003/028547

49/6881
FIGURE 47

MAQADIALIGLAVMGQNLILNMNDHGFVVCAFNRTVSKVDDFLANEAKGTKVVGAQSLKEMVSKLKKPRRIILLV
KAGQAVDDFIEKLVPLLDTGDIIDGGNSEYRDTTRRCRDLKAKGILEVSGSVSGGEEGARYGPSLMPGGNKEAW
PHIKTIFQGIAAKVGTGEPCCDWVGDEGAGHFVKMVHNGIEYGDMQLICEAYHLMKDVLGMAQDEMAQAFEDWNK
TELDSFLIEITANILKFQDTDGKHL LPKIRDSAGQKGTGKWTAI SALEYGVPVTLIGEAVFARCLSSSLKDERIQA
SKKLKGPQKFQFDGDKKSFLDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVFLGK
IKDAFDRNPELQNL LDDFFKSAVENCQDSWRRRAVSTGVQAGIPMPCFTTALSFYDGYRHEMLPASLIQAQRDYF
GAHTYELLAKPGQFIHTNWTGHGGTVSSSSSYNA

WO 2004/030615

PCT/US2003/028547

50/6881
FIGURE 48

CGCCGCTCCGGCCTCCCGCGACTTCTCGAAGGTGGGCAGGTCCACCTTGTGGAGGATGGAGGTGACCGGGGACG
CCGGGGTACCAGAATCTGGCGAGATCCGGA CTCTAAAGCCGTGTCTGCTGCGCCGCAACTACAGCCGCGAACAGC
ACGGCGTGGCCGCCTCCTGCCTCGAAGACCTGAGGAGCAAGGCCTGTGACATTCTGGCCATTGATAAGTCCCTGA
CACCAGTCACCCTTGTCTGGCAGAGGATGGCACCATAGTGGATGATGACGATTACTTTCTGTGTCTACCTTCCA
ATACTAAGTTTGTGGCATTGGCTAGTAATGAGAAATGGGCATACAACAATTCAGATGGAGGTACAGCTTGGATTT
CCCAGAGTCCCTTGTATGTAGATGAAACAGACAGCGGGGCGAGGGTTGAAGTGGAAGAATGTGGCCAGGCAGCTGA
AAGAAGATCTGTCCAGCATCATCCTCCTATCAGAGGAGGACCTCCAGATGCTTGTTGACGCTCCCTGCTCAGACC
TGGCTCAGGAACCTACGTGAGATTGTGCCACCGTCCAGCGGCTGCAGCACACACTCCAACAGGTGCTTGACCAAA
GAGAGGAAGTGCGTCAGTCCAAGCAGCTCCTGCAGCTGTACCTCCAGGCTTTGGAGAAAGAGGGCAGCCTCTTGT
CAAAGCAGGAAGAGTCCAAAGCTGCCTTTGGTGAGGAGGTGGATGCAGTAGACACGGGTATCAGCAGAGAGACCT
CCTCGGACGTTGCGCTGGCGAGCCACATCCTTACTGCACTGAGGGAGAAGCAGGCTCCAGAGCTGAGCTTATCTA
GTCAGGATTTGGAGTTGGTTACCAAGGAAGACCCCAAAGCACTGGCTGTTGCCTTGAACTGGGACATAAAGAAGA
CGGAGACTGTTTCAGGAGGCCTGTGAGCGGGAGCTCGCCCTGCGCCTGCAGCAGACGCAGAGCTTGCATTCTCTCC
GGAGCATCTCAGCAAGCAAGGCCTCACCACCTGGTGACCTGCAGAATGCTAAGCGAGCCAGACAGGATCCCACAT
AGCAGCAGCGGGGAAGTGTGCCAAGGAAGCTCTGTGGCGTTGTGTTATTGGTAGACACCCTCAGCCTCATCTTTG
ACTACCTATGTACTACTCTACCCCTGCCTTAGAGCACCTTCCAGAGAAGCTATTCCAGGTCTCAACATACGCCG
TTCCACCAATTTTTTTTTTAGCCCCACCAGCTTCAGGACTTCTGCCAATTTTGAATGATATAGCTGCACCAACAA
TATCCCGCTCCTCTAATTACATATGATGTTCTCTGTTCAAAAGTAATTGGCAGTGATTGGCCAGGCGCAGTGGC
TCACGCCTGTAATCCAGCACTGGGAGGCCGAGGGGGCGGATCGTGAAGTCAGGAGATCGAGACCATCCTGGCT
AACATGGTGAAACCTGTCTCTACTAAAAATACAAAAAAATTAGCCAGCCATGGTGGCGGGCGCCTGTAATCCC
AGCTACTTGGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAGGCAGAGCTTGCAGTGAGCTGAGATTGCGCC
ACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

51/6881
FIGURE 49

MEVTGDAGVPESGEIRTLKPCLLRNYSREQHGVAASCLEDLRSKACDILAIKSLTPVTLVLAEDGTIVDDDDY
FLCLPSNTKFVALASNEKWAYNNSDGGTAWISQESFDVDETDGAGLKWKNNVARQLKEDLSSIILLSEEDLQMLV
DAPCSDLAQELRQSCATVQRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQEESSKAAFGEEVDAVDT
GISRETSSDVALASHILTALREKQAPELSLSSQDLELVTKEDPKALAVALNWDIKKTETVQEACERELALRLQQT
QSLHSLRSISASKASPPGDLQNPKRARQDPT

WO 2004/030615

PCT/US2003/028547

52/6881
FIGURE 50

CGGCGGAGCTGGTCCCGTTGTGCTGCGGCGCCGCGCGGCCTGCAGTCCCGGGCCCGCGCCCCGCGCCGCCGCCGCC
GCCCCGCCATGGAGCCCCGCCCCGACGGCCCCGCGCGCTCCGGCCCCGCCGCCATCCGCGAGGGCTGGTTCCGCGA
GACCTGCAGCCTGTGGCCCCGGCCAGGCCCTGTGCTGCAGGTGGAGCAGCTGCTCCACCACCGGCCTCGCGCTA
CCAGGACATCCTCGTCTTCCGCAGTAAGACCTATGGCAACGTGCTGGTGTGGACGGTGTTCATCCAGTGCACGGA
GAGAGACGAGTTCTCCTACCAGGAGATGATCGCCAACCTGCCTCTCTGCAGCCACCCCAACCCGCGAAAGGTGCT
GATCATCGGGGGCGGAGATGGAGGTGTCTGCGGGAGGTGGTGAAGCACCCCTCCGTGGAGTCCGTGGTCCAGTG
TGAGATCGACGAGGATGTCATCCAAGTCTCCAAGAAGTTCTGCCAGGCATGGCCATTGGCTACTCTAGCTCGAA
GGTGACCCTACATGTGGGTGACGGTTTTGAGTTTCATGAAACAGAATCAGGATGCCTTCGACGTGATCATCACTGA
CTCCTCAGACCCCCATGGGCCCCGCCGAAAGTCTCTTCAAGGAGTCTATTACCAGCTCATGAAGACAGCCCTCAA
GGAAGATGGTGTCTCTGCTGCCAGGGCGAGTGCAGTGGCTGCACCTGGACCTCATCAAGGAGATGCGGCAGTT
CTGCCAGTCCCTGTTCCCCGTGGTGGCCTATGCCTACTGCACCATCCCCACCTACCCAGCGGCCAGATCGGCTT
CATGCTGTGCAGCAAGAACCCGAGCACGAACTTCCAGGAGCCGGTGCAGCCGCTGACACAGCAGCAGGTGGCGCA
GATGCAGCTGAAGTACTACAACCTCCGACGTGCACCGCGCCGCCCTTTGTGCTGCCCCGAGTTTGCCCCGAAGGCCCT
GAATGATGTGAGCTTGAGCCCCAGGCGCCACCACTGATGCCACCCAGGACCTCGGACCTTGGAGCCTGCGGGGTGCC
TCGGCCCCCTCCAGCCCCGGGCCGACCTCCTGCTGGCTCTCGCCCACCAACCAAGTGTACAAAGCCCCAGAATGC
TGCCCCGGCCTGCCCTGCTGGGCGGACTGTCTGTGTGTCTGTCTCTTGGCGTTCCACCTCCAAGCCTATACCAGC
TGTGTACAGCGCCATCTCTCTGCCTTCTGTTGCCCCCG

WO 2004/030615

PCT/US2003/028547

53/6881

FIGURE 51

MEPGPDGPAASGPAAIREGWFRETCSLWPGQALSLQVEQLLHRRSRYQDILVFRSKTYGNVLVLDGVIQCTERD
EFSYQEMIANLPLCSHPNPRKVLIIIGGDGGVLREVVKHPSVESVVQCEIDEDVIQVSKKFLPGMAIGYSSSKVT
LHVGDGFEFMKQNQDAFDVITDSSDPMGPAESLFKESYYQLMKTALKEDGVLCCQGECEWLHLDLIKEMRQFCQ
SLFPVVAYAYCTIPTPSGQIGFMLCSKNPSTNFQEPVQPLTQQQVAQMLKYNSDVHRAAFVLPEFARKALND
VS

WO 2004/030615

PCT/US2003/028547

54/6881
FIGURE 52

AGGCGCAGGCGCAGGCGAGGGGCTGGGTGGCGGTTGAGACAGCGGCGGTACTGGGAGGCGTAGGTGAGGGTCGCG
AGGCTGCCCCGAGCTTCTGAGCGAGCGCGGTGCTTTTGGGAACGCGGGACGGGCGATCTGCGGCGCCAGGAGCTGG
GCCGAGGCGCGGGCGGCGCGGCTGCCGGCTGCCCTGTGAATGGGAAGTTACGCGAAGTCCACCCAGCGTTTCTGAG
GCAATCTGAAGGCAAATCCTGTTTAGACCCAGGCGAAGGTTCCCGGTGACCCGGGCTCTCACCAGCCAATTGTCC
CTTGCCGTCCTCCTGAGGGTGCCCTGGAGCTTAAGCACTGTGTGCTCTTGGCCTCCACACTGGGGATGCCGCTGAC
TCCCACTGTCCAGGGCTTCCAGTGGATTCTCCGAGGCCCTGATGTAGAACTTCCCCATTGGGTGCACCAAGAGC
AGCCTCACATGGTGTGGGCTGACATCAAGAGCTGCCAGATCCAACAGGAAGATGGCCAATCTTTCCTAAGCTGCT
CACCTTACAAGAAAACGAATCGTACTGCTAAGAATTCAAACCTTCAGCAGTCATGGGGAGCCTTGGAAGGAGCCCG
AATCACTGATGGAATTGGACAGTGCATGGAGATGGTTCAGCAGGACAAGGGTAAGTGCAGGGGCAAGTCCAGGTC
ATACTGAGAGACAACGAGTGGCGCTGACAGAGACAGACAAAGATAAAATCAAAAGTTTGTGCTTCATCTTCAAAA
ACTCAAACCTAATAACAACTTGGCCTT

WO 2004/030615

PCT/US2003/028547

55/6881
FIGURE 53

MPLTPTVQGFQWILRGPDVETSPLGAPRAASHGVG

WO 2004/030615

PCT/US2003/028547

56/6881
FIGURE 54

CTGCGCCCGCGACGGAGGCGCGCTTCAAAGCGCAGGCGCGGGGAGGGGGTGGGGGAGGAGGGAAAGCGGCGAGTA
AGATGGAAGATGAGGAGGTGCTGAGAGCTGGGAAGAGGCGGCAGACAGCGGGGAAATCCAAATCTCCTCCCAAA
GTGCCCATTGTGATTCAGGACGATAGCCTTCCCGCGGGGCCCCCTCCACAGATCCGCATCCTCAAGAGGCCCCACC
AGCAACGGTGTGGTCAGCAGCCCCAACTCCACCAGCAGGCCCCACCCTTCCAGTCAAGTCCCTAGCACAGCGAGAG
GCCGAGTACGCCGAGGCCCCGAAGCGGATCCTGGGCAGCGCCAGCCCCGAGGAGGAGCAGGAGAAACCCATCCTC
GACAGGCCAACCAGGATCTCCAACCCGAAGACAGCAGGCAGCCCCAATAATGTGATCAGACAGCCTTTGGGTCTT
GATGGGTCTCAAGGCTTCAAACAGCGCAGATAAATGCAGGCAAGAAAAGATGCCGCCGTTGCTGCCGTACCCGCC
TCCTGGGTCTGTCGCCACGGGTTGCACTGCCGTGGCAGACAGCTGGACTTGAGCAGAGGGGAACGACCTGACTTAC
TTGCACTGTGATCCCCCTTGCTCCGCCCCACTGTGACCTTGAACCCCATGCACTGTGACCTCCCCCTTCTCCCCC
TTCCCACTGTGATTGGCACATCGACAAGGGCTGTCCCAAGTCAATGGAAAGGGAAAGGGTGGGGGTAGGGGAAG
GTTGGGGGACCCAGCAAGGACTCAGAGAGTCAGACAGTGCCACTTGGCCACTTGGGGTAAAGCCAGTGCCAGCA
ATAACAGTTTATCATGCTCATTAAATTTGGGATTTCAAACACAAATGAAACTCACACCCACCCACCCCAAGTG
CATGTCTCCATCACTTAAAAAGTAAGTTCCATTTGAAAATATCCTTTCTTTTTTTTTTCTTCTATTTTGTGTTG
TTTATACAAATATCTGATTTGCAAGAAAAAGTGATGGGAGGGGTTTTAGTGGTTTAAATGAATTTTAAATTAAGA
AAGGGTAGTTTGGTAGTCTACTTAAAAATGTTTCTGGGAAATTCAGTAGAAACATTAACCAATAGGATTTTGGTG
AGCTTAGCTTCTGTATTCTACTGCCGCCAGAAAAGGGGCAGGGCTCTGCAGCCGCCAGGACAGACGAGCACC
CATGCCTATACCTCCCTCCCCGAGCTAAGTCCCAGGGCATCTGGGCCTTGCCCTGGAGACTGGGCTAGCTCTGTAG
GCTCGGAGAGCCTGGGGAGGGTGCCAACCCACCTCTAGTATTTGGGAGATAGGGAAAGTGAACCGACTTCCCC
TTCCCATACCCCTCAGGGTGGTTCCCTACCAGCCAGGCTTACTACTTCTAGAAGAAAGCAGAGTGCCAGGGAGTG
AGATTGCATCCCTGGGCTTAGAAGTGACGGAGAGAAGACTTGTTTAGTATTTGCCATCAGCACAAGGAAAACCA
GGAGAGAGTCTGCCTCCAGGACTCTGAGCCTTCTGCCTCGTATGTTTCAAGAGGTGGATAGGTCTTCCCACTCCAG
CATGGCTTGAACCTTAGGGGTCTGCAGTGCTCCATCTCCATTGGTGGCCCCAGCTCAGTAACCTATACCTGGTAC
ATTTCTGTGTGCAATCAGTACCTTGAAGGCAGAACATTCTGAATAAAGTTGAAAAAGAACA

WO 2004/030615

PCT/US2003/028547

57/6881
FIGURE 55

CCACCTGGCACTGCCCCACCACCTGTAGCAGTGTGCCAGCAGGAGAGTCTGTCCCTTTCAGAGCTGCCCGCCCTG
AAGCCCCCGAGCCAGTGTGTCTGGACCTTTTCCCTGTTGCCCCAGAGGAGCTTCGGGCTCCTGGCAGCCGCTGG
TCCCTGGGGACCCCTGCCCTCTCCAAGGGTTGCTATGGCCATTATCCCCAGGAGGCTCAGATACAGAGATCACC
AGCGGGGGGATGCGGGCCAGCAGGGCTGGCAGCTGGCCACACTGTCTGGTGCCAGCCCCAGCTCTGGAGGGA
CCCTGGAGTCCCCGACACACACAGCCACAGCGCCGGGCCAGCCACGGCTCGGAGAAGAAGTCTGCCTGGCGCAAG
ATGCGGGTGTACCAGCGTGAAGAGGTCCCCGGCTGCCCGAGGCCCCACGCTGTCTTCCTAGAGCCTGGCCAGGTA
GTGCAAGAGCAGGCCCTGAGCACAGAGGAGCCCAGGGTGGAGTTGTCTGGGTCCACCCGAGTGAGCCTCGAAGGT
CCTGAGCGGAGGCGCTTCTCGGCATCGGAGCTGATGACCCGGCTGCACTCTTCTCTGCGCTGGGGCGGAATTCA
GCAGCCCCGGGCACTCATCTCTGGGTCAAGCACCGGAGCAGCCCCGGGAAGGGAAGCATCTGGAATGGAGGCTCGA
AGTGTAGAGATGAGCGGGGACCGGGTGTGCGCGCCAGCCCCCTGGTGACTCACGAGAGGGCGATTGGTCCGAGCCC
AGGCTAGACACACAGGAAGAGCCGCCTTTGGGGTCCAGGAGCACCAACGAGCGGCGCCAGTCTCGATTCTCCTT
AACTCCGTCTCTATCAGGAATACAGCGACGTGGCCAGCGCCCCGCAACTGCGGCGGCAGCAGCGCGAGGAGGAG
GGCCCCGGGGACGAGGCCGAGGGCGCAGAGGAGGGGCCGGGGCCGCCGCGGGCCAACCTCTCCCCCAGCAGCTCC
TTCCGGGCGCAGCGCTCGGCGCGAGGCTCCACCTTCTCGCTGTGGCAGGATATCCCCGACGTACGCGGCAGCGGC
GTCTTGGCCACGCTGAGCCTGCGGGACTGCAAGCTGCAGGAGGCCAAGTTTGAGCTGATCACCTCCGAGGCCCTCC
TACATCCACAGCCTGTGCGTGGCTGTGGGCCACTTCTTAGGCTCTGCCGAGCTGAGCGAGTGTCTGGGGGCGCAG
GACAAGCAGTGGCTGTTTTCCAACTGCCCGAGGTCAAGAGCACAGCGAGAGGTTCTTGCAGGACCTGGAGCAG
CGGCTGGAGGCAGATGTGCTGCGCTTACAGCGTGTGCGACGTGGTGCTGGACCACTGCCCGGCCCTCCGAGAGTC
TACCTGCCCTATGTACCAACCAGGCCTACCAGGAGCGCACCTACCAGCGCCTGCTCCTGGAGAACCCAGGTTT
CCTGGCATCCTGGCTCGCCTGGAGGAGTCTCCTGTGTGCCAGCGTCTGCCCTTACCTCCTTCTTATCTGCC
TTCCAGAGGATCACCCGCCTCAAGATGTTGGTGGAGAATCCTGAAGCGGACAGCACAGGGCTCTGAAGACGAA
GACATGGCCACCAAGGCCTTCAATGCGCTCAAGGAGCTGGTGCAAGAGTGCAATGCTAGTGACAGTCCATGAAG
AGGACAGAGGAACATCCACCTGAGCAAGAAGATCCACTTTGAGGGCAAGATTTTCCCGCTGATCTCTCAGGCC
CGCTGGCTGGTTTCGGCATGGAGAGTTGGTAGAGCTGGCACCCTGCCTGCAGCACCCCTGCCAAGCTGAAGCTG
TCCAGCAAGGCAGTCTACCTCCACCTCTTCAATGACTGCTTGCTGCTCTCTCGGCGGAAGGAGCTAGGGAAGTTT
GCCGTTTTTCGTCCATGCCAAGATGGCTGAGCTGCAGGTGCGGGACCTGAGCCTGAAGCTGCAGGGCATCCCCGGC
CACGTGTTCTCTCCAGCTCCTCCACGGGCAGCACATGAAGCACCAGTTCTTGCTGCGGGCCCCGACGGAAAGT
GAGAAGCAGCGATGGATCTCAGCCTTGTCCTCCAGCCCCCAGGAGGACAAGGAGGTCATCAGTGAGGGGGAA
GATTGCCCCCAGGTTTCAAGTGTGTTAGGACATAACAAGGCACTGCACCCAGATGAGCTGACCTTGGAGAAGACTGAC
ATCCTGTCAAGTGGAGCCTGGACCAAGTGACGGCTGGCTGGAAGGGGTCCGCTGGCAGATGGTGAGAAGGGGTGG
GTGCCCCAGGCCTATGTGGAAGAGATCAGCAGCCTCAGCGCCCGCCTCCGAAACCTCCGGGAGAATAAGCGAGTC
ACAAGTGCCACCAGCAAACTGGGGGAGGCTCCTGTGTGATGGGCAGCCATGGCCTAGGACCCACCTCCATGCCCT
GGCTCCTGGATGGTCTTGAGGGGGCTGCAGTGTCTCCATTCCCCAAGCTGCTCCTGCTGGCACTTCGCTTCTGT
GGCCTTGGCATTGAGGGCACAGGCTGGACACAGGAATGGGGGCGCCTCCAGAGGGTCTCTCCGTCTCATGCTCC
TCAGTGTCCACACTTCAAGGCCAAGGATAGTTTCTTCTGACATGGGGACCATAACAGGTGATCACTGATAACC
TGGCAAAGACTGGGGCCCTCTCCTTTCTATGTCTCAATCCTGCCTGACTCTTGGTCTTCTGGCAGGGACCTGG
CTGGGGAACGTTCTGGTGCTGATGGTGCTGGGACCTATATGTATATTTATATATATCTGGGGTCTTGTCTACCAC
CTCC

WO 2004/030615

PCT/US2003/028547

58/6881
FIGURE 56

MDCGPPATLQPHLTGPPGTAHHPVAVCQQESLSFAELPALKPPSPVCLDLFPVAPEELRAPGSRWSLGTAPAPLQG
LLWPLSPGGSDTEITSGGMRPSRAGSWPHCPGAQPPALEGPWSPRHTQPQRRASHGSEKKSARWKMRYQREEVP
GCPEAHAVFLEPGQVVQEALSTEEPRVELSGSTRVSLEGPERRRFSASELMTRLHSSLRLGRNSAARALISGSG
TGAAREGKASGMEARSVEMSGDRVSRPAPGDSREGDWSEPRLDTQEEPPGSRSTNERRQSRFLNSVLYQEYSD
VASARELRRQOREEEGPGDEAEGAEAGPGPPRANLSPSSSFRAQRSARGSTFSLWQDIPDVRGSGVLATLSLRDC
KLQEAKFELITSEASYIHSLSVAVGHFLGSAELSECLGAQDKQWLFSKLPEVKSTSERFLQDLEQRLEADVLRFS
VCDVVLHDHCPAFRRVYLPYVTNQAYQERTYQRLLLENPRFPGILARLEESPVCQRLPLTSFLILPFQRITRLKML
VENILKRTAQGSSEDEDMATKAFNALKELVQECNASVQSMKRTEELIHLSKKIHFEKGIFPLISQARWLVRHGELV
ELAPLPAAPPKAKLKLSSKAVYLHLFNDCLLLSRRKELGKFVAVFHAKMAELQVRDLSLKLQGIPGHVFLQLLHG
QHMKHQFLLRARTSEKQRWISALCPSSPQEDKEVISEGEDCPQVQCVRTYKALHPDELTLEKTDILSVRTWTS
GWLEGVRLADGEKGWVPQAYVEEISSLSARLRNLRENKRVTSATSKLGEAPV

WO 2004/030615

PCT/US2003/028547

59/6881
FIGURE 57A

GAAGTTGCGCGCAGGCCGGCGGGCGGGAGCGGACACCGAGGCCGGCGTGCGGGTGTGCGGGAGCCGG
GCTCGGGGGGATCGGACCGAGAGCGAGAAGCGCGGCATGGAGCTCCAGGCAGCCCGCGCCTGCTTCGCCCTGCTG
TGGGGCTGTGCGCTGGCCGCGGCCGCGCGGCGCAGGGCAAGGAAGTGGTACTGCTGGACTTTGCTGCAGCTGGA
GGGGAGCTCGGCTGGCTCACACACCCGTATGGCAAAGGGTGGGACCTGATGCAGAACATCATGAATGACATGCCG
ATCTACATGTACTCCGTGTGCAACGTGATGTCTGGCGACCAGGACAACCTGGCTCCGCACCAACTGGGTGTACCGA
GGAGAGGCTGAGCGTATCTTCATTGAGCTCAAGTTTACTGTACGTGACTGCAACAGCTTCCCTGGTGGCGCCAGC
TCCTGCAAGGAGACTTTCAACCTCTACTATGCCGAGTCGGACCTGGACTACGGCACCAACTTCCAGAAGCGCCTG
TTCACCAAGATTGACACCAATTGCGCCCGATGAGATCACCGTCAGCAGCGACTTCGAGGCACGCCACGTGAAGCTG
AACGTGGAGGAGCGCTCCGTGGGGCCGCTCACCCGCAAAGGCTTCTACCTGGCCTTCCAGGATATCGGTGCCTGT
GTGGCGCTGCTCTCCGTCCGTGTCTACTACAAGAAGTGCCCCGAGCTGCTGCAGGGCCTGGCCCACTTCCCTGAG
ACCATCGCCGGCTCTGATGCACCTTCCCTGGCCACTGTGGCCGGCACCTGTGTGGACCATGCCGTGGTGCCACCG
GGGGGTGAAGAGCCCCGTATGCACTGTGCAGTGGATGGCGAGTGGCTGGTGGCCATTGGGCAGTGCCTGTGCCAG
GCAGGCTACGAGAAGGTGGAGGATGCCTGCCAGGCCTGCTCGCCTGGATTTTTTAAGTTTGAGGCATCTGAGAGC
CCCTGCTTGGAGTGCCCTGAGCACACGCTGCCATCCCCTGAGGGTGCCACCTCCTGCGAGTGTGAGGAAGGCTTC
TTCCGGGCACCTCAGGACCCAGCGTCGATGCCTTGACACGACCCCCCTCCGCCCCACACTACCTCACAGCCGTG
GGCATGGGTGCCAAGGTGGAGCTGCGCTGGACGCCCCCTCAGGACAGCGGGGGCCGCGAGGACATTGTCTACAGC
GTCACCTGCGAACAGTGCTGGCCCGAGTCTGGGGAATGCGGGCCGTGTGAGGCCAGTGTGCGCTACTCGGAGCCT
CCTCACGGACTGACCCGCAACAGTGTGACAGTGAAGCGACCTGGAGCCCCACATGAACCTACACCTTACCGTGGAG
GCCCCGAATGGCGTCTCAGGCCTGGTAACAGCCGAGCTTCCGTACTGCCAGTGTGAGCATCAACCAGACAGAG
CCCCCAAGGTGAGGCTGGAGGGCCGAGCACCACCTCGCTTAGCGTCTCCTGGAGCATCCCCCGCCGCGAGCAG
AGCCGAGTGTGGAAGTACGAGGTCACTTACCGCAAGAAGGGAGACTCCAACAGCTACAATGTGCGCCGACCCGAG
GGTTTCTCCGTGACCTTGGACGACCTGGCCCCAGACACCACCTACCTGGTCCAGGTGCAGGCACTGACGCAGGAG
GGCCAGGGGGCCGGCAGCAAGGTGCACGAATTCCAGACGCTGTCCCGGAGGGATCTGGCAACTTGGCGGTGATT
GGCGGCGTGGCTGTGCGTGTGGTCTGCTTCTGGTGTGGCAGGAGTTGGCTTCTTTATCCACCGCAGGAGGAAG
AACCAGCGTGCCCGCCAGTCCCCGGAGGACGTTTACTTCTCCAAGTCAGAACAACCTGAAGCCCCCTGAAGACATAC
GTGGACCCCCACACATATGAGGACCCCCAACAGGCTGTGTTGAAGTTCACTACCGAGATCCATCCATCCTGTGTC
ACTCGGCAGAAGGTGATCGGAGCAGGAGAGTTTGGGGAGGTGTACAAGGGCATGCTGAAGACATCCTCGGGGAAG
AAGGAGGTGCCGTGGCCATCAAGACGCTGAAAGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCCTCGGGAG
GCCGGCATCATGGGCCAGTTCAGCCACCACAACATCATCCGCCTAGAGGGCGTCATCTCAAATACAGCCCATG
ATGATCATCACTGAGTACATGGAGAATGGGGCCCTGGACAAGTTTCTTCGGGAGAAGGATGGCAGGTTTCAAGCTG
CTGCAGCTGGTGGGCATGCTGCGGGCATCGCAGCTGGCATGAAGTACCTGGCCAACATGAACATATGTGCACCGT
GACCTGGCTGCCCCGAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCTGACTTTGGCCTGTCCCGCGTG
CTGGAGGACGACCCCGAGGCCACCTACACCACAGTGGCGGCAAGATCCCCATCCGCTGGACCGCCCCGGAGGCC
ATTTCTTACCGGAAGTTCACTCTGCCAGCGAGTGTGGAGCTTTGGCATTGTGATGTGGGAGGTGATGACCTAT
GGCGAGCGGCCCTACTGGGAGTTGTCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCTCCCCACA
CCCATGGACTGCCCCCTCCGCCATCTACAGCTCATGTGAGTGTGCTGGCAGCAGGAGCGTGCCCGCCGCCCAAG
TTGCTGACATCGTCAGCATCCTGGACAAGCTCATTCTGCCCCCTGACTCCCTCAAGACCCTGGCTGACTTTGAC
CCCCGCGTGTCTATCCGGCTCCCCAGCACGAGCGGCTCGGAGGGGGTGCCCTTCCGCACGGTGTCCGAGTGGCTG
GAGTCCATCAAGATGCAGCAGTATACGGAGCACTTTCATGGCGGCCGGCTACACTGCCATCGAGAAGGTGGTGCAG
ATGACCAACGACGACATCAAGAGGATTGGGGTGCAGCTGCCCGGCCACCAGAAGCGCATCGCCTACAGCCTGCTG
GGACTCAAGGACAGGTGAACACTGTGGGGATCCCCATCTGAGCCTCGACAGGGCCTGGAGCCCCATCGGCCAAG
AATACTTGAAGAAACAGAGTGGCCTCCCTGCTGTGCCATGCTGGGCCACTGGGGACTTTATTTATTTCTAGTTCT
TTCTTCCCCCTGCAACTTCCGCTGAGGGGTCTCGGATGACACCCTGGCCTGAACTGAGGAGATGACCAGGGATGC
TGGGCTGGGGCCCTCTTTCCCTGCGAGACGCACACAGCTGAGCACTTAGCAGGCACCGCCACGTCCAGCATCCCT
GGAGCAGGAGCCCCGCCACAGCCTTCGGACAGACATATGGGATATTCCCAAGCCGACCTTCCCTCCGCTTCTCC
CACATGAGGGCATCTCAGGAGATGGAGGGCTTGGCCAGCGCCAAGTAAACAGGGTACCTCAAGCCCCATTTCTCT
CACACTAAGAGGGCAGACTGTGAACCTGACTGGGTGAGACCCAAAGCGGTCCCTGTCCCTCTAGTGCCTTCTTTA
GACCTCGGGCCCCATCCTCATCCCTGACTGGCCAAACCCTTGCTTCTCGGGCTTTGCAAGATGCTTGGTTGT

WO 2004/030615

PCT/US2003/028547

60/6881

FIGURE 57B

GTTGAGGTTTTTAAATATATATTTTGTACTTTGTGGAGAGAATGTGTGTGTGTGGCAGGGGGCCCCGCCAGGGCT
GGGGACAGAGGGTGTCAAACATTCGTGAGCTGGGGACTCAGGGACCGGTGCTGCAGGAGTGCCTGCCCCATGCCC
CAGTCGGCCCCATCTCTCATCCTTTTGGATAAGTTTCTATTCTGTCAGTGTTAAAGATTTTGTGTTGGACAT
TTTTTTCGAATCTTAATTTATTATTTTTTTTTATATTTATTGTTAGAAAATGACTTATTTCTGCTCTGGAATAAAG
TTGCAGATGATTCAAACCG

WO 2004/030615

PCT/US2003/028547

61/6881
FIGURE 58

GGTGGGCTGTAGGAATGAGGAGGAACCTAGGGAGAAACAGCTAGTGGGGAGGTAGGGCCTGGGGGAGCCGCCCCCT
TGCCCCAAGAGAAGGAGCCAGAACCCCCGGATCTGCATGCAAGGCCTGCTCCATGCCTCGCTCACAGCAGCCCCAT
CCCACAGCCCGCCCCGGTGGGGCAGGCAACATCAAGACCCTAGGAGACGCCTATGAGTTTGCGGTGGACGTGAGA
GACTTCTCACCTGAAGACATCATTGTCAACACCTCCAACAACCACATCGAGGTGCGGGCTGAGAAGCTGGCGGGCT
GACGGCACCGTCATGAACACCTTCGCTCACAAGTGCCAGCTGCCGGAGGACGTGGACCCGACGTGCGGTGACCTCG
GCTCTGCGGGAGGACGGCAGCCTCACTATCCGGGCACGGCGTCACCCGCATACAGAACACGTCCAGCAGACCTTC
CGGACGGAGATCAAAATCTGAGTGCTCTCCCTTCCCTTTCCCTGTCCCCCGCCCCACGCCTGCCAGCAAAGCC
TCGCTAACCCCATTAACAACAGCTCCAGGACATCTCAGCCCAGGTTCTAGCCCCACGCACCCAGACCCAGGTTG
GACCATCCTCCAAACTAGGGCCCTCCACTCTATCCAGGGCAGGCCAGGGACTCCCTGGCCTGACACATGATGCC
CAGATTTAGATTTGGCCTCCGTCACCTAATCCAGAGTACAGGGGCTGGGGTCAGGGAAGGAAGATCTAAAGAAC
CCACTGTGGGTCAGGGGAATGGGACCAGCAGGACATATGGGCAAGCTCTGCAGGACAGACAGGCAGACAAACCCT
CTGATCTATGA

WO 2004/030615

PCT/US2003/028547

62/6881
FIGURE 59

GCTCGTGTTAAATCTAGAACCGTAGCCAGACATGGGACTGGAGGACGAGCAAAAGATGCTTACCGAATCCGGAGA
TCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCTAACAACAGTGAGAGAGCAATGCGAGCAGTT
GGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTATGATGAGCATGTATCCTCTCGATCACATACAGAAGA
GGATTGCACGGAGGAGCTCTTTGACTTCTTGCAATGCAAAGGACCATTGCGTGGCCACAAACTCTTTAACAATT
GAAATAAATGTGTGGACTTAATTCACCCCAGCCTTCATCATCTGGGCATCAGAATATTTCTTATGGTTTCGGAT
GTACCATTGTGTTCTTATTTGTGTAAGTTCACATGAACCTCGTGGGTTTTGGCTTAGGCTGGTAGCTTC
TATGTAATTGCGAGTGATTCCATCTAAATAAAAGTTCTGTGATCTGC

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

64/6881

FIGURE 61

MIRTLTLLSTLVAGALSCGDPTYPYVTRVVGGEARPNSWPWQVSLQYSSNGKWYHTCGGSLIANSWVLTAHCI
SSSRTYRVGLGRHNLYVAESGLAVSVSKIIVVHKDWNSNQISKGN DIAL LKLANPVSLTDKIQLACLPPAGTILP
NNYPCYVTGWGRLQTNGAVPDVLQQGRLLVVDYATCSSAWWGSSVKTSMICAGGDGVISSCNGDSGGPLNCQAS
DGRWQVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDWINSVIANN

WO 2004/030615

PCT/US2003/028547

65/6881
FIGURE 62

CGGACGCGTGGGCCCCGGCCAAGGCGAGTGCCGCGCGGGCCACCATGGCCACGGACGAGCTGGCCACCAAGCTGAG
CCGGCGGCTGCAGATGGAGGGCGAGGGCGGCGGAGACCCCGGAGCAGCCCGGGCTGAACGGGGCAGCGGCGGC
GGCGGCGGGGGCACCCGACGAGGCGGCGGAGGCGCTGGGCAGCGCGGACTGCGAGCTGAGCGCCAAGCTGCTGCG
GCGCGCAGACCTCAACCAGGGCATCGGCGAGCCCCAGTCGCCAGCCGCGCGTCTTCAACCCCTACACCGAGTT
CAAGGAGTTCTCCAGGAAGCAGATCAAGGACATGGAGAAGATGTTCAAGCAGTATGATGCCGGGCGGGACGGCTT
CATCGACCTGATGGAGCTAAACTCATGATGGAGAACTTGGGGCCCCCTCAGACCCACCTGGGCCTGAAAAACAT
GATCAAGGAGGTGGATGAGGACTTTGACAGCAAGCTGAGCTTCCGGGAGTTCTCTCTGATCTTCCGCAAGGCGGC
GGCCGGGGAGCTTCAGGAGGACAGCGGGCTGTGCGTGCTGGCCCGCCTCTCTGAGATCGACGTCTCCAGTGAGGG
TGTC AAGGGGGCCAAGAGCTTCTTTGAGGCCAAGGTCCAGGCCATCAACGTGTCCAGCCGCTTCGAGGAGGAGAT
CAAGGCAGAGCAGGAGGAAAGGAAGAAGCAGGCGGAGGAGATGAAGCAGCGGAAAGCGGCCCTTCAAGGAGCTGCA
GTCCACCTTTAAGTAGCGGGGGCTGCAGCCGACCGCCCTGCTCCGGCCCCAGTGTGGTGGGCGAGGGTGGCGCAT
GGGAGGCGGAGCCTGAATCCTTGCTGTGTCTGACGGGACCCTACTAAAAACCTAAAAATATCTGTGAATGGAG
CAAGTTTCAGGGGTCTTATGGAGGTGGCCCGGCCCTCCCGCTCCCTTCCACTCTGCACGAGGCCGCCACACCGG
CGCTGGCTCCCTGCCCGGCCCGGCCCTCCCTGGCAATCCCTGGGCTCTCTTGCACCCCTAACTGCCCCCTGCCTG
CTCCGGCACTGCCCCAGGCCAGCTCCTGGCCCTAGGTCCCTCCCAGCCCCATGTGCTGCCGCTGCCCTCCAC
ACATCCCTGTCCCCCAACCCGGAACCCCTGCCCTCCTCCAGCAGGCCGCACCGCCCCCTGGGGCCCCCTGCCAG
CCCCCTTCCCAGGCTGGGAGACAGCAGAAGAGATAGAATCAGGGCTGCCCCACAGAGTGGGACCCAAGGGGCTAA
TTGGAGGCACGAGGGGACCCCTCCCCAGGGCCTTTTCTCTCTGCGTCTTCCATCTACTGAAATGGGAGAGGGG
GTGGGGAGCTTCTGTTCTGGTGAAGGGACCCGGGAGGCCCCAGCACCCCATGCTGACTTGGAGAACCCAGAT
CTCTGGGGCCCAGCCAGGCAGGGTGTGGGGGCGAGCTGTGCCAATCTACCTCACAGGCCCAACCCCTGCCGGGCAT
GCCGTGGGATCATGGGCAGGGAAGGCTCTGGGGGTCGGAGACACCGCTGCTTAGCACCCCCAGCCAGAACACCCCT
GAGGGTCTCGGGGCTCTGGAGAGAGTGGGGCGGGAGGAAGAATTGGCACCTTCTAGGGAAGGAGACGAGCGCTT
CGCCTTGATTCTCCGAGAAGCCTCCGAGAAGTGCTTTAAGTGTGTTTGCAATGCGCCAGGCGGTGGGCAGCGGGG
CCTGTCCAGCCCTCTCCCGCCATCCTTCCCCAAGTGACGTCCACTGCCCTTGTACACGCGACCTGCCTGTCTATGC
CCACCCCTGAGGAAGCATGGGGACCTAACACCCCTGGTGCCCTGCACCAGACAGGCCGTGGTCAGGCCCAGGCC
ACCGGCCGGGTCTGCCACAGCTTCCCACGTGCTTGCTGACATGCGTGTGCTGTGTGGTGTCTGTGTGCTGTG
TCGTGAACTGTGACCATCACTCAGTCCAAACAAGTGAGTGGCCCTCGAGGCCACAGTTATGCAACTTTCAGTGT
GTGTGATAACGACGTCACTGCTTTTTAACTCGATAACTCTTTATTTTAGTAAATGCCCAGGAGTCTTGGAAGC
TACGCGGACTTGCAGAGGTTTTATTTTTTGGCCTTAGAATCTGCAGAAATTAGGAGGCACCGAGCCCAGCGCAGC
AGCCTCGGACCCGATTGCGTTTGCCTTAGCGGATATGTTTATACAGATGAATATAAAATGTTTTTTCTTTGGG
AAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

66/6881
FIGURE 63

MATDELATKLSRRLQMEGEGGGETPEQPGLNGAAAAAAGAPDEAAEALGSADCELSAKLLRRADLNQGIGEPQSP
SRRVFNPYTEFKEFSRKQIKDMEKMFKQYDAGRDFIDLMELKLMMEKLGAPQTHLGLKNMIKEVDEDFDSKLSF
REFLLIFRCAAAGELQEDSGLCVLARLSEIDVSSEGVKGAKSFFEAKVQAINVSSRFEIEIKAEQEERKKQAEEM
KQRKA AFKELQSTFK

WO 2004/030615

PCT/US2003/028547

67/6881
FIGURE 64

GCCTCCCACTTGGTTGCTCGTACGCGGCTAGTGGGTCTCAGTGGATGTAGGCTGGGCGCCGCGATGTTGACGG
GACACCGGCGGAGAGCGACCTCGGGGTTAAGGGGTGGGGCTGACGTCAGGAGCCAAGATGGCGGCGGTGGTCGCC
CTCTCCTTGAGGCGCCGGTTGCCGGCCACAACCTTGCGGAGCCTGCCTGCAGGCCTCCCGAGGAGCCCAGACA
GCTGCAGCCACAGCTCCCCGTATCAAGAAATTTGCCATCTATCGATGGGACCCAGACAAGGCTGGAGACAAACCT
CATATGCAGACTTATGAAGTTGACCTTAATAAATGTGGCCCCATGGTATTGGATGCTTTAATCAAGATTAAGAAT
GAAGTTGACTCTACTTTGACCTTCCGAAGATCATGCAGAGAAGGCATCTGTGGCTCTTGTGCAATGAACATCAAT
GGAGGCAACACTCTAGCTTGACCCGAAGGATTGACACCAACCTCAATAAGGTCTCAAAAATCTACCCTCTTCCA
CACATGTATGTGATAAAGGATCTTGTTCCTGATTGAGCAACTTCTATGCACAGTACAAATCCATTGAGCCTTAT
TTGAAGAAGAAGGATGAATCTCAGGAAGGCAAGCAGCAGTATCTGCAGTCCATAGAAGAGCGTGAGAACTGGAC
GGGCTCTACGAGTGCATTCTCTGTGCTGTAGCACCAGCTGCCCCAGCTACTGGTGGAACGGAGACAAATAT
CTGGGGCCTGCAGTTCTTATGCAGGCCTATCGCTGGATGATTGACTCCAGAGATGACTTCACAGAGGAGCGCCTG
GCCAAGCTGCAGGACCCATTCTCTATACCGCTGCCACACCATCATGAACTGCACAAGGACCTGTCCTAAGGGT
CTGAATCCAGGGAAGCTATTGCAGAGATCAAGAAAATGATGGCAACCTATAAGGAGAAGAAAGCTTCAGTTTAA
CTGTTTCCATGCTAAACATGATTTATAACCAGCTCAGAGCTGAACATAATTTATATCTAATTTGAGTTTCCTTTAA
AGATCTTGGTTTTCCATGAATACAGCATGTATAATAAAAATTTTAAGAAATAAATGTTATTCTACTTTATTAAACA
AAAAA

WO 2004/030615

PCT/US2003/028547

68/6881
FIGURE 65

MAAVVALSLRRRLPATTLGGAQLQASRGATAAATAPRIKKFAIYRWDPDKAGDKPHMQTYEVDLNKCGPMVLDA
LIKIKNEVDSTLTFRRSCREGICGSCAMNINGNTLACTRRIDTNLNKVSKEYPLPHMYVIKDLVPDLSNFYAQY
KSIEPYLKKKDESGEGKQYQLQSIEREKLDGLYECILCACCSTSCPSYWWNGDKYLGPAVLMQAYRWMIDSRDD
FTEERLAKLQDPFSLYRCHTIMNCTRTCPKGLNPGKAIAEIKMMATYKEKKASV

WO 2004/030615

PCT/US2003/028547

69/6881
FIGURE 66

AGTGTGGGGTTGGCGGCCACAGCTAAGTCCAACACCAGCATGTCGCTGCAGAGAATCGTGCGTGTGTCCCTGGA
GCATCCCACCAGCGCGGTGTGTGTGGCTGGCGTGGAGACCCCTCGTGGACATTTATGGGTGAGTGCCTGAGGGCAC
AGAAATGTTTGAGGTCTATGGGACGCCTGGCGTGGACATCTACATCTCTCCCAACATGGAGAGGGGGCCGGGAGCG
TGCAGACACCAGGCGGTGGCGCTTTGACGCGACTTTGGAGATCATCGTGGTCATGAACTCCCCCAGCAATGACCT
CAACGACAGCCATGTTTACAGATTTCTTACCCTCCAGCCATGAGCCTCTGCCCCCTGGCCTATGCGGTGCTCTACCT
CACCTGTGTGACATCTCTCTGGATTGCGACCTGAACTGTGAGGGAAGGCAGGACAGGAACCTTTGTAGACAAGCG
GCAGTGGGTCTGGGGGCCAGTGGGTATGGCGGCATCTTGCTGGTGAAGTGTGACCGTGATGATCCGAGCTGTGA
TGTCCAGGACAATTGTGACCAGCACGTGCACTGCCGCAAGACCTGGAAGACATGTCTGTCTATGGTCCCTGCGGAC
GCAGGGCCCTGCAGCCCTCTTTGATGACCACAACTTGTCTCCATACCTCCAGCTATGATGCCAAACGGGCACA
GGTCTTCCACATCTGCGGTCTGAGGATGTGTGTGAGGCCATAGGCATGTGCTGGGCCAAGATAAGGTGTCTTA
TGAGGTACCCCGCTTGATGGGGATGAGGAGCGCTTCTCGTGGAAAGGCCTGTCTTCCCTGATGCCGGCTTCAC
AGGACTCATCTCTTCCATGTCACTCTGCTGGACGACTCCAACGAGGATTTCTCGGCATCCCTATCTTCACTGA
CACTGTGGTGTTCAGTGGCACCCCTGGATCATGACGCCAGCACTCTGCCACCCCTAGAGGTGTATGTGTGCCG
TGTGAGGAACAACAGTGTGTTTGTGGATGCGGTGGCAGAGCTGGCCAGGAAGGCCGGCTGCAAGCTGACCATCTG
CCCACAGGCCGAGAACCAGAACGACCGCTGGATCCAGGATGAGATGGAGCTGGGCTACGTTTACGGCGCCGACAA
GACCTTCCCGGTGGTCTTTGACTCCCCAAGGAATGGGGAAGTGCAGGATTTCCCTTACAAAAGAATCCTGGGTCC
AGATTTTGGTTACGTGACTCGGGAACCACGCGACAGGTCTGTGAGTGGCCTGGACTCCTTTGGGAACCTGGAGGT
CAGCCCTCCAGTGGTGGCCAATGGGAAAGAGTACCCCTGGGGAGGATCCTCATTGGGGGCAACCTGCCTGGGT
AAGTGGCCGAGGGTACCCAGGTGGTGGGGACTTCTCCATGCCAGAGGTGCAGCCCCCGTGGAGCTCTT
TGTGGACTGGTTGGCCGTGGGCCATGTGGATGAGTTTCTGAGCTTTGTCCCTGCCCCCGATGGGAAGGGCTTCG
GATGCTCCTGGCCAGCCCTGGGGCTGCTTCAAGCTCTTCCAGGAAAAGCAGAAGTGTGGCCACGGGAGGGCCCT
CCTGTTCCAGGGGGTTGTTGATGATGAGCAGGTCAAGACCATCTCCATCAACCAGGTGCTCTCCAATAAAGACCT
CATCAACTACAATAAGTTTGTGAGAGTGCATCGACTGGAACCGTGAGGTGCTGAAGCGGAGCTGGGCTGGC
AGAGTGTGACATCATTGACATCCACAGCTCTTCAAGACCGAGAGGAAAAAGCAACGGCCTTCTTCCCTGACTT
GGTGAACATGCTGGTGTGGGGAAGCACCTGGGCATCCCAAGCCCTTTGGGCCCATCATCAATGGCTGTCTGTG
CCTGGAGGAGAAGGTGCGGTCCCTGTGAGCCGCTGGGCCTCCACTGCACCTTCATTGATGACTTCACTCCATA
CCACATGCTGCATGGGAGGTGCACTGTGGCACCAATGTGTGCAGAAAGCCCTTCTCTTTCAAGTGGTGGAAAT
GGTGCCCTGAGACAGTCCCACCCACCATCTGTCCCCCTGGGGCGGGCATTGGCCAGGTGGTGGAGACAGAGA
CAGGCCCTGAACGATAAGCACCAAGAGACCCCAAGGCTCCAGATGGAACACTGAGGGTGACCGTCCCTCTCAGA
AGCCTTTTCCCTGGAAGTGTCCATGCCTCACCTGCAACCCATGTGGTTCTCAGACTTGAATCTTCTCGGCCCCC
AAAAAGAAGGACCTCATTCTTATAGCCTCTCCTGTGATTCAACACAACCCATGGAGATGTCCCCTTCTCACTCT
GAAATCATCCATTTGGGGACAAATCCACATTGGGGTCTAGAAACATCCACGTATCTCATCAGCCATCTTGTCTG
TGCATCCTAACAGAGGAAGGATCCATGATTCTGCTTTGGTCCAATTGCTTCTCTCTGCAGAGGAACAACCCATA
AACCAGACCACTCCACGCAGGACAGGCAGGAGAGATTCTTCTAAAGCCTCCCCCATAAAAAGGGAGCTGTGGAT
CCACTTAGATCAGGGCGGAACCATCTTTCACCCGGCCAAGCTCCTGCCAGATGTTGACCCTCACCCAGCGTGAG
CTGTACATAGTAGGAGCTTCTAGATGCATGTGGAAGCAATGAGAGTTGTCCCTTAGCCTTATAAACTCCCCATG
ATCTGACATGCAGAAATCCAGCCTTGTCCAGAATCTCCTGGAATTTCTTGGAGACGAAAGTATCTGGGGGATTG
TTGGGTACTAGGGAGACTGGGTACAAGGGTGAAAAGTAGTTCCCATATAACACATGGTTGACTATGGTGATCCAC
CTTGTGATGGTTAATATTAGGTGCTGAGAAAGGTGCTTCAATTGGCCCTGGGACTTCTCTCTGCAGGAGGAGAG
AACGCTGCCTCTCCTCTGGATTGGTCTCAGGCTCTCTGTTGGCCTTTGGTCAGCGTTTCCACATCCTGCTCTGCT
GCAGGAGAGGGGGCTAAGGGGCTGGATCCACCAAGGCAGCTCACAGCGGGAAGCTCTGGGAATGAACCACTGAA
TTCAGGGGATGGGGGTGGGGGGCGGTTCTCGAGGTGTGTGCCAGCTACACGTGTGTTCTGTATGGGTCCAGCTG
CGTTTCCATCACTCGCTAATAAATCAACAGAAACAC

WO 2004/030615

PCT/US2003/028547

70/6881
FIGURE 67

AGCCAGAGGGACGAGCTAGCCCGACGATGGCCCAGGGGACATTGATCCGTGTGACCCCAGAGCAGCCCACCCATG
CCGTGTGTGTGCTGGGCACCTTGACTCAGCTTGACATCTGCAGCTCTGCCCCTGAGGACTGCACGTCTTCAGCA
TCAACGCCTCCCCAGGGGTGGTCGTGGATATTGCCACGGCCCTCCAGCCAAGAAGAAATCCACAGGTTCTCCCA
CATGGCCCCCTGGACCCCTGGGGTAGAGGTGACCCTGACGATGAAAGTGGCCAGTGGTAGCACAGGCGACCAGAAGG
TTCAGATTTTCATACTACGGACCCAAGACTCCACCAGTCAAAGCTCTACTCTACCTCACCGGGGTGGAAATCTCCC
TGTGCGCAGACATCACCCGCACCGGCAAAGTGAAGCCAACCAGAGCTGTGAAAGATCAGAGGACCTGGACCTGGG
GCCCTTGTGGACAGGGGTGCCATCCTGCTGGTGAAGTGTGACAGAGACAATCTCGAATCTTCTGCCATGGACTGCG
AGGATGATGAAGTGCTTGACAGCGAAGACCTGCAGGACATGTGCGTGATGACCCCTGAGCACGAAGACCCCCAAGG
ACTTCTTCACAAACCATACTACTGGTGCTCCACGTGGCCAGGTCTGAGATGGACAAAGTGAGGGTGTTCAGGCCA
CACGGGGCAAAGTGTCTCTCAAGTGCAGCGTAGTCTTGGGTCCCAAGTGGCCCTCTCACTACCTGATGGTCCCCG
GTGGAAAGCACAAATGGAAGTCTTACGTGGAGGCCCTCGCTTTCCCGGACACCGACTTCCCGGGGGCTCATTACCC
TCACCATCTCCCTGCTGGACACGTTCAACCTGGAGCTCCCCGAGGCTGTGGTGTTCGAAGACAGCGTGGTCTTCC
GCGTGGCGCCCTGGATCATGACCCCCAACACCCAGCCCCCGCAGGAGGTGTACGCGTGCAGTATTTTTGAAAATG
AGGACTTCTGAAAGTCAGTGACTACTCTGGCCATGAAAGCCAAGTGCAAGCTGACCATCTGCCCTGAGGAGGAGA
ACATGGATGACCAGTGGATGCAGGATGAAATGGAGATCGGCTACATCCAAGCCCCACACAAAACGTGCCCCGTTG
TCTTCGACTCTCCAAGGAACAGAGGCCTGAAGGAGTTTCCCATCAAACGCGTGATGGGTCCAGATTTTGGCTATG
TAACTCGAGGGCCCCAAACAGGGGGTATCAGTGGACTGGACTCCTTTGGGAACCTGGAAGTGAGCCCCCAGTCA
CAGTCAGGGGCAAGGAATACCCGCTGGGCAGGATTCTCTTCGGGGACAGCTGTTATCCCAGCAATGACAGCCGGC
AGATGCACCAGGCCCTGCAGGACTTCTCAGTGCCAGCAGGTGCAGGCCCCCTGTGAAGCTCTATTCTGACTGGC
TGTCCGTGGGCCACGTGGACGAGTTCTTGAGCTTTGTGCCAGCACCCGACAGGAAGGGCTTCCGGCTGCTCCTGG
CCAGCCCCAGGTCTCTGCTACAAACTGTTCCAGGAGCAGCAGAATGAGGGCCACGGGGAGGCCCTGCTGTTCAAG
GGATCAAGAAAAAAAAACAGCAGAAAATAAAGAACATTCTGTCAAACAAGACATTGAGAGAACATAATTCATTG
TGGAGAGATGCATCGACTGGAACCGCGAGCTGCTGAAGCGGGAGCTGGGCCTGGCCGAGAGTGACATCATTGACA
TCCCGCAGCTCTTCAAGCTCAAAGAGTTCTCTAAGGCGGAAGCTTTTTTCCCAACATGGTGAACATGCTGGTGC
TAGGGAAGCACCTGGGCATCCCCAAGCCCTTCGGGCCCGTCATCAACGGCCGCTGCTGCCCTGGAGGAGAAGGTGT
GTTCCCTGCTGGAGCCACTGGGCCTCCAGTGACCTTCATCAACGACTTCTTCACCTACCACATCAGGCATGGGG
AGGTGCACTGCGGCACCAACGTGCGCAGAAAGCCCTTCTCCTTCAAGTGGTGGAACATGGTGCCCTGAGCCCATC
TTCCCTGGCGTCTCTCCTCCTGGCCAGATGTCGCTGGGTCTCTGCAAGTGTGGCAAGCAAGAGCTCTTGTGAA
TATTGTGGCTCCCTGGGGGCGGCCAGCCCTCCCAGCAGTGGCTTGCTTTCTTCTCCTGTGATGTCCAGTTTCCC
ACTCTGAAGATCCCAACATGGTCCTAGCACTGCACACTCAGTTCTGCTCTAAGAAGCTGCAATAAAGTTTTTTTA
AGTCACCTTGTAC

WO 2004/030615

PCT/US2003/028547

71/6881
FIGURE 68A

GGAAGCTCGTATTTACATTTTAAGTGTATCTGGTGAGTGGGCTGGAGCCCTCGTCTGGGCCGGAAAAAAAAGC
CCTCCGATCCGTCCTTTAGTTGCTTCTCTTCTTTTTTCTCTCCGGTTTCTCATCACTCCAACCAGCCGCGACCA
TGCCCAGGAAGAAGCGCGCGCGCGCGGCTGGGAGGAGCCGAGCTCGGGCAACGGCACTGCCCGCGCGGGGCCA
GGAAACGCGCGCGCCCCGGCGGGCAGGAAGCGCGAGCGGCCCCGAGCGCTGCAGTAGCAGCAGCGGCGGGCAGCA
GCGGCGACGAGGACGGCCTGGAGCTCGACGGGGCCCCCGCGGGGGCAAGCGCGCGGCGCGGCGGCGACAGCAG
GCAAGGCGGGCGCGCGCGCCGTGGTCATCACCGAACCCGAGCACACCAAGGAGCGCGTCAAACCTGAAGGGTCAA
AGTGCAAAGGGCAGCTTTTGATTTTTGGGGCAACCAACTGGGACTTGATTGGTCGAAAAGAAGTGCCTAAACAGC
AAGCTGCTTACCGCAATCTCGGTGAGAAATTTGTGGGGGCCCCACAGATATGGGTGCCTGGCGGGGTCCGGGTGC
GGACAGTGGTCTCGGGCTCGTGTGCTGCACACAGCCTCCTCATCACCGGAAGGGAAGCTGTGGAGCTGGGGTC
GAAATGAGAAGGGGCGAGCTGGGACATGGTGACACCAAGAGAGTAGAAGCCCCCTAGACTCATCGAGGGTCTTAGCC
ACGAAGTGATTGTGTCTGCAGCATGTGGGCGGAACACACCTTGGCCTTGACGGAACGGGCTCCGTGTTTTCGT
TTGGGGAAAAACAAGATGGGGCAGCTGGGCCTTGGCAACCAGACAGACGCTGTTCCAGCCCCGCGCAGATAATGT
ACAACGGCCAGCCAATTACCAAAATGGCCTGTGGGGCTGAATTCAGTATGATAATGGACTGCAAAGGAAACCTCT
ATTCTTTGGGTGCCCTGAATATGGTCAGCTGGGACACAACCTCAGATGGGAAGTTCATCGCCCGGGCACAGCGGA
TAGAGTACGACTGTGAAGTAGTTCCCCCGCGAGTGGCCATCTTCATTGAGAAGACGAAAGATGGACAGATTCTGC
CTGTACCAACGTGGTTGTACGAGACGTGGCCTGTGGCGCTAACCACACGCTGGTCTGGACTCCAGAAAGCGAG
TCTTCTCTGGGGCTTTGGTGGCTATGGCCGGCTGGGCCACGCAGAGCAGAAGGATGAGATGGTCCCCCGCCTGG
TGAAGCTGTTTGAATTCCTGGGCGTGGGGCTTCCCAGATCTATGCTGGTTACACCTGCTCCTTTGCTGTCACTG
AAGTGGGTGGTCTGTTTTCTGGGGGGCCACCAACACCTCCCGTGAATCTACCATGTACCCAAAAGAGCTGCAGG
ACCTCTGCGGCTGGAGAATTCGGAGCCTGGCTTGTGGGAAGAGCAGCATCATTGTGGCCCGCATGAGAGCACCA
TCAGCTGGGGTCCGTCACCGACCTTTGGGGAACCTGGGCTACGGGGACCACAAGCCCAAGTCTTCCACTGCAGCCC
AGGAGGTAAAGACTCTGGATGGCATTCTCAGAGCAGGTGCGCCACTGGGCTACTCACACTCCTTGGTGATAGCAA
GAGATGAAAGTGAGACTGAGAAAGAGAAGATCAAGAACTGCCAGAATACAACCCCCGAACCTCTGATGCTCCC
GGAGACTCCTCCGACTCCACACCTCTCGCGGCAGCTGTCAATTTCCATGTGCACTGGGACGGGAAGTCAAACGAGG
AATTTAAAAAAGCAAAAGTTGACCGAAGGTGCATTTTGTTTAGACTCCCTGAGGTTCCGTTTTACACATGATCC
AACGTTAACTACCTTTTTTCTGTATGCTTTCCAAAGTCTTTTTTCCCTTAATGTTGAATTAATACTTGC
TCATAGTTGATTTACCATTCCTACAAAAGAGGCAGAAACTTTAGCAATCTAGGTTTTTTTTTTTTTTAAGTTTT
TTCTTTCTTCTTCTGAATACACTCCCCAAACACCCCTTTCCAGTTACAATTAGCATCGTGATCCAAGCAGA
TGCCACATGGAAGAGGAATCGCCATTTACTCAGAAAAAATGTCCCTTACAGGAACCGGCAGCAGCTAGGCAGTCA
CCGCCCCGCTCCATCCAAATCAGCTCGCGTGCTTCGGAAGCATCCGGGTCACTCCTTCTCGCTTTTTCTTG
CAGATGGGCCTAGGCGGCTGTGCTTCTGTTTCTCCCTTGGCTGCCTGTACGCCACAGCCTTCTGGCTGCGAC
ATTATAGAATCGGCCGTGTCCCCCTGGTGGGGGATTGGGGATCTGTGTTTAGCCATTTATATCTACTTTAGCTG
TTAAAGAGGTCCAAATGAAAATCAGGTGATTGTGGAACCATGGGGACTTGGGGGTGGGGCAGAGGTGGGAACATT
TGATCAGTTGAGTCAGCTTGGTGGCTCCCTGTGGAGCCAGGGCTGAGCCTTGTACGCGCACTCGCCAATTAAG
AGATGGACCAGCCAGCAGTCAAGTGCACTTCCAGTCTTGAAGAAGGATCAGCCCTTTCTGTGCCAGCCTCGA
TCGCCTTGTGCTTTGGTCTCTTTTTCTCCCCCCCCGCTGGATCCTGCCTCGCGCGGGCGCTCCTGTTGCTGAGAC
TCGGGGTACCGTTCTGCTGACCCAGCTCCCTTTAGTCACGTTTGCTTGGCTCTGGTACCAATAGTTGGGATTAC
CGAAGAGTCCCCCTTCTTGCCTGTGAGCAGGATGCTGTGACTGCCACCTGCGTCTCTCAAGTGCCCGAGCTC
GCCGCCGTGTGTGCTGCGCTGAGTGAGTTATGAGGTGCCTTTCCCGGAACCTCCTCTCGCTGGACCCAAGAGA
GGCGACAGCTGTGGCTGGGGCTCTTGGTTTCCAGAGGGTCTGGACTGGTTTGGGTGCTTTAAATAGATATTTAG
TTCAGTGGTGCTTATGGGGGAGATGGGACTAGAACTTAAGTGTGAGACTTGGGTGGATGGGAAAGTTAAATATTG
GTCTCTTCAAGTTTTTTTTTTCTTTTGTGTTTGTACCACTTGTCACTGTCTCCATGTTAAATGCCAAAATGAT
GTAGTTGTTGTTGCTTTTTTCCCTATTTTCCACCCAGTCGCTCCTTACCGTGACTCCTGCCCTTGGAGGGCATG
TAGCAGTGTCTGTCTGCCAGTCCCAAGGCCCTGTGGGAGGAGACTGGCCTGCATCTCTTAAGACTTAGTCTGA
CGCCACGCGCATCTCTGTTCTGTGTTCAATCAGTAGTCCAGGGGAGAAGCTTCTGCTACTTCAGAGCTTTGCTA
AACTAACCTAATTTGTCCAAATCACCCAAAACCACCATCTCTGACGTAAGCTTCCATGCGACAGCCTGATCCGT
TTCCCTGGACAGGTCTCTTCTGGAATGCAGCCAGGCACCTGTGCTCCTGGCACCTTGGAGTCTCTTCTTG
AGCCGTGGTCACCGAGAGGGTTGAGGACGCAGCACCCGAGGTCCAGCCTTTGCAGGAGCCTCCCTGGGCTTAGC

WO 2004/030615

PCT/US2003/028547

72/6881
FIGURE 68B

TGGACTTAGATCTTCGGTGGCCTCATGTAAACGTGGCAGCCAGCCTCTTCTAGAACCCTAGCCCAGGGACTGGAG
CAGGAAAGGGACCTTCAAAGTGAAGACTGCCTTGTCCCGCAGCTCCTTCTGGCTTAGATTGAAACATGGGCTTCC
TAATGGGTAAATCCTTTAAACAAGGAGTTGTGGGGGAAGGGTGTCGTGCACTCCTAGAGAAAGGTACACAGTT
GCCCCGTTGGGAATGTGCTTGGCGCTGACCCTGCGGGCATCTGACTGGTCTTCCAGCTCAGGAAAAAGAAATTTGA
AAGAGGCTTAGCGTGAAGGGGAATCAAAGAGGAGGTTGTGATTGGTTCGAAGGTGCCTGGTTTAGTGCTGTAATT
GTCTTATTATTTTTTTTATATATATATTTCTTGGAGTAAACATTTTAAAT

WO 2004/030615

PCT/US2003/028547

73/6881
FIGURE 69

ATGAGTGATCAGCAGCTGGACTGTGCCTTGGACCTAATGAGGCGCCTGCCTCCCCAGCAAATCGAGAAAAACCTC
AGCGACCTGATCGACCTGGTCCCCAGTCTATGTGAGGATCTCCTGTCTTCTGTTGACCAGCCACTGAAAATTGCC
AGAGACAAGGTGGTGGGAAAGGATTACCTTTTGTGTGACTACAACAGAGATGGGGACTCCTATAGGTCACCATGG
AGTAACAAGTATGACCCTCCCTTGGAGGATGGGGCCATGCCGTGAGCTCGGCTGAGAAAGCTGGAGGTGGAAGCC
AACAATGCCTTTGACCAGTATCGAGACCTGTATTTTGAAGGTGGCGTCTCATCTGTCTACCTCTGGGATCTGGAT
CATGGCTTTGCTGGAGTGATCCTCATAAAGAAGGCTGGAGATGGATCAAAGAAGATCAAAGGCTGCTGGGATTCC
ATCCACGTGGTAGAAGTGCAGGAGAAATCCAGCGGTGCGACCGCCATTACAAGTTGACCTCCACGGTGATGCTG
TGGCTGCAGACCAACAAATCTGGCTCTGGCACCATGAACCTCGGAGGCAGCCTTACCAGACAGATGGAGAAGGAT
GAAACTGTGAGTGACTGCTCCCCACACATAGCCAACATCGGGCGCCTGGTAGAGGACATGGAAAATAAAATCAGA
AGTACGCTGAACGAGATCTACTTTGGAAAAACAAAGGATATCGTCAATGGGCTGAGGTCTGTGCAGACTTTTGCA
GACAAATCAAAACAAGAAGCTCTGAAGAATGACCTGGTGGAGGCTTTGAAGAGAAAGCAGCAATGCTTAAACCTCT
GTTTCATGCTAACCAGACACGCCGTGCACTCGTTAGATTCTTTCTTAGAAAACTCGTTTTCTGCTCCCTTCCCT
CGTCCCTTCCCTCCCCGACAGGTCACATAACAGCTGCATCATTGACCGCACAGCGCCATCTCTCCCTGAGAATAA
AGCCGATAGCCACCTCCTCCGGCTCCGAGCCTGCTTCTGCCACACCTCGCTCTCAGTCTCTCCACATTTCCATAG
AGACCGTGTGGTTTTTGTTCACCCGGG

WO 2004/030615

PCT/US2003/028547

74/6881
FIGURE 70

MSDQQLDCA LDLMRRLPPQQIEKNLS DLIDLVP SLCEDLLSSVDQPLKIARDKVVGKDYLLCDYNRDGDSYRSPW
SNKYDPPLEDGAMP SARLRKLEVEANNAFDQYRDLYFEGGVSSVYLWDL DHGFAGVILIKKAGDGSKKIKGCWDS
IHVVEVQEKSSGRTAHYKLTSTV MLWLQTNKSGSGTMNLGGS LTRQMEKDETVSDCSPHIANIGRLVEDMENKIR
STLNEIYFGKTKDIVNGLRSVQTFADKSKQEALKNDLVEALKRKQQC

WO 2004/030615

PCT/US2003/028547

75/6881
FIGURE 71

CCGCGTCTCGCGTAGTCTCCCGCGCCGCGCTCCACTGCGCGCTTCGCTCTCCGCCGCCCGAGGCCCGCGCGCTCG
CCATGTCCCGGCCACCGCCACCGCGGGTCGCCTCGGTGCTGGGCACCATGGAGATGGGGCGCCGCATGGACGCGC
CCGCCAGCGCCGCGGCCGTGCGCGCCTTTCGGAGCGCGGCCACACCGAACTGGACACGGCCTTCATGTACAGCG
ACGGCCAGTCCGAGACCATCCTGGGCGGCCTGGGGCTCGGGCTGGGCGGTGGCGACTGCAGAGTGAAAATTGCCA
CCAAGGCCAACCCTTGGGATGGAAAATCACTAAAGCCTGACAGTGTCCGGTCCCAGCTGGAGACGTCATTGAAGA
GGCTGCAGTGTCCCCAAGTGGACCTCTTCTACCTACACACACCTGACCACGGCACCCCGGTGGAAGAGACGCTGC
ATGCCTGCCAGCGGCTGCACCAGGAGGGCAAGTTCGTGGAGCTTGGCCTCTCCAACCTATGCTAGCTGGGAAGTGG
CCGAGATCTGTACCCTCTGCAAGAGCAATGGCTGGATCCTGCCCCACTGTGTACCAGGGCATGTACAACGCCACCA
CCCGGCAGGTGGAACGGAGCTCTTCCCTGCCTCAGGCACTTTGGACTGAGGTTCTATGCCTACAACCCTCTGG
CTGGGGGCTGCTGACTGGCAAGTACAAGTATGAGGACAAGGACGGGAAACAGCCTGTGGGCCGCTTCTTTGGGA
ATAGCTGGGCTGAGACCTACAGGAATCGCTTCTGGAAGGAGCACCACTTCGAGGCCATTGCGTTGGTGGAGAAGG
CCCTGCAGGCCGCATATGGCGCCAGCGCCCCAGTGTGACCTCGGCTGCCCTCCGGTGGATGTACCACCACTCAC
AGCTGCAGGGTGCCACGGGGACGCGGTCATCCTGGGCATGTCCAGCCTGGAGCAGCTGGAGCAGAACTTGGCAG
CAACAGAGGAAGGGCCCCCTGGAGCCGGCTGTCGTGGATGCCTTTAATCAAGCCTGGCATTGTTGTTGCTCACGAAT
GTCCCAACTACTTCCGCTAGGCCCATCATGGCTCAGGCTGCCCAAGGCTTTTCTGTACCTCTTTGTTCTCTCA
CACTGACCAGTCTTGGCCTTAAGCTGACTTAGAAGGGTTTTCTGAATTGTCTAGATCCATGCATTATTTTCTA
GCTTCCTGCCTTGCTCCCTATTCACTTTACACTGTGAAAGGTGGGGGGTGAGTCCCACTTGAGCGCTTCCTGTTG
AATAAAGCAGGCACTTGACCTGGCTGTAGCCTAGGTCTTGAGTGAACCCCAAAAAA

WO 2004/030615

PCT/US2003/028547

76/6881
FIGURE 72

MSRPPPPRVASVLGTMEMGRRMDAPASAAVRAFLERGHTELDTAFMYSDGQSETILGGLGLGLGGGDCRVKIAT
KANPWDGKSLKPDsvRSQLETSKRLQCPQVDLFYLHTPDHGTPVEETLHACQRLHQEGKFVELGLSNIASWEVA
EICTLCKSNGWILPTVYQGMYNATTRQVETELFPCLRHFGLRFYAYNPLAGGLLTGKYKYEDKDQKQPVGRFFGN
SWAETYRNRFWKEHHFEAIALVEKALQAAYGASAPSVTSAALRWMYHHSQIQGAHGDAVILGMSSLEQLEQNLA
TEEGPLEPAVVDAFNQAWHLVAHECPNYFR

WO 2004/030615

PCT/US2003/028547

77/6881
FIGURE 73

ACCGTCTTCCGCCGCACGTGGATTGAGCGCGATGCCCAAATCCAAGCGCGACAAGAAAGTCTCCTTAACCAAAAC
TGCCAAGAAAGGCTTGGAATTGAAACAAAACCTGATAGAAGAGCTTCGGAAATGTGTGGACACCTACAAGTACCT
TTTCATCTTCTCTGTGGCCAACATGAGGAACAGCAAGCTGAAGGACATCCGGAACGCCTGGAAGCACAGCCGGAT
GTTCTTTGGCAAAAACAAGGTGATGATGGTGGCCTTGGGTTCGGAGCCCATCTGATGAATACAAAGACAACCTGCA
CCAGGTCAGCAAAAGGTTGAGGGGTGAGGTGGGTCTCCTGTTTACCAACCGCACAAAGGAAGAGGTGAATGAGTG
GTTACGAAATACACAGAAATGGACTACGCCCAGCTGGTAACAAAGCAGCTTTCACTGTGAGCCTGGATCCAGG
GCCCCGGAGCAGTTCCCCCACTCCATGGAGCCACAGCTCAGGCAGCTGGGCCTGCCACCGCCCTCAAGAGAGG
TGTGGTGACTCTGCTGTCTGACTACGAGGTGTGCAAGGAGGGCGATGTGCTGACCCCAGAGCAGGCTCGCGTCCT
GAAGCTTTTTGGGTATGAGATGGCTGAATTCAAGGTGACCATCAAATACATGTGGGATTACAGTCGGGAAGGTT
CCAGCAGATGGGAGACGACTTGCCAGAGAGCGCATCTGAGTCCACAGAAGAGTCAGACTCAGAAGATGATGACTG
AAAGGGACTCGGGACTGAAGGTCTCCTGGAAGCTTCTGGGTCTCACTGGACCATCAGGACTGCTGCCGCCCCCTCT
GGAGAGAGCAGCTTTTTATTTGTCTGTAGACAGGGAACATGATGGGCACTGACCTCCTGTAAAGAATAAACTGT
GGGCCGGGCGCGGTGGCTCACGCCTGGAATCCCAGCACTTTGGGAAGCCGAGGTGGGCAGATCATAAGGTCAGGA
GATTAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATAGAAAAAAAAGTGTGGGCATAG
TGGCATGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGAGGTTG
CCGTGAGTTGAGATTGGACCACTGCTCTCCAGCCTGGGCAACAGAGTAAACTCTGTCCC

WO 2004/030615

PCT/US2003/028547

78/6881

FIGURE 74

MPKSKRDKKVS LTKTAKKGLELKQNLIEELRKCVDTYKYL FIFSVANMRNSKLKDIRNAWKHSRMFFGKNKVMV
ALGRSPSDEYKDN LHQVSKRLRGEVGLLFTNRTKEEVNEWFTKYTEM DYARAGNKAFTVSLDPGP LEQFPHSME
PQLRQLGLPTALKRGVVTLLSDYEVCKEGDVLTP EQARVLKLFGYEMAEFKVTIKYMWDSQSGRFQQMGGDDL PES
ASESTEESDSEDD

WO 2004/030615

PCT/US2003/028547

79/6881
FIGURE 75

ATCGCTGGGCGACTGATTTTCGAGTTTCCGGTCAGGTTAGGCCGGGGGGGTGCGGTCTTGGTCGGAAGGAGGTGGA
GAGTCGGGGGTACACAGGCCTATCCTTGCGGCCACAGTCGGCCACCGGGGCTCGCCGCCGTATGGAGAGCGGAG
GGCGGCCCTCGCTGTGCCAGTTTCATCCTCCTGGGCACCACCTCTGTGGTCACCGCCGCCCTGTACTCCGTGTACC
GGCAGAAGGCCCGGGTCTCCCAAGAGCTCAAGGGAGCTAAAAAAGTTTCAATTTGGGTGAAGATTTAAAGAGTATTC
TTTCAGAAGCTCCAGGAAAATGCGTGCCTTATGCTGTTATAGAAGGAGCTGTGCGGTCTGTTAAAGAAACGCTTA
ACAGCCAGTTTGTGGAAGAACTGCAAGGGGGTAATTCAGCGGCTGACACTTCAGGAGCACAAAGATGGTGTGGAATC
GAACCAACCCACCTTTGGAATGATTGCTCAAAGATCATTTCATCAGAGGACCAACACAGTGCCCTTTGACCTGGTGC
CCCACGAGGATGGCGTGGATGTGGCTGTGCGAGTGCTGAAGCCCTGGACTCAGTGGATCTGGGTCTAGAGACTG
TGTATGAGAAGTTCCACCCCTCGATTTCAGTCCTTCACCGATGTCATCGGCCACTACATCAGCGGTGAGCGGCCCA
AAGGCATCCAAGAGACCGAGGAGATGCTGAAGGTGGGGGCCACCTCACAGGGGTGGCGAACTGGTCTTGGAACA
ACAATCTGTCCGCTGCAGCCGCCCAAACAAGGCATGCAGTACTATCTAAGCAGCCAGGACTTCGACAGCCTGC
TGCAGAGGCAGGAGTCGAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTTTTTGGCTTTGCCACATGTGCCACCC
TCTTCTTCATTCTCCGGAAGCAGTATCTGCAGCGGCAGGAGCGCCTGCGCCTCAAGCAGATGCAGGAGGAGTTCC
AGGAGCATGAGGCCAGCTGCTGAGCCGAGCCAAGCCTGAGGACAGGGAGAGTCTGAAGAGCGCCTGTGTAGTGT
GTCTGAGCAGCTTCAAGTCTGCGTCTTTCTGGAGTGTGGGCACGTTTGTTCCTGCACCGAGTGCTACCGCGCCT
TGCCAGAGCCCAAGAAGTGCCCTATCTGCAGACAGGCGATCACCCGGGTGATACCCCTGTACAACAGCTAATAGT
TTGGAAGCCGCACAGCTTGACCTGGAAGCACCCCTGCCCTTTTTCAGGGATTTTTATCTCGAGGCCCTTTGGAGG
AGCAGTGGTGGGGGTAGCTGTACCTCCAGGTATGATTGAGGGAGGAATTGGGTAGAACTCTCCAGACCCATGC
CTCCAATGGCAGGATGCTGCCTTTCCACCTGAGAGGGGACCCTGTCCATGTGCAGCCTCATCAGAGCCTCACCC
TGGGAGGATGCCGTGGCGTCTCCTCCCAGGAGCCAGATCAGTGCAGTGTGACTGAAAATGCCCTCATCACTTAAG
CACCAAAGCCAGTGATCAGCAGCTCTTCTGTTTCTGTGCTTCTGTTTTTTTCTGGTGAATCGTTGCTGTG
GACTTGGTGGAGGACTCAGAGGGGAGGAAAGGCTGGGCCCCGAGTACAACGGATGCCTTGGGTGCTGCCTCCGAA
GAGACTCTGCCGCAGCTTTTCTTCTTTTCTCCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATTGTCAGGCTGGG
CAGGTCAACTTGTGTTTCTTTTCCCTCACCTGCTTGCTTCTTAAACGCCTGCACGTGTGTGTAGAGGACAAAAGA
AAGTGAAGTCAGCACATCCGCTTCTGCCCAGATGGTTCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAA
GGGCAGTTGGTCAGGCAGGCCTCCTGGTTTCGCCACTGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGG
GGTGGTCCCTGGTTTTTCCCTCCTGGAGAATGAGGCGCAGAGGCCTCGCCTCCTGAAGGACGCAGTGTGGATGCCA
CTGGCCTAGTGTCTTGGCCTCACAGCTTCCTTGCAAGGCTGTCAAGGAAAAGCAGCCGGCTGGCACCTGAGC
ATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCGCAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCCTT
GTGTTACCCCTCCCAGTATTACCATTTGCCCTCACCTGCCCTTGGTGAGCCTTTTAGTGCAAGACAGATGGGG
CTGTTTTCCCCACCTCTGAGTAGTTGGAGGTCACATACAGCTCTTTTTTTATTGCCCTTTTCTGCCTCTGAA
TGTTTCATCTCTCGTCCTCCTTTGTGCAGGCGAGGAAGGGTGCCCTCAGGGGCCGACACTAGTATGATGCAGTGT
CCAGTGTGAACAGCAGAAATTAAACATGTTGCAACC

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

81/6881

FIGURE 76B

TTTGTATTTGTTTTAGTATTGTGAAGTTGTGTTAAATAGTACTAGCTAGAAATACAAATTTCTGGTTATCATTTT
TCTTCCCTGTGGCACTTGACATTTTAATTGCTTAAAGTTTTTGAAGTACATCTTCTGGCCCCCTTGAGTACTGCC
AGAGGCAAAAGATGTTTGTTCCTTATTCCACTTTTGTCTCCTGGGATCCCTTCTGTAGCCTAAAGTATGGC
TGGGAAATGGACTTGAGAAGATTGGCTTGAATTAGATCATAATCATGTGTGATCCCATCATGAATTCATTGGAAT
TTGTGTTGCATGTAAGGCAATCTTTCCTGTTGTAAATCTTCCTTTTTTAATGTACATATATTTTGAAAAATATGA
ATAAACATGAAATTTT

WO 2004/030615

PCT/US2003/028547

82/6881
FIGURE 77

GGCGCCGAGTAGCCGGGCGGGCCGGAGCGCGGGCGGGCGGGAGGCAGCTGCGCCCCGCGCCTCCTGCCCTCCCA
GGCCCCGCGCCCCGCGCCCCGGGCCCCGGCGATGGTGACACATGCGGCGGGCGGCGGCCAGCGGCAGGACCATGGT
TGAGCGCGCCAGCAAGTTTCGTGCTGGTGGTGGCGGGCCCCGGTGTGCTTCATGCTCATCTTGTACCAGTACGCGGG
CCCAGGACTGAGCCTGGGCGCGCCCCGGGCGGGCGCGCCGCCGACGACCTGGACCTGTTCCCCACGCCCCGACCC
CCACTACGAGAAGAAGCACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGCTTCGACATGAAGGGCGACGA
CGTGATCGTCTTCTGACATCCAGAAGACGGGCGGCACCACCTTCGGCCGCCACCTCGTGCAGAACGTACGCCT
CGAGGTGCCGTGCGACTGCCGGCCCCGGCCAGAAGAAGTGACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCT
CTTCTCCCGCTTCTCCACCGGCTGGAGCTGCGGGCTGCGCGCCGACTGGACCGAGCTCACCAACTGCGTGCCCCG
CGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCAGGAAGTTCTACTACATCACCTGCTACGAGACCC
CGTGTCCTCGCTACCTGAGCGAGTGGCGGCATGTGCAGAGGGGTGCCACGTGGAAGACGTGCTTGACATGTGTGA
TGGGCGCACGCCACGCCTGAGGGGCTGCCGCCCTGCTACGAGGGCACGGACTGGTCGGGCTGCACGCTACAGGA
GTTTCATGGACTGCCCGTACAACCTGGCCAACAACGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGCTG
CTACAACCTGTCTTCATCCCCGAGGGCAAGCGGGCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGG
CATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCACTACCTGTTTCGAGCGGACGTTCAACCTCAAGTT
CATCCGGCCCTTCATGCAGTACAACAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAGGACACCATCCGGCGCAT
CGAGGAGCTCAACGACCTGGACATGCAGCTGTATGACTACGCCAAGGACCTCTTCAGCAGCACTACCAGTACAA
GCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCGCT
GCCGCGGGAGGACGCCGACGAGCCGGGCGCGTGCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGGTA
GTGGCGGTGGTGGCCACGGGGAGGCCTCTTGGGGTGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAA
GACTGTCAAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCCTGAAAAAAACACAGCAGGGACA
TAGTGGGGCTGGGCAGGGATGGGGCTTGAGAAATCAACAGGTGCAGCCAGTGGGTCAGAGGAAAGCGTGCTCGA
AGGATGCCATGGTCAGGGCAGAGCCTCCAGAGCAGGTGTTGTGCCTGGAGCTGCTCTCCTGGCCTCCTTGGATTT
ATCGCAAAACTGAAGGTTTTCGTGAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCCT
CACCAACTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAAC
TGCCCCAGCTCCAGGCCATCCATAGCTCCTCCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCCC
AGCTACCCATCTGTAGCTCCCTCAAAGTCAGGGCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCCC
AGGAAGCCTGCTCCCCTCTCTGGCCATGGTCTGCTTCATGCTTTGGGTGAGGAGCCAAAGCTGATGTTTCAGG
CCCCACCCACTCCCTACAGTCCTCAGACC

WO 2004/030615

PCT/US2003/028547

83/6881
FIGURE 78

AGAAACTCCCGGTGTGGCAGCTGAGATGGCCCAGGAAAGAACTATATTACCTTCAAAAAGAGAGGTACATGCCGAT
GTTTGAGGTGGCATGAAGCTCAGTGGTGTTATATTGGAATGAGTGAGTGACCATCCTGGAGCCTTCCTGAAAAGAG
GATTGGAACATCAGTTAACATCTGACCACTGCCAGCCCACCCCTCCACCCACGTCGATTGCATCTCTGGGCTC
CAGGGATAAAGCAGGTCTTGGGGTGCACCATGATTTACCATTCCTTAGTACTGGCCATTGGCACCTGCCTTACTA
ACTCCTTAGTGCCAGAGAAAGAGAAAGACCCCAAGTACTGGCGAGACCAAGCGCAAGAGACACTGAAATATGCCC
TGGAGCTTCAGAAGCTCAACACCAACGTGGCTAAGAATGTCATCATGTTCTGGGAGATGGGATGGGTGTCTCCA
CAGTGACGGCTGCCCCGATCCTCAAGGGTCAGCTCCACCACAACCCCTGGGGAGGAGACCAGGCTGGAGATGGACA
AGTTCCCCTTCGTGGCCCTCTCCAAGACGTACAACACCAATGCCAGGTCCCTGACAGTGCCGGCACCGCCACCG
CCTACCTGTGTGGGGTGAAGGCCAATGAGGGCACCGTGGGGGTAAGCGCAGCCACTGAGCGTTCCCGGTGCAACA
CCACCCAGGGGAACGAGGTACCTCCATCCTGCGCTGGGCCAAGGACGCTGGGAAATCTGTGGGCATTGTGACCA
CCACGAGAGTGAACCATGCCACCCCCAGCGCCGCTACGCCCACTCGGCTGACCGGGACTGGTACTCAGACAACG
AGATGCCCCCTGAGGCCTTGAGCCAGGGCTGTAAGGACATCGCTACCAGCTCATGCATAACATCAGGGACATTG
ACGTGATCATGGGGGGTGGCCGGAATACATGTACCCCAAGAATAAACTGATGTGGAGTATGAGAGTGACGAGA
AAGCCAGGGGCACGAGGCTGGACGGCTGGACCTCGTTGACACCTGGAAGAGCTTCAAACCGAGATACAAGCACT
CCCATTCTATCTGGAACCGCACGGAACCTCTGACCCCTGACCCCCACAATGTGGACTACCTATTGGGTCTCTTCG
AGCCAGGGGACATGCAGTACGAGCTGAACAGGAACAACGTGACGGACCCGTCACTCTCCGAGATGGTGGTGGTGG
CCATCCAGATCCTGCGGAAGAACCCCAAGGCTTCTTCTGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
ATGAAGGAAAAGCCAAGCAGGCCCCTGCATGAGGCGGTGGAGATGGACCGGGCCATCGGGCAGGCAGGCAGCTTGA
CCTCCTCGGAAGACACTCTGACCGTGGTCACTGCGGACCATTCACAGTCTTACATTTGGTGGATACACCCCC
GTGGCAACTCTATCTTTGGTCTGGCCCCATGCTGAGTGACACAGACAAGAAGCCCTTCACTGCCATCCTGTATG
GCAATGGGCCTGGCTACAAGGTGGTGGGCGGTGAACGAGAGAATGTCTCCATGGTGGACTATGCTCACAACAAC
ACCAGGCGCAGTCTGCTGTGCCCCCTGCGCCACGAGACCCACGGCGGGGAGGACGTGGCCGTCTTCTCCAAGGGCC
CCATGGCGCACCTGCTGCACGGCGTCCACGAGCAGAACTACGTCCCCACGTGATGGCGTATGCAGCCTGCATCG
GGCCAACCTCGGCCACTGTGCTCCTGCCAGCTCGGCAGGCAGCCTTGCTGCAGGCCCCCTGCTGCTCGCGCTGG
CCCTCTACCCCTGAGCGTCTGTCTGAGGGCCAGGGCCCCGGGCACCCACAAGCCCGTGACAGATGCCAACTT
CCCACAGGCAGCCCCCCCCCTCAAGGGGCAGGGAGGTGGGGGCCCTCCTCAGCCTCTGCAACTGCAAGAAAGGGGA
CCCAAGAAACCAAAGTCTGCCGCCACCTCGCTCCCCCTCTGGAATCTTCCCCAAGGGCCAAACCCACTTCTGGCC
TCCAGCCTTTGCTCCCTCCCCGCTGCCCTTTGGCCAACAGGGTAGATTCTCTTGGGAGGCAGAGAGTACAGAC
TGCAGACATTCTCAAAGCCTCTTATTTTCTAGCGAACGTATTCTCCAGACCCAGAGGCCCTGAAGCCTCCGTG
GAACATTCTGGATCTGACCTCCAGTCTCATCTCTGACCTCCCACTCCCATCTCTTACCTCTGGAACCCCC
CAGGCCCTACAATGCTCAITGTCCTGTCCCCAGGCCCCAGCCCTCCTTCAGGGGAGTTGAGGTCTTTCTCCTCAGG
ACAAGGCTTGCTCACTCACTCACTCCAAGACCACAGGGTCCAGGAAGCCGGTGCCTGGGTGGCCATCCTACC
CAGCGTGGCCCAGGCCGGAAGAGCCACCTGGCAGGGCTCACACTCCTGGGCTCTGAACACACACGCCAGCTCCT
CTCTGAAGCGACTCTCCTGTTTGGAAACGGCAAAAAAAATTTTTTTTTCTTTTTTGGTGGTGGTTAAAGGGAA
CACAAAACATTTAAATAAAACTTTCCAAATATTTCCGAGG

WO 2004/030615

PCT/US2003/028547

84/6881
FIGURE 79

GAACCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCACCCAATAGATGTTCT
CCAGGCCTTTTAGAAAACATGGAGTTGTTCCCTTTGGCCACGTATATGCGAATCTATAAGAAAGGTGATATTGTAG
ACATCAAGGGAATGGGTACTGTTCAAAAAGGAACGCCCCACAAGTGTTACCATGGCAAACTGGAAGAGTCTACA
ATGTTATCCAGTATGCTGCTAGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATG
TGCGTATTGAGCACATTAAGCACTCTGAGAGCCGAGATAGCTTCCTGAAACGCGTGAAGGAGAATGATCAGAAAA
AGAGAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGCTCCACCCAGCAAAGCACACTTTG
TGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCTCTATGAATTCACGGCATAATAGGTATTTAAAA
AAAAAAAAAGACCTCTGGGCTGT

WO 2004/030615

PCT/US2003/028547

85/6881
FIGURE 80

DRTQREERGEAPNRMFSRPFRKHGVVPLATYMRIYKKGDIVDIKGMGTVQKGTPHKCYHGKTGRVYNVIQYAASIV
V NKQVKGKILAKRINVRIEHIKHSES RDSFLKRVKENDQKKREAKEKGTWVQLKRQPAPPSKAHFVRTNGKEPEL
LEPILYEFTA

PCT/US2003/028547

FIGURE 81

[illegible]

WO 2004/030615

PCT/US2003/028547

87/6881

FIGURE 82

MQTIKCVVVGDAVGKTCLLISYTTNKFPSEYVPTVFDNYAVTVMIGGEPYTLGLFDTAGQEDYDRLRPLSYPQT
DVFLVCF SVVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETA EKLARDLK
AVKYVECSALTQKGLKNVFDEAILAALEPPEPKSRRCVLL

WO 2004/030615

PCT/US2003/028547

88/6881
FIGURE 83

CGCGCGCGCCATTTCTAGTCGTTTTCAAAGCGCCTCGCGCTGATTCTCACGGGCCCGGCTGCCGGCCCCCGCTCT
GCCCTGCATAATAAAATGGCTAATCAGGTGAATGGTAATGCGGTACAGTTAAAAGAAGAGGAAGAACCAATGGAT
ACTTCCAGTGTAACCTCACACAGAACTACAAGACACTGATAGAGGCAGGCCTCCACAGAAAGTGGCAGAAAGA
CTTGATGAAATATTTAGACAGGATTGGTAGCTTATGTCGATCTTGATGAAAGAGCAATTGATGCTCTCAGGGAA
TTTAATGAAGAAGGAGCTCTGTCTGTACTACAGCAGTTCAAGGAAAGTGAATTATCACATGTTTCAAGCAAAAGT
GCATTTTTATGTGGAGTTATGAAGACCTACAGGCAGAGAGAGAAACAGGGGAGCAAGGTGCAAGAGTCCACAAAG
GGACCTGATGAAGCGAAGATCAAGGCCTTGCTTGAGAGAACTGGTTATACTCTGGATGTAACCAAGGACAGAGG
AAGTATGGTGGTCCTCCACCAGACAGTGTGTACTCTGGCGTGCAACCTGGAATTGGAACGGAGGTATTTGTAGGC
AAAATACCAAGGGATTTATATGAGGATGAGTTGGTGCCCTTTTTGAGAAGGCCGGACCCATTTGGGATCTACGT
CTTATGATGGATCCACTGTCCGGTCAGAATAGAGGGTATGCATTTATCACCTTCTGTGGAAGGAAGCTGCACAG
GAAGCCGTGAACTGTGTGACAGCTATGAAATTCGCCCTGGTAAACACCTTGGAGTGTGCATTTCTGTGGCAAAAC
AACAGACTTTTTGTTGGATCCATTCCGAAGAATAAGACTAAAGAAAACATTTTGGAAAGATTTCAGTAAAGTCACA
GAGGGTTTGGTGGACGTTATTTCTCTATCATCAACCCGATGACAAAAAGAAGATCGGGGGTTCTGCTTCTCTTGA
TATGAGGATCACAAGTCAGCAGCACAAAGCCAGACGCCGGCTGATGAGTGGAAAAGTAAAAGTGTGGGGAAATGTA
GTTACAGTTGAATGGGCTGACCCTGTGGAAGAACCAGATCCAGAAGTCATGGCTAAGGTAAAAGTTTGTGTTGTG
AGAACTTGGCTACTACGGTGACAGAAGAAATATTGGAAGTCAATTTCTGAATTTGGAAAAGTTCGAAAGAGTA
AAGAAGTTGAAAGATTATGCATTTGTTCATTTTGAAGACAGAGGAGCAGCTGTTAAGGCTATGGATGAAATGAAT
GGCAAAGAAATAGAAGGGGAAGAAATTGAAATAGTCTTAGCCAAGCCACCAGACAAGAAAAGGAAAGAGCGCCAA
GCTGCTAGACAGGCCTCCAGAAGCACTGCGTATGAAGATTATTACTACCACCTCCTCCTCGCATGCCACCTCCA
ATTAGAGGTGCGGGTCTGTGGTGGGGGAGAGGTGGATATGGCTACCCTCCAGATTACTACGGCTATGAAGATTAC
TATGATGATTACTATGGTTATGATTATCACGACTATCGTGGAGGCTATGAAGATCCCTACTACGGCTATGATGAT
GGCTATGCAGTAAGAGGAAGAGGAGGAGGAAGGGGAGGGCGAGGTGCTCCACCACCACCAAGGGGGAGGGGAGCA
CCACCTCCAAGAGGTAGAGCTGGCTATTCACAGAGGGGGGCACCTTTGGGACCACCAAGAGGCTCTAGGGGTGGC
AGAGGGGGTCTGCTCAACAGCAGAGAGGCCGTGGTTCCCGTGGATCTCGGGGCAATCGTGGGGGCAATGTAGGA
GGCAAGAGAAAGGCAGATGGGTACAACCAGCCTGATTCGAAGCGTCGTCAGACCAACAACCAACAGAAGTGGGGT
TCCCAACCCATCGCTCAGCAGCCGCTTCAGCAAGGTGGTGACTATTCTGGTAACTATGGTTACAATAATGACAAC
CAGGAATTTTATCAGGATACTTATGGGCAACAGTGGAAAGTAGACAAGTAAGGGCTTGAAAATGATACTGGCAAGA
TACGATTGGCTCTAGATCTACATTCTTCAAAAAAAAAAATTGGCTTAAGTGTTCATCTTTAAGTAGCATTTTGC
TGCCATTTGTATTGGGCTGAAGAAATCACTATTGTGTATATACTCAAGTCTTTTTATTTTCTCTTTTCATAAA
TGCTCTTGGACATTATTGGGCTTGCAGAGTTCCCTTATTCTGGGGATTACAATGCTTTTATCGTTTCAGGCTTCA
TTTTAGCTTCAAAACAAGCTGGGCACACTGTTAAATCATGATTTTGCAGAACCTTTGGTTTTGGACAGTTTCATT
TTTTTGGATTTGGGATAGATTACATAGGAGTATGGAGTATGCTGTAAATAAAAAATACAAGCTAGTGCTTTGTCTT
AGTAGTTTTAAGAAATTAAAGCAAACAAATTTAAGTTTTCTGTATTGAAAATAACCTATGATTGTATGTTTTGC
ATTCCTAGAAGTAGGTTAACTGTGTTTTTAAATTGTTATAACTTCACACCTTTTGAATCTGCCCTACAAAATT
TGTTTGGCTTAAACGTCAAAAGCCGTGACAATTTGTTCTTTGATGTGATTGATTTCCAATTTCTTGTTCATGTA
AGATTTCAATAAAACTAAAAAATCTATTCAAACATTA

WO 2004/030615

PCT/US2003/028547

89/6881
FIGURE 84

MANQVNGNAVQLKEEEEPMDTSSVTHTEHYKTLIEAGLPQKVAERLDEIFQTGLVAYVDLDERAIDALREFNEEG
ALSVLQQFKESDLSHVQNKSAFLCGVMKTYRQREKQGSKVQESTKGPDEAKIKALLERTGYTLDVTTGQRKYGGP
PPDSVYSGVQPGIGTEVFVGKIPRDLYEDELVPLFEKAGPIWDLRLMMDPLSGQNRGYAFITFCGKEAAQEAVKL
CDSYEIRPGKHLGVCISVANNRLFVGSIPKNKTKENILEEFSKVTEGLVDVILYHQPDDKKKNRGFCFLEYEDHK
SAAQARRRLMSGKVWVWGNVTVWADPVEEPDPEVMAKVKVLFRNLATTVTEEILEKSFSEFGKLERVKKLKD
YAFVHFEDRGA AVKAMDEMNGKEIEGEEIEIVLAKPPDKKRKERQAARQASRSTAYEDYYYHPPPRMPPPIRGRG
RGGGRGGYGYPPDYGYEDYYDDYYGYDYHDYRGGYEDPYGYDDGYAVRGRGGGRGGRGAPPPPRGRGAPPPRG
RAGYSQRGAPLGPPRGSRGGRGGAQQQRGRGSRGSRGNRGGNVGGKRKADGYNQPD SKRRQTNNQQNWGSQPIA
QQPLQQGGDYSGNYGYNNDNQEFYQDTYQQWK

WO 2004/030615

PCT/US2003/028547

90/6881
FIGURE 85

CGGACTGGCAGGGGGCAGGGAAGCTCAAAGATCTGGGGTGCTGCCAGGAAAAAGCAAATTCTGGAAGTTAATGGT
TTTGAGTGATTTTTTAAATCCTTGCTGGCGGAGAGGCCCGCCTCTCCCCGGTATCAGCGCTTCCTCATTCTTTGAA
TCCGCGGCTCCGCGGTCTTCGGCGTCAGACCAGCCGGAGGAAGCCTGTTTGCAATTTAAGCGGGCTGTGAACGCC
CAGGGCCGGCGGGGGCAGGGCCGAGGCGGGCCATTTTGAATAAAGAGGCGTGCCTTCCAGGCAGGCTCTATAAGT
GACCGCCGCGGCGAGCGTGC CGCGTTCAGGTCAGTGTAGCGGGACTTCTTTTGGTTTTCTTTCTCTTTGGGGC
ACCTCTGGACTCACTCCCCAGCATGAAGGCGCTGAGCCCGGTGCGCGGCTGCTACGAGGCGGTGTGCTGCCTGTC
GGAACGCAGTCTGGCCATCGCCCGGGGCCGAGGGAAGGGCCCGGCAGCTGAGGAGCCGCTGAGCTTGCTGGACGA
CATGAACCACTGCTACTCCCGCCTGCGGGAAC TGGTACCCGGAGTCCCGAGAGGCACTCAGCTTAGCCAGGTGGA
AATCCTACAGCGCGTCATCGACTACATTCTCGACCTGCAGGTAGTCTTGCCGAGCCAGCCCCCTGGACCCCTGA
TGGCCCCACCTTCCCATCCAGACAGCCGAGCTCACTCCGGAAC TTGTCATCTCCAACGACAAAAGGAGCTTTTG
CCACTGACTCGGCCGTGTCCTGACACCTCCAGGTGAGTATCTCCTCTCTTGAGAGGGAGGTTTAAACGGCAAGT
CCTGGAGTTGGCAGACGTTTTGAAAATTGCCACTCACTCGGTTTAGGGAACTGAGGCCAGAGAGGGACAAGTG
ACTTGCCCATGTTG

WO 2004/030615

PCT/US2003/028547

91/6881
FIGURE 86

MKALSPVRGCYEAVCCLSERSLAIARGRGKGPAEEPLSLDDMNHCSRLRELVPGVPRGTQLSQVEILQRVID
YILDQLQVLAEPAPGPPDGPHLPITAEITPELVISNDKRSFCH

WO 2004/030615

PCT/US2003/028547

92/6881
FIGURE 87

TTCTCTTCCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACTTCGCATCCGCA
AACTCTGTCTCAACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAGCTCA
CAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATCCGGAGAAATGAAAAGATTG
CTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATCTTGAGAAAGGGTCTAAAGGTGCGGGAGTATGAGT
TAAGAAAAACAACCTTCTCAGATACTGGAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAAT
ATGACCCAAGCATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCAGACA
AGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCCATGCGCTGGTTCCAGCAGA
AGTATGATGGGATCATCCTTCCTGGCAAATAAATTCCCGTTTCTATCCAAAAGAGCAATAAAAAGTTTTTCAGTGA
AATGTGCAA

WO 2004/030615

PCT/US2003/028547

93/6881
FIGURE 88

MAQDQGEKENPMRELRIKLCNICVGESGDLTRAQKVLEQLTGQTPVFSKARYTVRSFGIRRNEKIAVHCTVR
GAKAEEILEKGLKVREYELRKNNFSDTGNFGFGIQEHIDLGIKYDPSIGIYGLDFYVVLGRPFGFSIADKKRRTGC
IGAKHRISKEEAMRWFQKYDGIILPGK

WO 2004/030615

PCT/US2003/028547

94/6881
FIGURE 89

GGAAGTTCCGGCGGGGGCGGCCGAGGGGGAAGAGTGTGTCTGCGGGAGAAAGAGGAGAATCGCCCCAAGCGGCCTC
GGAAGTCCCAGGGAGTGGAGGCCCCCGCCGTGGAGCCGTGTGGTGTATGTGTGGTAACACCATGTCTGTGCCCCCT
GCTCACCGATGCTGCCACCGTGTCTGGAGCTGAGCGGGAAACGGCCGCGGTTATTTTTTACATGGACTTGGAGA
CACAGGGCACAGCTGGGCTGACGCCCTCTCCACCATCCGGCTCCCTCACGTCAAGTACATCTGTCCCCATGCGCC
TAGGATCCCTGTGACCTCAACATGAAGATGGTGTATGCCCTCCTGGTTTGACCTGATGGGGCTGAGTCCAGATGC
CCCAGAGGACGAGGCTGGCATCAAGAAGGCAGCAGAGAACATCAAGGCCTTGATTGAGCATGAAATGAAGAACGG
GATCCCTGCCAATCGAATCGTCTCTGGGAGGCTTTTTCAGGGCGGGGGCCCTGTCCCTCTACACGGCCCTCACCTG
CCCCACCTCTGGCTGGCATCGTGGCGTTGAGCTGCTGGCTGCCTCTGCACCGGGCCCTCCCCCAGGCAGCTAA
TGGCAGTGCCAAGGACCTGGCCATACTCCAGTGCCATGGGGAGCTGGACCCCATGGTGCCCGTACGGTTTGGGGC
CCTGACGGCTGAGAAGCTCCGGTCTGTTGTACACCTGCCAGGGTCCAGTTCAGACATACCCGGGTGTCATGCA
CAGCTCCTGTCTCAGGAGATGGCAGCTGTGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTCTAAGTAGTCGC
TGGCCCCAGTGCAGTACCCAGCTCATGGGGGACTCAGCAAGCAAGCGTGGCACCATCTTGGATCTGAGCCGGTC
GAGCCCCGTGTCCCCACCTTCCCTGACCTGTCTTTTTCCACAGGCCTCTGGGGGCAGGTGGCAAGGCCTGGCCGG
GCCTTCCTTCTGGCCTTAGCCACCTGGCTCTGTCTGCAGCAGGGGCAGGCTGCTTTCTATCCATTTCCCTGGA
GGCGGGCCCCCCTGGCAGCAGTATTGGAGGGGCTACAGGCAGCTGGAGAAAGGGGGCCAGCCGCTGACCCACTCA
CTCAGGACCTCACTCACTAGCCCCGCTTTGGGCCCCCTCCTGTGACCTCAGGGTTTGGCCCATGGGGCCCCCCA
GGCCCCCTGCCCCAACTGATTCTGCCAGATAATCGTGTCTCCTGCCTCCACTCAGCTGCTTCTCAGTCATGAATG
TGGCCATGGCCCCGGGGTCCCCCTTGTCTGTGGGCTCCCTGTCCCTGGGCAGGAGTGCTGGTGAGGAGGTGGAG
CCTTTTGAGGGGGGCCTTCCCTCAGCTGTTTCCCCACACTGGGGGGCTGGGCCCTGCCTCCCCGTTACCTCCTT
CCCTGCAGGCCTGGAGCCTGTAGGGCTGGACTGAGGTTTCAAGTCTCCCCCAGCTGTCTCACCCCCACTTTGTCC
CCACTCTAGAGCAGGGAGGCAGTGGGGGAGGAGTTGTGTCTCGTCTTCTGTCTCCATGTGGTTTTTGGGTGTTTT
TCTTGTGTGTCTCTGGATTCCGATAAAATTAAAGAAATTGCTTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

95/6881
FIGURE 90

MCGNTMSVPLLTDAA TVSGAERETA AVIFLHGLGDTGHSWADALSTIRLPHVKYICPHAPRIPVTLNMKMVMP
FDLMGLSPDAPED EAGIKKAAENIKALIEHEMKN GIPANRIVLGGFSQGGALSLYTALTCPHPLAGIVALSCWLP
LHRAFPQAANGSAKDLAILQCHGELDPMVPVRF GALTAEKLRSVVTPARVQFKTYPGVMHSSCPQEMAAVKEFLE
KLLPPV

WO 2004/030615

PCT/US2003/028547

96/6881
FIGURE 91

AGAAGGAGAAGGTCGGGTGTAGAACTGGGGTGGCCGGCAGCTCGCTCATCGGTGTTTCGTGGGCTTTGTTCGGTC
CGTGCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCGACGTCGAGAGGGAGCCGCTGCCGCGTTAGTTCGGAGC
TTGAAGTCACTAGGACTTCTCTCAAACCTTGTGTGCTGAGGAGACTCAGATGTTGGCCTCAGCTCCTAGGCTGAAC
TCAGCAGATCGGCCCATGAAAACCTTCTGTATTGAGACAAAGGAAGGGATCTGTCAGAAAGCAACACTTGTATCT
TGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAGCAGACTGAAAGGTGACAAAGA
AGCTGAAGATGGGTGGTGGAGAGAGGTATAACATTCCAGCCCCCTCAATCTAGAAATGTTAGTAAGAACCAACAAC
AGCTTAACAGACAGAAGACCAAGGAACAGAATTCAGATGAAGATTGTTTCATAAGAAAAAGAAAGAGGACATG
GTTATAACTCATCAGCAGCTGCCTGGCAGGCCATGCAAAATGGGGGAAGAACAAAAATTTCCAAATAATCAAA
GTTGGAATTCTAGCTTATCAGGTCCCAGGTTACTTTTTAAATCTCAAGCTAATCAGAACTATGCTGGTGCCAAAT
TTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCAAGCCACTGGGTCCCTGTTTCCTTTAATCCTTCAG
ATAAGGAAATAATGACATTTCAACTTAAAACCTTACTTAAAGTACAGGTATAAATAAGACAAATGTTTAAATTT
AGTTATGTTACGGATAGTTGTCAATTGGTCTGAAACAAATTCGCTAGGGAATCTATTGTGTAGAACTAATTAA
TGTAACAAAAACAGACCATCTCGTGTTGTGTGCACTGTGATATAATGGTAGTATCAGTGCAACTTTAATGATTGT
ACTTGATATTAAGTGTTCTCAACTGAGTAACTTTTTAAGTGGAAACCAAGTTTAGATTGGGGAGTGGTAAAGGAA
TCAGCTTTTTCTATTGTTAGGGGAAGACAGTAATTTATCATTATGGACCAGTAGATTGTTGAAAGTTGGTGAAT
CGGATTATAAGCTTCTAGCTAACACAAGGATTGAGAATTAGGTAAACATCTGAAGGTTTAGTATATTAGAAACAC
CCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAAATGTGAATTTTCGTAATAATTGCATTTTAGTG
AATTGTACAGTGGGTGGAAAGGGCATTGGAGCTCATTAGAATGAGACATAGTACACCCCAATGGCCCTGTTTAT
TAAATGTAGTGGATTAAAGTGCTGTCAACAAATACACCAAAACCATTTTTTATAGAAACAGTATTTAATGGTCAC
TCAATAGCTTTCAAATAACATTTTTGTATTACAGCACTGCACAAGCTATTCTAATAGTGCTCTCGCCTCATCATT
CCTGCAAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTAAGTACCTAGGGGAGAAAGAGCCATGTAAATA
TCTGTAATAAACTTGTAGCATATGTAAAGTTTCTTGGCCTTTATCTTACAAAATGGAGTATTTTAGTATGAAT
TTGCTGAATGTAAGACCGTGGACTGTTTTTATAATATGGCCTAATTTTAAAGGTCCAAAATAACTTGTTTTAA
AGTTTGCCCTTGTGCTAAAGTGCCAGTGTATGTATGTTTATCTTGATTGGTTGTAACTATATTTCAAAGTAA
CCCTAGTGTAATAAGTTTATAACTAAAAAGGTTTAAAGCTGCTAAACTATTTTAAAGAGATGTGAAATGCAGTA
TGGGACTATCTTTTTTCTCCTCTAAGCCCAAAGATTAACTAGAGTCCCTCCAACCTTATAGATTGTTGGCTTT
CACAATCTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGTGATGTTTTGTTTTGTTTGGTCAAGGG
GTAGGTGCAACCAATGGACCACTTATGCAAAAGATGTAACTCTTGCATAATACATTGATAACATGTTTGCCA
ACTTTAAATGCTTAAACATAAGCGAAACCAAGTAGCAAGTATGTGGGTGAGCTTAAAAATTTTGATTGTTAATGCC
CTATTTTCTAATTTGGCACCTCTTGATGCCTAAGCAGGTAAGCAGATGCCTAAGCTGTATTTCTCCAAATAAATC
AAGATGAAGTACTGCCCAAGTTAAATATTGATAGCCTAAAGACAAGTTTATGTAGTACTTAAATGTACATGATATG
AATGTGAAGCATAAAATTAATAAAATTTTTCCCATTAATAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

97/6881
FIGURE 92

MGGGERYNIPAPQSRNVSKNQQLNRQKTKEQNSQMKIVHKKKERGHGYNSSAAAWQAMQNGGKNKNFPNNQSWN
SSLSGPRLLFKSQANQNYAGAKFSEPPSPSVLPKPPSHWVPVSFNPSPDKEIMTFQLKTLLKVQV

WO 2004/030615

PCT/US2003/028547

98/6881
FIGURE 93

GTCTGAGGGCTCGGCCGCTGAGCCGCGGACGGTTTGCTGAGCCCCTTAGTGCGCCCGGCCGAGACACGCCGCCGC
CATGTCCCCGTACCTGCGTCCCCCAACACGTCTCTGTTGCTCAGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTCTGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAATATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCGTAGCAGAAGCCATTCCGACAATGATAGACCAAACCTGCAGCTGGAATACCCAGTACAGTTC
TGCTTACTACACTTCAAGAAAGATCT**TGAA**AGCGGAAAAAGAACCAAAGAAGGGCAGTTCAAGCGACCAAAGGGTG
GGTGGAAGGTGCTGCAGTATGAATACTGTACGAATATTTTGACTCTGGTCTGAAAAGATAAAAGAATGTTATCGA
AAACTACATGGAATAATTGAAGTCCCTTCAAGTTTGAAAGTAAGCATTTTAGGACAAATAAAAGGAAATTCAACT
TTGTACTTGTGGAACTAATCCCTAAATATGAATAGGTTTATATTGATTCATGGGTAACAGGTCCATAATAAATT
ATTGGAACTAGGATGTCTGAATATCAAGGAAGACAGCCATAGTCTCTTACAGTGCCTCTGTTGGTCTGTCTCAA
ACTGAATTGGGTGGGAAAAGGTATGGTCCAATATAAAAGTTCCATTTTGCCATTATTGGCAAATCTTGCCTTTG
TTTATTTTGGTGCCAGTGTTTTCTGCTTAATCATTGCTTTGTTGGCATCTGTGTTTATTTACTTGTACACCACA
TGCAGTTTACATCTGTCTTAACACTCCTTCCAGGTAAATTCGAATTATTTTACATCCAGCTAAGAGGGGCC
ATCTCTTCTCACTCTTTCTAGTCAGTATATTCAGCAAATATTTATTGAGCCCTTACTGTGGGCAAATCATTGT
ACTGGATAATTGAGAAAAATAGATAATCCCTTATTCAGTAAATGTCTACTGAGCACAATCTAGTGAATCATTAC
AGTATGGCCTCATTGTTTTGTTGAGGTGTGTTATTCATAACAATATTTTACACCATTTCGTATCAATGTAATTAT
AGAACACAATATACGATCAAGGATAAGTAATTGTGTGGTTATCTGCCATTTAAAAGTATCCAGTATTTGATCACA
TTATTATAAATAATGAAAAAATGATTTAATCTGTAATAAACTGGTTTATTGTGCACTGACTGTAATATACTAGAG
TTATAATAAATTGTTTACTCTGCCTCACCAAACACATGCTAGGATATAACCCCCAAAATAAGTATTTAACTTTGC
ATTAGGTATAAAGGAGACTGGGTGCTATAATTAGATTATTTGAGGCAGACAGAGAGCTGTTATCCTAACTGATT
TAGTATGTTCTGTAATTGAGAAAATGTTCAACCAATATATACTTTTATGATTTACATGTACATTTTATAGGGGA
CATGTTCTGTGTATAGCGAATAAATAACTTTTATAGTATCAC

WO 2004/030615

PCT/US2003/028547

99/6881
FIGURE 94

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDRKW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSSRYYDDYDRYRRSRRSYERRRSRSRSFDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRPNCSWNTQYSSAYYTSRKI

WO 2004/030615

PCT/US2003/028547

100/6881
FIGURE 95

GTCTGAGGCTCGGCCGCCTGAGCCGCGGACGGTTTGCTGAGCCCGTTAGTGCGCCCGGCCGAGACACGCCGCCGC
CATGTCCCCGCTACCTGCGTCCCCCAACACGTCTCTGTTTCGTAGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTTCGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAACCTATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCTAGCAGAAGCCATTCCGACAATGATAGATTCAAACACCGAAATCGATCTTTTTCAAGATC
TAAATCCAATTCAGATCACGGTCCAAGTCCCAGCCCAAGAAAGAAATGAAGGCTAAATCACGTTCTAGGTCTGC
ATCTCACACCAAACTAGAGGCACCTCTAAACAGATTCCAAAACACATTATAAGTCTGGCTCAAGATATGAAAA
GGAATCAAGGAAAAAAGAACCACCTAGATCCAAATCTCAGTCAAGATCACAGTCTAGGTCTAGGTCAAAATCTAG
ATCAAGGTCTTGGACTAGTCCTAAGTCCAGTGGCCAC**TGAT**AGTATAAACCATGGTCATTTTTTAGGCATGTATCA
TTCATTTACTCATAGTTTGGTTTACTTAAATATCAGGAATACAATGTTGCAATGATGCTTAAAAAACACTTGTT
AGTTTTCCCTGTACCAGGCAATGGTTATAAATTAATGATATGCTGTTGAGAAGCCACTCTTAAGAGTCCAGTTT
GTTTAAATGTTATGGGCAGCTACCAATTTGTGGTGCTCTGTATATTTTGTAAAGATTCTCATTTTTTATGCTTG
AAGTATTTGGTGAAAAGATGTTGGTTGACCATAATTTGCAACATTGTCTCATTAATAAATAAACTTTTCATATTCAT
ATTTGGTAGAACTGTTAACCTAGAAATGTAGCTTGCTAATAAGATAGAATGATACAAAAGTGAAGTAGTAGCCAC
AGTACAACACTGACTGCTCAGACACATTTAGGTTTCAGGTGGACCTTTATGCTTGTCAAGATGTCTAGGCCCGG
CTGGGCGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGCGGATCACGAGGTACAGGAGTT
CGAGACCAGCCTGACCAACACGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTATCCGGGCATGGTGGCACA
TGCTGTAAATCTCAGCTACTCAGGAGGCTGAGGCAACAGAGATCGCTTGAACCTGGGAGGTAGAAGTTGCAGTGAG
CCAAATCACGCCACTGCCTCCAGCCTGGGCAACAGATGTAGACTCCGTCTCAAAAAAAAAAAAAACCGGATG
TCTAGGCCAATGATAATTATTTTGTATGCAGTGTTGATTAGTTCTTTTGTAAACCCCACTGTCTTGGGGAATGAT
GCCAGCTGGGAAATGAGTTTGTGAC.TGAAACATGGAGCCTTCACTGCTTTTTTCTGTTTCTATGAAGATTTG
GAACATAGAAAACACAAAACTCACCTTAAATTTGAGCAGGTGCTTGATGGCAAAAAATAATTTAAGGAAAAAG
GAATATTCCTATGTAGTTATTTCTAAAGTTTAAGGAGCGTTGTTGACCATAATATTGCTTAGTTTTCTTACTGCTG
TTAAGTAAGTAAATTGTTTCAAAGTAGGTTTTGTGTGTGTGCTAGTGTAAGAAGAACTGAAATTTTGATGCTT
ACAGCACTTGGCTCGTGCAATTTGTATCAAAATTTGCCTGCCTCTTTATGAGGGAGGCCTGCTTTTCACACCTCAG
TTTATTTAATACGAGGCAAGTTGTAAGACAACACTCATTCTAGGTGATTCTGTGGTGCCATGAAATTTAAGGTAA
TTTGGGAAAAGGATTAGTCAGTTTTAAGCAAGAGTCACATCTTTTGAGCTTTCGATTATCAGTGTAGTACCTGA
CTAAAAATGAAGTAATACCCTTAAACATTTATAATTTCTAGTATTTCTCTGAAAGATCGTTTTGGGGACAAAAG
TGACTTGACATGTCCAATTTCAATTCAGAATAAAAAGCTAGCATCTTAAAAATCTCAGATTGCTTGCTTACAGA
TACAAGTACGAATTATGGACAAACGATTCCCTTTAGAGGATTACTTTTTCAATTCGGTTTTAGTAATCTAGGC
TTTGCCTGTAAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTCTAGAACC
TTTGTATATTTGATAGTATTTCTAATTTCTTTTACTGTTTGCAGTTAATGTTTATGTTCTGCTATGCAAT
CGTTTATATGCACGTTTCTTTAATTTTTTTAGATTTTCTGGATGTATAGTTTAAACAACAAAAAGTCTATTTAA
AACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAACTTTGTATTTTCTTTCTTATAGA
GGCTTCTAAAAAGGTATTTTTATATGTTCTTTTTAACAAATATTGTGTACAACCTTTAAACATCAATGTTTGGA
TCAAAACAAGACCCAGCTTATTTTCTGCTTGCTGTAAATTAAGCAAACATGCTATAATAAAAAACAAATGAAGG

WO 2004/030615

PCT/US2003/028547

101/6881
FIGURE 96

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDRKW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSSRYYDDYDRYRRSRRSYERRRSRRSRFDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRFKHRNRSFSRSKSNRSRRSKSPKKEMKAKSRRSASHTKTRGTSKTDKTHYKSGSRYEK
ESRKKEPPRSKSQSRSQSRRSRKSRSRSPKSSGH

WO 2004/030615

PCT/US2003/028547

102/6881
FIGURE 97

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGC GGTGCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTTCATGGGGATGCCTCGCAGAAAGCTGCCAAGGCAGGGCTTTTGGCATTTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTGGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTTAATCACAAGATTATTTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

WO 2004/030615

PCT/US2003/028547

103/6881
FIGURE 98

CAGGAACGAGATGGCGGTTCCCTGGAGGCTGAGTGCCGTTTGC GGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACACTTGTCAACGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTTACTGATTATGTTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCTCTGCTTTGTCTATGCCATTAAGCTCACAATAAGGAAGAAATAACAGATAAGCCCATTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAATCTTTGAGGAAAAGGTTTGAGAGGAATTATATCT
AAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAATAT
AACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTATTATGATTA
GTACATGATCAAATTTCCATATTTGCCTTGGGAATAATGGACAAAGGGAAATACTCTTAATTCATGAATAAAAAC
TTTGAGAAAATTAGACAGTGTTTAATTTCAAAAACCTCCCTCTCTAGTCAGTAGATACCACCTACTGATGGTT
ACATATACTAGGGAAATTTTAAAATTAGGAAATGCTGCTATCTCATATTATAAATTTCTAAATCCTAGGAAGAAA
CGCTTGGAGTGCTTCTGAAGATACAGAAGTTCCATTTAAGGGCAAGTTTCCCCAGAGACATATCAAAATATTATC
CATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTCTAAAACAATCTGTCCACAAATATAAACTAT
AAGTAATAAATTGTTATTTCCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTATGAAAATAATTTTTTTAA
ATAAAATGTTGTATAAAAAAA

WO 2004/030615

PCT/US2003/028547

104/6881
FIGURE 99

AGAGAGAAAGGTTGTGATGCGCGCTATAGCTGCATCCGAGGTGCTGGTGGACAGCGCGGAGGAGGGGTCCCTCGC
TGCGGCGGCGGAGCTGGCCGCTCAGAAGCGCGAACAGAGACTGCGCAAATTCCGGGAGCTGCACCTGATGCGGAA
TGAAGCTCGTAAATTAAATCACCAGGAAGTTGTGGAAGAAGATAAAAGACTAAAATTACCTGCAAATTGGGAAGC
CAAAAAAGCTCGTTTGGAGTGGGAATAAAGGAAGAGGAAAAGAAAAGGAATGTGCGGCAAGAGGAGAAGACTA
TGAGAAAGTGAAGTTGCTGGAGATCAGTGCAGAAGATGCAGAAAGATGGGAGAGGAAAAAGAGAGGAAAAACCC
TGATCTGGGATTTTCAGATTATGCTGCTGCCCAGTTACGCCAGTATCATCGGTTGACCAAGCAGATCAAACCTGA
CATGGAAACATATGAGAGACTGAGAGAAAAACATGGAGAAGAGTTTTTCCCAACATCCAATAGTCTTCTTCATGG
AACACATGTGCCTTCCACAGAGGAAATTGACAGGATGGTCATAGATCTGGAAAAACAGATTGAAAAACGAGACAA
ATATAGCCGGAGACGTCCTTATAATGATGATGCAGATATCGACTACATTAATGAAAGGAATGCCAAATTCAACAA
GAAAGCTGAAAGATTCTATGGGAAATACACAGCTGAAATTAAACAGAATTTGGAAAGAGGAACAGCTGTCTAATC
CCTTCAAGAACTGTTTATAGAAGCTTGAGAATGGGGTAAAAATTTCTGCTAGCAAATCAAGTTCTTTTGAAT
TTTATCAGTAATCCAGAATTTAGTAGTCCATGCCTTCTCACTCAGCATTAGAAATAAAAAATGGTTTCTTAAA
CGTATATCCTTTTCATGTATATTTCCACATTTTTGTGCTTGGATATAAGATGTATTTCTTGTAGTGAAGTTGTTTT
GTAATCTACTTTGTATACATTCTAATTATATTATTTTCTATGTATTTTAAATGTATATGGCTGTTTAACTTTG
AAGCATTTTGGGCTTAAGATTGCCAGCAGCACACATCAGATGCAGTCATTGTTGCTATCAGTGTGGAATTTGATA
GAGTCTAGACTCGGGCCACTTGGAGTTGTGTACTCCAAAGCTAAGGACAGTGATGAGGAAGATGGCAGTGGCCAC
CGGAGGACTGGAGCAGTCCCTCCTCATGGCGGCCTGTGACCAAGGTCGGGGAGGAGTGGAGCTATCCTTCCATGA
TCTGATCATGTACAGTTCCTTTTTTAAAAAGCAATAAATGCTTGGGATTAGAATTTCTAAAAA

WO 2004/030615

PCT/US2003/028547

105/6881
FIGURE 100

MAAIAASEVLVDSAEEGSLAAAAELAAQKREQRLRKFREHLHMRNEARKLNHQEVVEEDKRLKLPANWEAKKARL
EWELKEEEKKKKECAARGEDYEKVKLLEISAEDAERWERKKRKNPDLGFSYAAAQLRQYHRLTKQIKPDMETYE
RLREKHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLEKQIEKRDKYSRRRPYNDDADIDYINERNAKFNKKAERF
YGKYTAEIKQNLERGTA

WO 2004/030615

PCT/US2003/028547

106/6881
FIGURE 101A

GGCGGCCCCACTCTGCTCTGTCTGTCAGCTTCGGAGCTCCTCCACCCTGGCTGCCGAAAGCCCCCTTCCCGCCATCTAATG
ATACACTCTGCATACGCTTCTGTTGAGAATTTGTGGCTAGACATTCTGTGGGACCGGGAATCCAAATTCCTGGT
AGCTAGAGGAAAAAAAATAAAACAACAGCCAACCAAGTGAATCCCAACCCAACCCCTGAAGGGCTGAAAATTC
TCGCCTTCTTCAGAGCGGGGCATGGCATCGAACAGCATCTTCGACTCCTTCCCGACCTACTCGCCGACCTTCATC
CGCGACCCAAGCACCAGCCGCCGCTTCACACCTCCCTCCCCGGCCTTCCCCTGCGGCGGCGGCGGCGCAAGATG
GGCGAGAACAGCGGCGCGCTGAGCGCGCAGGCGGCCGTGGGGCCCGAGGGCGCGCCCGGCCCGAGGTGCGCTCG
ATGGTGGACGTGCTGGCGGACCACGCAGGCGAGCTCGTGCACCCGACAGCCCCAACTTCCTCTGCTCCGTGCTG
CCCTCGCACTGGCGCTGCAACAAGACGCTGCCCGTCGCCTTCAAGGTGGTGGCATTGGGGGACGTGCCGGATGGT
ACGGTGGTGAATGTGATGGCAGGCAATGACGAGAACTACTCCGCTGAGCTGCGCAATGCCCTCGGCCGTGATGAAG
AACCAGGTGGCCAGGTTCACGACCTTCGCTTCGTGGGCGCAGTGGGCGAGGGAAGAGTTTCACCTGACCATC
ACTGTGTTACCAACCCCAACCAAGTGGCGACCTACCACCGAGCCATCAAGGTGACCGTGGACGGACCCCGGGAG
CCCAGACGGCACCGGCAGAAAGCTGGAGGACCAGACCAAGCCGTTCCCTGACCGCTTTGGGGACCTGGAACGGCTG
CGCATGCGGGTGACACCGAGCACACCCAGCCCCGAGGCTCACTCAGCACACAAGCCACTTCAGCAGCCAGCCC
CAGACCCCCAATCCAAGGCACCTCGGAATGAACCCATTCTCCGACCCCCGCCAGTTTGACCGCTCCTTCCCCACG
CTGCCAACCCTCACGGAGAGCCGCTTCCAGACCCCCAGGATGCATTATCCCGGGGCCATGTCAGTGCCTTCCCC
TACAGCGCCACGCCCCTCGGGCACGAGCATCAGCAGCCTCAGCGTGGCGGGCATGCCGGCCACCAGCCGCTTCCAC
CATACTACCTCCCCGCCACCCTACCCGGGGGCCCCGAGAACCAGAGCGGGCCCTTCCAGGCCAACCCGTCCCC
TACCACCTCTACTACGGGACATCCTCTGGCTCCTACCAAGTTCCTATGGTGGCGGGCAGCAGCAGTGGGGCGAC
CGCTCACCTACCCGATGCTGGCCTCTTGACACAGCAGCGCTGCCTCTGTGCGCGCGGCAACCTCATGAACCCC
AGCCTGGGCGGCCAGAGTGATGGCGTGGAGGCCGACGGCAGCCACAGCAACTCACCCACGGCCCTGAGCACGCCA
GGCCGCATGGATGAGGCGGTGTGGCGGCCCTACTGACCGCCCTGGTGGACTCCTCCCGCTGGAGGCGGGGACCCT
AACAACTTCAAGACCAAGTGATGGGCGGCTCCGAGGCTCCGGGCGGGAATGGGACCTGCGCTCCAGGGTGGTCT
CGGTCCAGGGTGGTCCAGCTGGTGGGAGCCTCTGGCTGCATCTGTGCAGCCACATCCTTGTACAGAGGCATAG
GTTACACCCCCACCCCGGCCCGGGATACTGCCCCCGGCCAGATCCTGGCCGTCTCATCCATACTTCTGTGGG
GAATCAGCCTCCTGCCACCCCCCGGAAGGACCTCACTGTCTCCAGCTATGCCAGTGCTGCATGGGACCCATGT
CTCCTGGGACAGAGGCCATCTCTTCCAGAGAGGCGACATTGGCCACAGGATAAGCCTCAGGCCCTGGGAA
ACCTCCCGACCCCTGCACCTTCGTTGGAGCCCCCTGCATCCCTGGGTCCAGCCCCCTCTGCATTTACACAGATTT
GAGTCAGAACTGGAAAGTGTCCCCACCCCCACCCCTCGAGCGGGGTTCCCTCATTGTACAGATGGGGCAGG
ACCCAGCACGCTGCTGGCAGAGATGGTTTGAGAACACATCCAAGCCAGTCCCCCAGCCAGCTTCCCCTCCGTT
CCTAACTGTTGGCTTTCCCCCAGCCGACGGGTCCCAGGCCCCAGAGAAGATGAGTCTATGGCATCAGGTTCTTA
AACCAGGAAAGCACCTACAGACCGGCTCCTTCATGCATTTTACCAGCTCAACGCATCCACTCTCTGTTCTCTTG
GCAGGGCGGGGAGGGGGGATAGGAGGTCCCCCTTTCCCTAGGTGGTCTCATAATTCCATTTGTGGAGAGAACAG
GAGGGCCAGATAGATAGGTCCTAGCAGAAGGCATTGAGGTGAGGGATCATTTTGGGTGAGACATCAATGTCCCTG
TCCCCCTGGGTCCAGCCAAGCTGTGCCCCATCCCCAAGCCTCCTGGGAGGATCCAGCCAAATCTTGCGACTCC
TGGCACACACCTGTCTGTAACCTGTTTTGTGCTCTGAAAGCAAATAGTCTGAGCAAAAAAAAAAAAAAAAAACAA
AAAAAAAAAAAAAAAAACAAACAGTTTTTAAAACTGATTTTAGAAAAAGAGCTTAATCTAACGTTTTCAAACACA
AGGTCTCTTACAGGTATAGTTCCGTGATTATGATAGCTCTGTGATTATAAGCAACATCCCCGCCCCCTCTCCCC
CCGCGGACCCCCAGCTGCCTCCTGAGGGTGTGGGGTTATTAGGGTCTCAATACTTTCTCAAGGGGCTACACTCCC
CATCAGGCAGCATCCCACCAGCCTGCACCACAGGCTCCCCTGGGAGGACGAGGGAACGCTGATGAGACGCTGGG
CATCTCTCCTCTGTGGCTCTAGGACATCTGTCCAGGAGGCTGGGCGGAGGTGGGCAGGATGTGAGAGGTGGGGAG
TACTGGCTGTGCGTGGCAGGACAGAAGCACTGTAAAGGGCTCTCCAGCCGAGCTCAGCTGCACTGCGTTCCGAG
GTGAAGTCTTGCCCTGAATTTTGCAAAATGGGAAAGTGGGCGCTTGCCCAAGGGCCAGGCTGCATGGATTCTCA
CATCAGAGTTCTCTGGCCCTAGAAAGGCTTAGAAAAGGCGTAAGGGAACCTATAAAGGCTAGCAGCATGCGGTAT
TTTAACTTTCTGCTCGGCCCTCTGTGGATGCAGAAATCTGCCCTACAAAATGCTCTTCATTGGTTGTCTCTGTGA
GAGCACTGTCCCCACCAACCTGTCACAACGGCCAGAACCATACACCAGAGACACACTGGCAGGTTAGGCAGTCC
TTCTGGTGATCCTATTCCATTCCCTCCTGCTGCGGTTTCTCTTGGCCTGTCTCACTGGAAAAACAGTCTCCATC
TCCTCAAAATAGTTGCTGACTCCCTGCACCAAGGGGCTCTCCATGCCTTCTTAGGAAGCAGCTATGAATCCAT
TGTCCTTGATGTTTCTTCCCTCCTGTTCTCTGTTATAGCTGGTCCAGGTCAGCGTGGGAGGCACCTTTGGGTT

PCT/US2003/028547

FIGURE 101B

CCCAGTGCCCAGCACTTTGTAGTCTCATCCCAGATTACTAACCCCTTCCTGATCCTGGAGAGGCAGGGATAGTAAATAAATTGCTCTTCCCTACCCCATCCCCATCCCTGACAAAAAGTGACGGCAGCCGTACTGAGTCTGTAAGGCCCAAGTGGGTACAGACAGCCTGGGCTGGTAAAAGTAGGTCCTTATTTACAAGGCTGCGTTAAAGTTGTACTAGGCAAACACACTGATGTAGGAAGCACGAGGAAAGGAAGACGTTTTGATATAGTGTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCTGAGGTGTGACACCTGCTGCACCTCATCTGATGTAAACCATCCCAGAGCTGGCGAGAGGATGGAGCTGGGTGGAAACTGCTTTCGCACTATCGTTTGCTTGGTGTGTTTTTAACGCACAACTTGCTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGT

WO 2004/030615

PCT/US2003/028547

108/6881
FIGURE 102

CAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACACTTGTACCGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGACAAAGTTGTTACTGACTATGTTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAAGGAAGAAATAACAGATAAGTCCATTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACTTTGAGGAAAAGGTTTGAGAGGAATTATATTTA
AGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAGTATA
ACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTAGTATGATTAG
CATATGATCAAACCTCCATATTTGCCTTGGAATAATGGACTAAGGGAAATACTCTTAATTCATGAATAAAAACT
TTGCAGAAAATTAGACAGTGTTTAAATTTTCAAAAACCTCCCTCTCTAGTCGGTAGATACCACCTACCGATGGTTA
CATATACTAGGGAAATTTTAAAATTAGGAAATGCTGATATCTCATATTATAAATTTCTAAATCCTAGGAAGAAAC
GCTTGGAGTGCTTCTGAAGATACAGAAGTTCCATTTAAGGGCAAGTTTCCCATAGACGTATCAAAATATTACCC
ATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTCTAAAACAATCTGTCCACAAATATAAACTATA
AGTAATAAATTGTTATTTTCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTGTGAAAATAAATTTTAAAT
AAAATGTTGTATAATAA

WO 2004/030615

PCT/US2003/028547

109/6881
FIGURE 103

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGC GGTGCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCATGGTCAC TGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTTCATGGGGATGCCTCGCAGAAAGCTGCCAAGGCAGGGCTTTTGGCATT TTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTTGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

WO 2004/030615

PCT/US2003/028547

110/6881
FIGURE 104

MAVLRRRLSALYGAQGGRALLLRTPVIRPAHISAFIQDRPIPEWCGVQHLHLSPSHHPGSKAASLHWTSERVVSVL
LLGLLPAAAYLNPCSAMDYSLAATLTLPGHWGLRQVVTMFMGMPRRKLPRQGFWHFQL

WO 2004/030615

PCT/US2003/028547

111/6881
FIGURE 105

AGTGTGGTCAGGCGGCTCGGACTGAGCAGGACTTTCCCTTATCCCAGTTGATTGTGCAGAATACACTGCCTATCGC
TTGTCTTCTATTCACCAATGGCTTCTTCTGATATCCAGGTGAAAGAAGCTGGAGAAGCGTGCCTCAGGCCAGGCTTT
TGAGCTGATTCTCAGCCCTCGGTCAAAGAATCTGTTCCAGAATTCCCCCTTTCCCCTCCAAAGAAGAAGGATCT
TTCCCTGGAGGAAATTCAGAAGAAATTAGAAGCTGCAGAAGAAAGACGCAAGTCCCATGAAGCTGAGGTCTTGAA
GCAGCTGGCTGAGAAACGAGAGCACGAGAAAGAAGTGCTTCAGAAGGCAATAGAAGAGAACAACAACCTTCAGTAA
AATGGCAGAAGAGAACTGACCCACAAAATGGAAGCTAATAAAGAGAACCGAGAGGCACAAATGGCTGCCAACT
GGAACGTTTGCAGAGAAGGATAAGCACATTGAAGAAGTGCGGAAGAACAAGAATCCAAAGACCCTGCTGACGA
GACTGAAGCTGACTTAATTTGTCTGAGAAGTGACTTTCTCCCCATCCCCTTCCTAAATATCCAAAGACTGTACTG
GCCAGTGTCATTTTATTTTTTCCCTCCTGACAAATATTTTAGAAGCTAATGTAGGACTGTATAGGTAGATCCAGA
TCCAGACTGTAAGATGTTGTTTTAGGGGCTAAAGGGGAGAACTGAAAGTGTTTTACTCTTTTTCTAAAGTGTTG
GTCTTTCTAATGTAGCTATTTTTCTTGTTCATCTTTTCTACTTCAGTACACTTGGTGTACTGGGTAAATGGCTA
GTACTGTATTGGCTCTGTGAAAACATATTTGTGAAAAGAGTATGTAGTGGCTTCTTTTGAAGTGTTAGATGCTGA
ATACTGTTCACCTTTTCAATCCCAATTCTGTCCCAATCTTACCAGATGCTACTGGACTTGAATGGTTAATAAAAC
TGCACAGTGCTGTTGGTGGCAGTGACTTCTTTTGTAGTTAGGTAAATAAATCAAGCCATAGAGCCCCCTCCTGGTTG
ATACTTGTTCAGATGGGGCCTTTGGGGCTGGTAGAAATACCCAACGCACAAATGACCGCACGTTCTCTGCCCCG
TTTCTTGCCCCAGTGTTGGTTTGCATTGTCTCCTTCCACAATGACTGCTTTGTTTGGATGCCTCAGCCCAGGTCAG
CTGTTACTTTCTTTTCTAGATGTTTATTTGCAAACAACCATTTTTTGTCTGTGTCCCTTTTAAAAGGCAGATTAAA
AGCACAAGCGTGTTTCTAGAGAACAGTTGAGAGAGAATCTCAAGATTCTACTTGGTGGTTTGCTTGCTCTACGTT
ACAGGTGGGGCATGTCTCATCCTTTTCTGCCATAAAAGCTATGACACGAGAATCAGAATATTAATAAAACTTTA
TGTAAGTCTGT

WO 2004/030615

PCT/US2003/028547

112/6881
FIGURE 106

MASSDIQVKELEKRASGQAFELILSPRSKESVPEFPLSPPKKKDLSEELIQKKLEAAEERRKSHEAEVLKQLAEK
REHEKEVLQKAIEENNNFSKMAEEKLTHKMEANKENREAQMAAKLERLREKDKHIEEVRKNKESKDPADETead

WO 2004/030615

PCT/US2003/028547

113/6881
FIGURE 107

GTGCAACGGCCGTTAGAGGAGCTGAGGGAGGGAACACCGCTCACCGCAGACGTAGTGGCTGCAGTCAGTCTTCC
CGAGTGAGGGATTTGCGCGCCCGCTTTCAGGCCCCGTTTGGCTTAAATAACTGTGATTGATGGCCATGCAGGAGAA
ATATCCAACCTGAGGGGATCTCTCACGTCACTTCACCGAGTTCCGATGTGATTGATGAGAGGGCAGTTCCTGGGGAC
TGAATGGCAGACCCAGTTATCTCGGAGCCCTTTCGGAGCCGCTTCAGCCGCTGTTCAAGTGTAGCCGACAGTGG
GGACACAGCCATTGGTACATCATGCTCAGATATTGCGGAGGATTTTTGTCAGCTCAAGTGGCAGTCTCTCTTTCCA
GCCCATCAAAAGCCACGTAACCATTCCAACAGCCCCATGTGATGCCTTCTACTTTAGGGACCTCTCCTGCCAAGCC
AAATTCTACACCTGTTGGACCTCTTCTCTAAACTCCCTTTGTGAGGGTTGGCTGAAAGTGTGGGAATGACAAG
AAATGGAGACCTCGGTGCAATGAAACATTTCTCCAGGCCTATCTAGAGATCTCATGATTTCTCTGGTGCTACTGG
AGAAAATGGAATTGAGCAGTCTGTTTCCAGCAGTGGGCCATGAAAGACAAGAAGAGGCGAGGAAGTTTGATAT
TCCTAGCATGGAATCTACCTCAATCAGTCGGCAATGATGGAGACACTTTATTGAGATCCTCACCACCGAGTCCG
CTTCCACAACCCAAGAACAGCACAAGTAAGGAGTTGTACAGAGTGTGCTGAGGCCAAGAAGGCACCGGGCAG
CGGGGCAGTGTGTTGAGCGGAATGGACCACATTCTAATAGCAGTGGGGTCTCTCTTTGGGACTCCAGCCTGCTCC
CGGGCAGTCCAGCCAGCCTCTGCCCTCTCAGGTGTGGCAGCCGAGTCTGACACTTGGCATCCCCGAGAGCAATC
TTGTGAACCTCAGCACTTGTGCGGAGCAGCTGGAATTGATTGCTTTACAGATGGAGCAAATGCAGCTTCAGAAATGG
AGCCATCTGCCACCATCCTGCTGCTTTTGGTCTTCACTGCCCATCTTAGAGCCAGCACAGTGGATCAGCATCTT
GAACAGTAATGAACACCTTCTGAAGGAAAAAGAGCTTCTCATTGACAAGCAGAGGAAACACATCTCTCAGCTGGA
GCAGAAAGTGCGAGAGAGCGAACTGCAAGTCCACAGTGCCCTCTTGGGCCGCCCTGCCCCCTTTGGTGATGTCTG
CTTGCTGAGGGCTACAGGAATTGCAGCGAGAAAAACATTTCTTACGTGCACAGTTTGCACAGAAGACAGAAGCCTT
GAGCAGAGAAAAAGATTGACCTTGAAAAGAACTCTCTGCTTCTGAAGTTGAAGTCCAGCTCATCAGAGAGTCGCT
CAAAGTGGCGTTGCAGAAAGCATTTCTGAGGAAGTGAAGAAACAGGAAGAAAGGGTCAAAGGTCTGTATAAACATAT
CAATAATTTGAAAAAGAAATGCCAGAAGGAATCAGAGCAGAACCGGGAGAAGCAGCAGCGTATTGAGACCTTGGA
GCGCTACCTGGCTGACCTGCCACACTGGAAGACCATCAGAAGCAGAGCCAGCAGCTTAAGGATTCTGAGTTGAA
GAGCACAGAGCTGCAGGAGAAAGTGACTGAGCTGGAGAGTTTGCTGGAGGAGACCCAGGCAATCTGCAGAGAGAA
GGAGATTCAACTGGAAGCCTGAGGCAGAGAGAAGCAGAAATCTCCTCCGCTGGACATAGCCTGCAAGATAAACA
GTCTGTGGAGGAGACCAGTGGAGAAGGTCCAGAAGTGGAAATGGAGTCTTGGCAGAAGCGATACGATTGCTCCA
AAAGATTGTGGAGAAGCAGCAGCAGAAGATGGATCAGTTGCGCTCACAAGTACAGAGCCTAGAGCAGGAAGGCTGC
TCAAGAAGAAGGAACAAGCCAGGCCCTGAGAGAGGAGGCCAGCGAAGGGATTGAGCCCTGCAGCAGCTGCGCAC
AGCCGTGAAGGAGCTTTCAGTGCAAAACCAGGACTTGATTGAGAAGAACTGACACTCCAGGAACACCTGCGCCA
GGCCCAACCAGGGTCTCCACCTTCACCAGACACGGCCAGCTGGCACTTGAGCTGCACCAGGAGTTGGCCAGTTG
CCTTCAAGATCTGCAGGCTGTCTGTAGCATTGTGACCCAGAGGGGCCAGGGCCATGACCCCAATCTCTCCCTGCT
CCTGGGCATTCACTCACAGCACCAGAGACTCAGTAGATTGTCAGAAGCCAGATGTGATCAAGAGGAACTAGA
AGAGGTTCAACAGCTGCGTCTGTGACATTGAGGACTTAAGGACCACCATGTGACAGAGATATGCCAGGACATGGG
AGAAAACCTGTGTCACACAGTGAAGGAATTCTGGGGGATTCCTCCAGGGAGGAGCTGGGCTGCTGAGAGCCTAGTCC
AGCAGGTTTCTGCCCTGACATTCTTGTCTGCTATTCCAGAGAGGTCTCAGAGGGGAGGGGAGAGCCTGCATC
TGGGGGCCAAGGGCTGATTAGGGAAGTGTGCTCTACCCACACTGGCATGTTGGATTACGTTTGTCTGTTAATTC
ACTCTCGACGGTGAGTTACTAATTAACTTTGGCAGGTACAACAGATAAGTCTCACAACCTGTTCCAGCCCTA
GGCTGACATTGAGAGACGAACAGGCTGTCCACCTTCTTCTCCATCCAATGGGATGGATCCATGTTTCAATCCACT
TCACACCTTGGTCTGCTGATTAGAGAGCTCATCAGAGGGGCCCTGGAAAGGCTGAGCAAGTACCAGTGACAATGG
CCATTTAAGAATTTCTCAGGCCCCATGTGCCAGCCTTCTTGGGAAGTGAAGTGGCTTTCTGGGTTTTCTCATGCCT
GGTCTTACTGCTTCTTCTCAGGGCTCTTGTCTCTCCAGAGCCTCAGGGTAATGTGTTGGTTAGCACGTAACATA
CTAGGATTGGGGCCCTAGGGATTATAGCCAGGACTCTAATCTGCCTACCATGCCATTTAACAAGAGATCCCACTC
TCCAGCTGCCTTGTGTCCTAGGGTCTGCGCATGTGTTAGTGTGCTAAACTTTCTCTTTGTTCTCAGGCCTT
CCAGGTAGTCCCCCTCTGGACTTAAGAGTGCAAACTCTTCTGTGTTTCTAGCCTTGGGCAGAAATATATCCC
AGAGACCACAGAGCAACTGTCAAGCTGCTTACCCCTCACCCAGGGCTACAGCCTGTGCCAGCCCTCTAATTTG
TGCTCTCTTGTGTTGGGGGTGGTGGGGGTATTTCCTTTCCCTTTCTGCTCTGGCTCCTTGAAAGTTGAGAGT
ACCCAGTACAAGTCAGCCACCATGCTGACGGGTATTTTCTCATAAAGTTTATAACCAGTTATTTATATGAATC
TTTGTATGTCCATTTGTTTGTATTGCGTATTTTGATTATAAAATAAAGTATCTTAACAG

WO 2004/030615

PCT/US2003/028547

114/6881
FIGURE 108

MAMQEKYPTEGISHVTSPSSDVIQKGSSLGTEWQTPVISEPFRSRFSRCSSVADSGDTAIGTSCSDIAEDFCSSS
GSPPFQPIKSHVTIPTAHVMPSTLGTSPAKPNSTPVGPSSSKLP LSGLAESVGMTRNGDLGAMKHSPGLSRDLMY
FSGATGENGIEQSWFFPAVGHERQEEARKFDIPSMESTLNQSAMMETLYSDPHHRVRFHNPRTSTSKELYRVLPEA
KKAPGSGAVFERNGPHSNSSGVLPLGLQPAPGHSSQPLPSQVWQPSPTDTHPREQSCELSTCRQQLELIRLQMEQ
MQLONGAICHHPAAFGPSLPILPAQWISILNSNEHLLKEKELLIDKQRKHISQLEQKVRESELQVHSALLGRPA
PFGDVCLLRLLQELQRENTFLRAQFAQKTEALSREKIDLEKKLSASEVEVQLIRESLKVALQKHSEEVKKQEERVK
GRDKHINNLLKKKCQKESEQNREKQQRIETLERYLADLP TLEDHQKQSQQLKDSELKSTELQEKVTELESLLLEETQ
AICREKEIQLESLRQREAEFSSAGHSLQDKQSVEETS GEGPEVEMESWQKRYDSLQKIVEKQQQKMDQLRSQVQS
LEQEVAQEEGTSQALREEAQRDSALQQLR TAVKELSVQNQDLIEKNLTLQEHRLQAQPGSPSPDQAQLALELH
QELASCLQDLQAVCSIVTQRAQGHDPNLSLLLGIHSQHPETQLDLQKPDVIKRLKEEVQQLRRDIEDLRTTMSDR
YAQDMGENCVTQ

WO 2004/030615

PCT/US2003/028547

115/6881
FIGURE 109

GTAGCAGCTTCTTCTCCGAACCAACCCTTTGCCTTCGGACTTCTCCGGGGCCAGCAGCCGCCGACCAGGGGCCCC
GGGGCCACGGGCTCAGCCGACGACCATGGGCTCCGTGTCCAACCAGCAGTTTGCAGGTGGCTGCGCCAAGCGGGC
AGAAGAGGCGCCCCGAGGAGGCGCCGGAGGACGCGGCCCGGGCGGGACGAGCCTCAGCTGCTGCACGGTGCGGG
CATCTGTAAGTGGTTCAACGTGCGCATGGGGTTGGGCTTCTGTCCATGACCGCCCGCGCCGGGGTCCGCTCGA
CCCCCAGTGGATGTCTTTGTGCACCAGAGTAAGCTGCACATGGAAGGGTTCCGGAGCTTGAAGGAGGGTGAGGC
AGTGGAGTTCACCTTTAAGAAGTCAGCCAAGGGTCTGGAATCCATCCGTGTCACCGGACCTGGTGGAGTATTCTG
TATTGGGAGTGAGAGGCGGCCAAAAGGAAAGCATGCGAGAAGCGCAGATCAAAAGGAGACAGGTGCTACAACCTG
TGGAGGTCTAGATCATCATGCCAAGGAATGCAAGCTGCCACCCAGCCCAAGAAGTGCCACTTCTGCCAGAGCAT
CAGCCATATGGTAGCCTCATGTCCGCTGAAGGCCAGCAGGGCCCTAGTGCACAGGGAAAGCCAACCTACTTTTCG
AGAGGAAGAAGAAGAAATCCACAGCCCTACCCTGCTCCCGAGGCACAGAATTGAGCCACAATGGGTGGGGGCTA
TTCTTTTGGCTATCAGGAAGTTTTGAGGAGCAGGCAGAGTGGAGAAAGTGGGAATAGGGTGCATTGGGGCTAGTTG
GCACTGCCATGTATCTCAGGCTTGGGTTCACACCATCACCTTTCTTCCCTCTAGGTGGGGGGAAAGGGTGAGTC
AAAGGAACCTCAACCATGCTCTGTCCAATGCAAGTGAGGGTTCTGGGGGCAACCAGGAGGGGGGAATCACCTTA
CAACCTGCATACTTTGAGTCTCCATCCCCAGAATTTCCAGCTTTTGAAAGTGGCCTGGATAGGGAAGTTGTTTTT
CTTTTAAAGAAGGATATATAATAATTCCTATGCCAGAGTGAAATGATTAAGTATAAGACCAGATTCTAGGAGCCA
AGCCACTACATTCTGTGGAAGGAGATCTCTCAGGAGTAAGCATTGTTTTTTTTTTCACATCTTGATCCTCATACC
CACTTTTGGGATAGGGTGTCTGGCAGCTGTCCCAAGCAATGGGTAAATGATGATGGCAAAAAGGGTGTGGGGGAA
CAGCTGCAGACCTGCTGCTCTATGCTCACCCCGCCCCATTCTGGGCCAATGTGATTTTATTTATTTGCTCCCTT
GGATACTGCACCTTGGGTCCCACTTTCTCCAGGATGCCAAGTGCAGTGTGTGCGAATGACGTATCTTGTC
ATTTTAACTTTTTTTTCTTAATATAAATATTCTGGTTTTGTATTTTGTATATTTTAACTAAGGCCCTCATTTT
CTGCACTGTGTTCTCAGGTACATGAGCAATCTCAGGGATAGCCAGCAGCAGCTCCAGGTCTGCGCAGCAGGAATT
ACTTTTTGTTGTTTTTGGCACCGTGGAGAGCAACTATTGGAGTGCACAGCCTATTGAACTACCTCATTTTTGCC
AATAAGAGCTGGCTTTTCTGCCATAGTGTCTCTTGAACCCCCCTCTGCCTTGAAATGTTTTATGGGAGACTAG
GTTTTAACTGGGTGGCCCCATGACTTGATTGCCTTCTACTGGAAGATTGGGAATTAGTCTAAACAGGAAATGGTG
GTACACAGAGGCTAGGAGAGGCTGGGCCCCGTGAAAAGGCCAGAGAGCAAGCCAAGATTAGGTGAGGGTTGTCTA
ATCCTATGGCACAGGACGTGCTTTACATCTCCAGATCTGTTCTTACCAGATTAGGTTAGGCCTACCATGTGCCA
CAGGGTGTGTGTGTTTTGTAAGTGTGTAAGGATAAGTTTTAAAGACCAATACCCCTGTACTTAATCCT
GTGCTGTGAGGGATGGATATATGAAGTAAGGTGAGATCCTTAACCTTTCAAATTTTGGGTTCCAGGGAGACA
CACAAGCGAGGGTTTTGTGGTGCCTGGAGCCTGTGCTGCTGCTACAGTAGTGATTAATAGTGTATGGTAG
CTAAAGGAGAAAAAGGGGGTTTTGTTTTACACGCTGTGAGATCACCGCAAACCTACCTTACTGTGTTGAAACGGGA
CAAATGCAATAGAACGCATTGGGTGGTGTGTGCTGATCCTGGGTCTTGTCTCCCTAAATGCTGCCCCCAAG
TTACTGTATTTGTCTGGGCTTTGTAGGACTTCACTACGTTGATTGCTAGGTGGCCTAGTTTGTGTAATATAATG
TATTGGTCTTTCTCCGTGTTCTTTGGGGTTTTGTTTACAACTTCTTTTTGTATTGAGAGAAAAATAGCCAAAG
CATCTTTGACAGAAGGTTCTGCACCAGGCAAAAAGATCTGAAACATTAGTTTGGGGGGCCCTCTTCTTAAAGTGG
GGATCTTGAACCATCCTTTCTTTTGTATTCCCTTCCCTATTACCTATTAGACCAGATCTTCTGTCTTAAAC
TTGTCTTCTACCTGCCCTCTTTCTGTTTACCCCCAAAAGAAAACCTTACACACCCACACACATACATTTTCAT
GCTTGGAGTGTCTCCACAACCTCTTAAATGATGTATGCAAAAATACTGAAGCTAGGAAAACCCCTCCATCCCTTGTT
CCCAACCTCCTAAGTCAAGACCATTACCATTTCTTTCTTTTCTTTTTTTTTTTTTTAAATGGAGTCTCACTGT
GTCACCCAGGCAGAGGTTGCAGTGAGCTGAGATCGCACCCTGCACTCCAGCCTGGTTACAGAGCAAGACTCTGT
CTCAACAAAAACAAAACAAAACAAAACACACTACTGTATTTTGGATGGATCAAACCTCCTTAATTTTAAATTTCT
AATCCTAAAGTAAAGAGATGCAATTGGGGCCCTCCATGTAGAAAGTGGGGTCAGGAGGCCAAGAAAGGGAATAT
GAATGTATATCCAAGTCACTCAGGAACTTTATGCAGGTGCTAGAAACCTTATGTCAAAGTGGCCACAAGATTGT
TTAATAGGAGACGAACGAATGTAACCTCATGTTTACTGCTAAAAACCAAAGCTTTGTGTAATCTTGAATTTAT
GGGGCGGGAGGGTAGGAAAGCCTGTACCTGTCTGTTTTTTTCTGATCCTTTTCCCTCATTCCTGAACCTGCAGGA
GACTGAGCCCCCTTTGGGCTTTGGTGACCCCATCACTGGGGTGTGTTTTATTTGATGGTTGATTTTGTGTACTGGG
TACTTCTTTCCCATTTTCTAATCATTTTTTAACACAAGCTGACTCTTCCCTTCCCTTCTCCTTTCCCTGGGAAA
ATACAATGAATAAATAAAGACTTATTGGTACGC

WO 2004/030615

PCT/US2003/028547

116/6881
FIGURE 110

GAGCAGTGTGAAGAAGAGGCGAGAACGACCCCCGGACCGACCAAAGCCCGCGCGCCGCTGCATCCCGCGTCCAGC
ACCTACGTCCCGCTGCCGTCGCCGCCGCCACCATGCCCAAGAGAAAGGCTGAAGGGGATGCTAAGGGAGATAAAG
CAAAGGTGAAGGACGAACCACAGAGAAGATCCGCGAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCA
AGCCTAAAAAGGCCCTTGCAAAGAAGGGAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCTGGCAAGG
AGGGGAATAACCTGCAGAAAAATGGAGATGCCAAAACAGACCAGGCACAGAAAGCTGAAGGTGCTGGAGATGCCA
AGTGAAGTGTGTGCATTTTTGATAACTGTGTACTTCTGGTGACTGTACAGTTTGAAATACTATTTTTTATCAAGT
TTTATAAAATGCAGAATTTTGTCTTTACTTTTTTTTTTTTTTTTAAAAGCTATGTTGTTAGCACACAGAACTTC
ATTGTTGTTTTTGGGGGAAGGGGCATATGTCATAATAGAATGTCTCCAAAGCTGGATTGATGTGGAGAAAACAC
CTTTCCTTCTAGTTTTGAGAGACTTCTCTTGGCTCCAGGAGGAGGGATTCCCTGACTTTGACACACATGGCC
ACCTTGGCACAAAAGCCTTGTGGTATAGAAAAACAAATTTGTTTTTATGTCTCTTCTCCCTTTCCATCTTTTCAG
CATAGACTTAACCTCCCTTAAGCCCAGACATCTGTTGAGACCTGACCCCTAGTCATTGGTTACCAGTGTGTGAGGC
AATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAAGAGCAGTGTTCCATTTCTAGATTGTGGAT
CTTCAGATAAATTCTGCCATTTTCATTTCACTTCCCTGAAAGTCAGGGTCGGCTTGTGAAAAAGTTGTTAAACAACA
TGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTTCAGAGCATCAGATGAAGACTTCATTGGGTTT
TATAGTGGCTTTCTGATTTTTGGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTATACTGTTAACGATTGT
CTGCCCATGTCCTGCCTGAAATACCATGATTGTTTATGGAAAGTATCTTTAATAAAGCTGGATACAGTTTGGC

WO 2004/030615

PCT/US2003/028547

117/6881
FIGURE 111

MPKRKAEGDAKGDKAKVKDEPQRRSARLSAKPAPPKPEPKPKKAPAKKGEKVPKGKKGKADAGKEGNNPAENGDA
KTDQAQKAEGAGDAK

WO 2004/030615

PCT/US2003/028547

118/6881
FIGURE 112A

GAAAGCGGAGAGTCACAGCGGGGCCAGGCCCTGGGGAGCGGAGCCTCCACCGCCCCCTCATTCCCAGGCAAGGG
CTTGGGGGGAATGAGCCGGGAGAGCCGGGTCCCGAGCCTACAGAGCCGGGAGCAGCTGAGCCGCCGGCGCCTCGG
CCGCCGCCGCCGCTCCTCCTCCTCCGCCGCCGCCAGCCCGGAGCCTGAGCCGGCGGGGCGGGGGGAGAGGAGC
GAGCGCAGCGCAGCAGCGGAGCCCCGCGAGGCCGCCGGCGGGTGGGGAGGGCAGCCCGGGGACTGGGCCCC
GGGGCGGGGTGGGAGGGGGGAGAAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTCGAGGCGGCGGCTGCGGCAGCGGC
CGAGCGCGGTGGAATGAAGGCAGCCGCCGGGCAGGAAAGCGAGGGCCCCGCCGTGGGGCGCCGCATCCGCTGG
GAAAGGAGCTGCTGGACGGGGCCGAGAGCAATGGGGTGGCGCGGCGGCGGAGCCGGCAGCGGCGGCGGGCCCG
GCGCGGAGCCGGACCTGAAGAACTCGAACGGGAACGCGGGCCCTAGGCCCGCCCTGAACAATAACCTCACGGAGC
CGCCCGGCGGCGGCGGTGGCGGCAGCAGCATGGGGTGGGGGCGCCTCCTCACTCAGCCGCGGCGGCCTTGCCGC
CCCCAGCCTACGGCTTCGGGCAACCTACGGCCGAGCCCGTCTGCCGTGCGCGCCGCGCGGCGGCGCGCTTCC
ACCAACAACATGGCGGACAACAAAGCCCTGGCCTGGCAGCGCTGCAGAGCGGCGGCGGGGGGCTGGAGCCCT
ACGCGGGGGCCCCAGCAGAACTCTCAGACCACGGCTTCCCCAACCCAGTACAACCTCTACTACCCCAACCGCA
GCGCTACCCCCCGCCGCCCGGCTACGCGCTGAGCTCCCCGAGAGGTGGCACTCCGGGCTCCGGCGCGGCGG
CGGCTGCCGGCTCCAAGCCGCTCCCTCCTCCAGCGCCTCCGCCTCCTCGTCTCTTCGTCCTTCGCTCAGCAGC
GCTTCGGGGCCATGGGGGAGGCGGCCCTCCGCGGCCGCGGGGGAACCTCCCGAGCCACCGCCACCCCAACC
TCAACCAACTGCTCACGTCGCCCAGCTCGGCCCGGGGCTACCGGGCTACCCCGGGGGCGACTACAGTGGCGGGC
CCCAGGACGGGGGCGCCGGCAAGGGCCCGGCGGACATGGCCTCGCAGTGTGGGGGGCTGCGGCGGCGGCGAGCTG
CGGCGGCGGCGCCTCGGGAGGGGGCCAAAGAGGCCACACGCGCCATGAGCCCCGGGAGCAGCGGCGGCG
GGGGGCGAGCCGCTCGCCCGGACCCCTCAGCCATCCAGTCCAATGGATCAGATGGGCAAGATGAGACCTCAGCCAT
ATGGCGGGGACTAACCCTACTCGCAGCAACAGGGACCTCCGTGAGGACCGCAGCAAGGACATGGGTACCCAGGGC
AGCCATACGGGTCCCAGACCCCGCAGCGGTACCCGATGACCATGCAGGGCCGGGCGCAGAGTGCCATGGGCGGCC
TCTCTTATACACAGCAGATTCTCTTATGGACAACAAGGCCCGAGCGGGTATGGTCAACAGGGCCAGACTCCAT
ATTACAACCAGCAAGTCTCTACCCCTCAGCAGCAGCAGCCACCTACTCCCAGCAACCACCGTCCCAGACCCCTC
ATGCCCAACCTTCGTATCAGCAGCAGCCACAGTCTCAACCACACAGCTCCAGTCTCTCAGCCTCCATACTCCC
AGCAGCCATCCCAGCCTCCACATCAGCAGTCCCCGGCTCCATACCCCTCCCAGCAGTCGACGACACAGCAGCACC
CCCAGAGCCAGCCCCCTACTCACAGCCACAGGCTCAGTCTCCTTACCAGCAGCAGCAACCTCAGCAGCCAGCAC
CCTCGACGCTCTCCCAGCAGGCTGCGTATCCTCAGCCCCAGTCTCAGCAGTCCCAGCAAACTGCCTATTCCCAGC
AGCGCTTCCCTCCACCGCAGGAGCTATCTCAAGATTCAATTTGGGTCTCAGGCATCCTCAGCCCCCTCAATGACCT
CCAGTAAGGGAGGGGAAGAAGATATGAACCTGAGCCTTCACTCAAGACCCTCCAGCTTGCCGTGATCTATCTGGTT
CAATAGATGACCTCCCCATGGGGACAGAAGGAGCTCTGAGTCTGGAGTGAGCACATCAGGGATTTCCAGCAGCC
AAGGAGAGCAGAGTAATCCAGCTCAGTCTCCTTTCTCTCTCATACCTCCCTCACCTGCCTGGCATCCGAGGCC
CTTCCCCGTCCCTGTTGGCTCTCCCGCCAGTGTGCTCAGTCTCGCTCAGGACCACTCTCGCTGCTGCAGTGC
CAGGCAACCAGATGCCACCTCGGCCACCCAGTGGCCAGTGGACAGCATCATGCATCCTTCCATGAACCAATCAA
GCATTGCCCAAGATCGAGGTTATATGCAGAGGAACCCCGATGCCCGAGTACAGTCCCCCGAGCCCGGCTCAG
CCTTATCTCCGCTCAGCCTTCCGGAGGACAGATACACACAGGCATGGGCTCCTACCAGCAGAACTCCATGGGGA
GCTATGGTCCCCAGGGGGTCAATATGGCCACAAGGTGGCTACCCAGGCAGCCAACTATAATGCCTTGCCCA
ATGCCAACTACCCAGTGCAGGCATGGCTGGAGGCATAAACCCCATGGGTGCCGGAGGTCAAATGCATGGACAGC
CTGGCATCCACCTTATGGCACACTCCCTCCAGGGAGGATGAGTCACGCTCCATGGGCAACCGGCTTATGGCC
CTAACATGGCCAATATGCCACCTCAGGTTGGGTGAGGATGTGTCCCCACAGGGGGCATGAACCGGAAACCC
AAGAAACTGCTGTGCGCATGCATGTTGCTGCCAACTCTATCCAAAACAGGCCGCCAGGCTACCCCAATATGAATC
AAGGGGGCATGATGGGAAGTGGACCTCCTTATGGACAAGGGATTAATAGTATGGCTGGCATGATCAACCTCAGG
GACCCCATATTCCATGGGTGGAACCATGGCCAACAATTCTGCAGGGATGGCAGCCAGCCAGAGATGATGGGCC
TTGGGGATGTAAAGTTAACTCCAGCCACCAAAATGAACAACAAGGCAGATGGGACACCAAGACAGAATCCAAAT
CCAAGAAATCCAGTTCTTCTACTACAACCAATGAGAAGATCACCAGTTGTATGAGCTGGGTGGTGAGCCTGAGA
GGAAGATGTGGGTGGACGTTATCTGGCCTTCACTGAGGAGAAGGCCATGGGCATGACAAATCTGCCTGCTGTGG
GTAGGAAACCTCTGGACCTCTATCGCCTCTATGTGTCTGTGAAGGAGATTGGTGGATTGACTCAGGTCAACAAGA
ACAAAAATGGCGGGAACCTGCAACCAACCTCAATGTGGGCACATCAAGCAGTGCTGCCAGCTCCTTGAAAAAGC

WO 2004/030615

PCT/US2003/028547

119/6881
FIGURE 112B

AGTATATCCAGTGTCTCTATGCCTTTGAATGCAAGATTGAACGGGGAGAAGACCCTCCCCCAGACATCTTTGCAG
CTGCTGATTCCAAGAAGTCCCAGCCCAAGATCCAGCCTCCCTCTCCTGCGGGATCAGGATCTATGCAGGGGGCCCC
AGACTCCCCAGTCAACCAGCAGTTCCATGGCAGAAGGAGGAGACTTAAAGCCACCAACTCCAGCATCCACACCAC
ACAGTCAGATCCCCCATTTGCCAGGCATGAGCAGGAGCAATTCAGTTGGGATCCAGGATGCCTTTAATGATGGAA
GTGACTCCACATTCCAGAAGCGGAATTCCATGACTCCAAACCTGGGTATCAGCCCAGTATGAATACCTCTGACA
TGATGGGGCGCATGTCTATGAGCCAAATAAGGATCCTTATGGCAGCATGAGGAAAGCTCCAGGGAGTGATCCCT
TCATGTCTCAGGGCAGGGCCCCAACGGCGGGATGGGTGACCCCTACAGTCGTGCTGCCGGCCCTGGGGCTAGGAA
ATGTGGCGATGGGACCACGACAGCACTATCCCTATGGAGGTCTTATGACAGAGTGAGGACGGAGCCTGGAATAG
GGCCTGAGGGAAACATGAGCACTGGGGCCCCACAGCCGAATCTCATGCCTTCCAACCCAGACTCGGGGATGTATT
CTCCTAGCCGCTACCCCCCGCAGCAGCAGCAGCAGCAGCAACGACATGATTCTATGGCAATCAGTTCTCCA
CCCAAGGCACCCCTTCTGGCAGCCCCCTTCCCCAGCCAGCAGACTACAATGTATCAACAGCAACAGCAGAATTACA
AGCGGCCAATGGATGGCACATATGGCCCTCCTGCCAAGCGGCACGAAGGGGAGATGTACAGCGTGCCATACAGCA
CTGGGCAGGGGCGAGCCTCAGCAGCAGCAGTTCGCCCCAGCCAGCCCGAGCCTGCCAGCCAGCAACAAGCTGCCC
AGCCTTCCCCCTCAGCAAGATGTATACAACCAGTATGGCAATGCCTATCCTGCCACTGCCACAGCTGCTACTGAGC
GCCGACCAGCAGGCGGGCCCCCAGAACCAATTTCCATTCCAGTTTGGCCGAGACCGTGTCTCTGCACCCCTGGCA
CCAATGCCCAGCAAAACATGCCACCACAAATGATGGGCGGGCCCATACAGGCATCAGCTGAGGTTGCTCAGCAAG
GCACCATGTGGCAGGGGCGTAATGACATGACCTATAATTATGCCAACAGGCAGAGCACGGGCTCTGCCCCCAGG
GCCCCGCCTATCATGGCGTGAACCGAACAGATGAAATGCTGCACACAGATCAGAGGGCCAACCACGAAGGCTCGT
GGCCTTCCCATGGCACACGCCAGCCCCCATATGGTCCCTCTGCCCCCTGTGCCCCCATGACAAGGCCCCCTCCAT
CTAACTACCAGCCCCCACCAGCATGCAGAATCACATTCTCAGGTATCCAGCCCTGCTCCCCCTGCCCCGGCCAA
TGGAGAACC GCACCTCTCCTAGCAAGTCTCCATTCTGCACTCTGGGATGAAAATGCAGAAGGCAGGTCCCCCAG
TACCTGCCTCGCACATAGCACCTGCCCCGTGTGCAGCCCCCATGATTTCGGCGGGATATCACCTTCCCACCTGGCT
CTGTTGAAGCCACACAGCCTGTGTTGAAGCAGAGGAGGCGGCTCACAATGAAAGACATTGGAACCCCGGAGGCAT
GGCGGGTAATGATGTCCCTCAAGTCTGGTCTCCTGGCAGAGAGCACATGGGCATTAGATACCATCAACATCCTGC
TGTATGATGACAACAGCATCATGACCTTCAACCTCAGTCAGTCCCAGGGTTGCTAGAGCTCCTTGTAAGATATT
TCCGACGATGCCTGATTGAGATCTTTGGCATTTTAAAGGAGTATGAGGTGGGTGACCCAGGACAGAGAACGCTAC
TGGATCCTGGGAGGTTTACGAAGGTGTCTAGTCCAGCTCCCATGGAGGGTGGGGAAGAAGAAGAAGAACTTCTAG
GTCCTAAACTAGAAGAGGAAGAAGAAGAGGAAGTAGTTGAAAATGATGAGGAGATAGCCTTTTCAGGCAAGGACA
AGCCAGCTTCAGAGAATAGTGAGGAGAAGCTGATCAGTAAGTTTGACAAGCTTCCAGTAAAGATCGTACAGAAGA
ATGATCCATTTGTGGTGGACTGCTCAGATAAGCTTGGGCGTGTGCAGGAGTTTGACAGTGGCCTGCTGCACTGGC
GGATTGGTGGGGGGGACACCACTGAGCATATCCAGACCCACTTCGAGAGCAAGACAGAGCTGCTGCCTTCCCGGC
CTCACGCACCTTGCCACCAGCCCCCTCGGAAGCATGTGACAACAGCAGAGGGTACACCAGGGACAACAGACCAGG
AGGGGCCCCCACCTGATGGACCTCCAGAAAACGGATCACAGCCACTATGGATGACATGTTGTCTACTCGGTCTA
GCACCTTGACCGAGGATGGAGCTAAGAGTTTCAAGAGGCATCAAGGAGAGCAGCAAGTTTCCATTGGCATTAGCC
CAGCACAGAGCCACCGGAACATCAAGATCCTAGAGGACGAACCCACAGTAAGGATGAGACCCCACTGTGTACCC
TTCGGACTGGCAGGATTCTCTTGCCAAGCGCTGCGTGTGTGTCCAATACCATTGGAAGCCTGTCTTTGTGC
CAGGCAATGACTTTGAGATGTCCAACACCCAGGGCTGCTGCTCATCCTGGGCAAGCTGATCCTGCTGCACCACA
AGCACCCAGAACGGAAGCAGGCACCACTAAGTTATGAAAAGGAGGAGGAACAGGACCAAGGGGTGAGCTGCAACA
AAGTGGAGTGGTGGTGGGACTGCTTGGAGATGCTCCGGGAAAACACCTTGGTTACACTCGCCAACATCTCGGGGC
AGTTGGACCTATCTCCATACCCCGAGAGCATTGTCCTGCCTGTCTGGACGGACTCCTACACTGGGCAGTTTGGC
CTTCAGCTGAAGCCAGGACCCCTTTTCCACCCTGGGCCCCAATGCCGTCTTTCCCCGAGAGACTGGTCTTGG
AAACCCTCAGCAAACTCAGCATCCAGGACAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCTGG
AGAAGTTGTATAGCACTATGGTGGCCTTCTCAGTGACCGAAAGAACCCGGTGTGCCGGGAGATGGCTGTGGTAC
TGCTGGCCAACCTGGCTCAGGGGGACAGCCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACC
TCCTGGGCTTCTAGAGGACAGCCTTGCCGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGA
ACCCACCCCTTTGAGCCAACCTAGTGTGGACATGATGCGCGGGCTGCCCGCGCGCTGCTTGCTTGGCCAAGGTGG
ACGAGAACCCTCAGAGTTTACTCTGTACGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACCTCAT
TGGTTTACAAAGTCATTTGTGATGTACTGTTTTTATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCC

WO 2004/030615

PCT/US2003/028547

120/6881
FIGURE 112C

GTGTGTGTGTGCGTGTGTGGAGAACTTAGAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCA
GTTTACCCTGTGCTGTCCAGCTTCTCCCTTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCT
CCCTCCATCACCTCAGCCTTTCTGTTCCCTTGTCCTCACCTTACTCCCCTCAGGACCCTACCCACCCCTCTTTGA
AAAGACAAAGCTCTGCCTACATAGAAGACTTTTTTTATTTTAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGG
GAAAAAAAAATAAAATAAAATGGCTTTCCAGTCCTTGTCATCAACGGGATGCCACATTTCATAACTGTTTTTAAT
GGTAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

121/6881
FIGURE 113

CAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCCTGGAGAAGTTGTATAGCACTATGGTGCGCTT
CCTCAGTGACCGAAAGAACCCGGTGTGCCGGGAGATGGCTGTGGTACTGCTGGCCAACCTGGCTCAGGGGGACAG
CCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACCTCCTGGGCTTCCTAGAGGACAGCCTTGC
CGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGAACCCACCCTTTGAGCCAACTAGTGTGGA
CATGATGCGGCGGGCTGCCCCGCGCTGCTTGCCTTGGCCAAGGTGGACGAGAACCACCTCAGAGTTTACTCTGTA
CGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACCTCATTGGTTTCACAAGTCATTGTGTATGTACT
GTTTTTGATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCCCGTGTGTGTGTGCGTGTGTGGAGAACTTA
GAAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCAGTTTACCCTGTGCTGTCCAGCTTCTCCC
TTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCTCCCTCCATCACCTCACGCCTTCTGTTC
CTTGTCCTCACCTTACTCCCCCTCAGGACCCCTACCCACCCCTCTTTGAAAAGACAAAGCTCTGCCTACATAGAAGA
CTTTTTTTATTTTAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGGGAAAAAAAATAAAATAAAATGGCTTTC
CCAGTCCTTGTCATCAACGGGATGCCACATTTTATAACTGTTTTTAATGGTAAAAAAAAAAAAAAAAATAAAAA
AAAAATTCTGAAGGACAAAAAAGGTGACTGCTGAACTGTGTGTGGTTTATTGTTGTACATTCACAATCTTGCAGG
AGCCAAGAAGTTTCGCAGTTGTGAACAGACCCTGTTCACTGGAGAGGCCTGTGCAGTAGAGTGTAGACCCTTTCAT
GTACTGTACTGTACACCTGATACTGTAAACATACTGTAATAATAATGTCTCACATGGAAACAGAAAACGCTGGGT
CAGCAGCAAGCTGTAGTTTTTAAAAATGTTTTTAGTTAAACGTTGAGGAGAAAAAAAAAAAAAGGCTTTTCCCCCA
AAGTATCATGTGTGAACCTACAACACCCTGACCTCTTCTCTCCTCCTTGATTGTATGAATAACCCTGAGATCAC
CTCTTAGAACTGGTTTTTAACCTTTAGCTGCAGCGGCTACGCTGCCACGTGTGTATATATATGACGTTGTACATTG
CACATACCCCTGGATCCCCACAGTTTGGTCCTCCTCCCAGCTACCCCTTTATAGTATGACGAGTTAACAAGTTGG
TGACCTGCACAAAGCGAGACACAGCTATTTAATCTCTTGCCAGATATCGCCCCTCTTGGTGCGATGCTGTACAGG
TCTCTGTAAAAAGTCCTTGCTGTCTCAGCAGCCAATCAACTTATAGTTTATTTTTTCTGGGTTTTTGTGTTTGT
TTGTTTTCTTTCTAATCGAGGTGTGAAAAAGTTCTAGGTTTCAAGTTCTGATGAAGAAACACAATTGAGAT
TTTTTCAGTGATAAAATCTGCATATTTGTATTTCAACAATGTAGCTAAACTTGATGTAAATTCCTCCTTTTTTT
CCTTTTTTGGCTTAATGAATATCATTTATTTCAGTATGAAATCTTTATACTATATGTTCCACGTGTTAAGAATAAA
TGTACATTAAATCTTGGT

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

123/6881
FIGURE 115

MERASLIQKAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVVGQRAAWRVLSSIEQKSNEEGSE
EKGPEVREYREKVETELQGVCDTVLGLLDSHLIKEAGDAESRVFYLMKGDYYRYLAEVATGDDKKRIIDSARSA
YQEAMDISKEMPPTNP IRLGLALNFSVFHYEIANSPEEAISLAKTTFDEAMADLHTLSEDSYKDSTLIMQLLRD
NLTLWTADNAGEEGGEAPQEPQS

WO 2004/030615

PCT/US2003/028547

124/6881
FIGURE 116

CCGGAAGTCGAGTTAGTCTAGTTAGTATCGGCCTGTTATCTCCTTTTGGCGGACACGGTCTCAGCTGTTCCGCCT
GAGGCGAGTGACGCTGGCCGCCAACGAGGTATACGTACTGGGACCCTCGCCCTCAGTCTCGTCTCCGGCGCGGCT
ACCTGCCCCGTTTTCCCTGTGAGTTGACCTGCTCCGGGCCGCGGGCCGCCAATGGCAGGGGCGCTCCGACCACG
GCCTTCGGGCAGGCGGTGACCGGCCCCGCCGGGCTCAGGGAAGACCACGTACTGCCTGGGCATGAGTGAGTTCCTG
CGCGCGCTGGGCCGGCGCGTGGCGGTGGTGAACCTGGACCCGGCCAACGAGGGGCTGCCGTACGAGTGTGCCGTG
GACGTGGGCGAGCTGGTGGGGCTGGGCGACGTGATGGACGCGCTGCGCCTGGGGCCCAACGGCGGCTGCTCTAC
TGCATGGAGTACCTGGAAGCCAACCTGGACTGGCTGCGTGCCAAGCTCGACCCCTCCGCGGCCACTACTTCCTC
TTCGACTGCCCAGGCCAGGTGGAGCTCTGCACGCATCACGGCGCCTTGCGCAGCATCTTCTCCCAAATGGCGCAG
TGGGACCTCAGGCTGACTGCCGTCCACCTCGTGGATTCTCACTACTGCACAGACCCTGCCAAGTTCATTTCAGTA
CTGTGTACCTCCCTGGCCACCATGCTGCACGTGGAAGTGGCCACATCAACCTCCTTTCCAAGATGGACCTCATT
GAGCATTATGGGAAGCTGGCCTTCAACCTGGACTACTACACAGAGGTTCTGGACCTCTCCTACCTGCTTGACCAC
CTGGCTTCTGACCCCTTCTTCCGCCACTACCGCCAGCTCAATGAGAAGCTAGTGCAGCTCATCGAAGACTATAGC
CTTGCTCTCCTTTATCCCTCTCAACATCCAGGACAAGGAGAGCATCCAGCGAGTCCTGCAGGCTGTGGATAAAGCC
AATGGATACTGTTTCAGAGCCCAAGAGCAGCGAAGCTTGGAAGCCATGATGTCTGCCGCAATGGGAGCCGACTTC
CATTCTCTTCCACACTGGGCATCCAGGAGAAGTACCTGGCACCCTCGAACCAGTCAGTGGAGCAGGAAGCCATG
CAGCTGTAGCAACAAGGTGGACCCTGGAGAGCAGGATGCATAATCCAGCACTGGGGAAAGTGGAGGCTCCTGATG
CAGGCTGCAGACCCAAGAGCAAGTCCTCCAGCCAGAGCTGGCGGGCTGGCAAGGGGATATTAGCTCTGCAAAG
GACTTCTGGCCAAAAGCCAGACATGGTGCCAAGCAGAACACCCCCATACTGTGAGTGGTGTCCGTGAGCTCTG
GGCCCTGCCACCAGAAAGTCGAGCACTGGTCCTAGTCAGGCTGTGATGAAATGTGCTACAATAAGAGTTTATT
TTCT

WO 2004/030615

PCT/US2003/028547

125/6881
FIGURE 117

MAGAAPTTAFGQAVTGPPGSGKTTYCLGMSEFLRALGRRVAVVNLDPANEGLPYECAVDVGELVGLGDVMDALRL
GPNGGLLYCMEYLEANLDWLRKLDPLRGHYFLFDCPGQVELCTHHGALRSIFSQMAQWDLRLTAVHLVDSHYCT
DPAKFISVLCTSLATMLHVELPHINLLSKMDLIEHYGKLAFNLDYYTEVLDLSYLLDHLASDPFFRHYRQLNEKL
VQLIEDYSLVSFIPLNIQDKESIQRVLQAVDKANGYCFRAQEQRSLEAMMSAAMGADFHFSSSTLGIQEKYLAPSN
QSVEQEAMQL

WO 2004/030615

PCT/US2003/028547

126/6881
FIGURE 118

TAGAGTCGTTGGGCCCCGGCGCGACCCGCAGGAGCGTAGAGAGCGCGGGACTAGAGTGCAGAGCTCCGGGACGTGG
ATCGGAGCCGGCGCGATGGGCGGAGAGCAGGAGGAGGAGCGGTTTCGACGGCATGTTGCTGGCCATGGCTCAGCAG
CACGAGGGCGGCGTGCAGGAGCTTGTGAACACCTTCTTCAGCTTCCTTCGACGCAAAACAGACTTTTTCATTGGA
GGAGAAGAAGGGATGGCAGAGAAGCTTATCACACAGACTTTCAGCCACCACAATCAGCTGGCACAGAAGACCCGG
CGGGAGAAGAGAGCCCCGGCAGGAGGCCGAGCGGGGAGAAGGCGGAGCGGGCGGCCAGACTGGCCAAGGAAGCC
AAGTCAGAGACCTCAGGGCCCCAGATCAAGGAGCTAACTGATGAAGAGGCAGAGAGGCTGCAGCTAGAGATTGAC
CAGAAAAAGGATGCAGAGAATCATGAGGCCAGCTCAAGAACGGCAGCCTTGACTCCCCAGGGAAGCAGGATACT
GAGGAAGATGAGGAGGAAGATGAGAAGGACAAAGGAAAACTGAAGCCCAACCTAGGCAACGGGGCAGACCTGCCC
AATTACCGCTGGACCCAGACCCCTGTCGGAGCTGGACCTGGCGGTCCCTTTCTGTGTGAACCTCCGGCTGAAAGGG
AAGGACATGGTGGTGGACATCCAGCGGCGGCACCTCCGGGTGGGGCTCAAGGGGCAGCCAGCGATCATTGATGGG
GAGCTCTACAATGAAGTGAAGGTGGAGGAGAGCTCGTGGCTCATTGAGGACGGCAAGGTGGTGAAGTGTGCATCTG
GAGAAGATCAATAAGATGGAGTGGTGGAGCCGCTTGGTGTCCAGTGACCCTGAGATCAACACCAAGAAGATTAAAC
CCTGAGAATTCCAAGCTGTCAGACCTGGACAGTGAGACTCGCAGCATGGTGGAAAAGATGATGTATGACCAGCGA
CAGAAGTCCATGGGGCTGCCAACTTCAGACGAACAGAAGAAACAGGAGATTCTGAAGAAGTTTCATGGATCAACAT
CCGGAGATGGATTTTCCAAGGCTAAATTCAACTAGCCCCCTGTTTTTTCCTCCCTGAACTCTTGGGGCTGAGCTG
CAACCACCCAACCTTCTTTCCTCTCTCTGGGACTTGTGGGCCTCAGGGCTTGGGGCAGGCATGGGACTGGC
CCAGGCACACAGGTCCCCGGGGCATCAGGAGAAAGGCTGGGTCTTGGGACCTTGTCTCTCCCCAGTTGGCCTACTGT
TACACATTAAAAACGATTTGCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

127/6881
FIGURE 119

MGGEQEEERFDGMLLAMAAQQHEGGVQELVNTFFSFLRRKTDFFIGGEEGMAEKLITQTFSHHNQLAQKTRREKRA
RQEAERREKAERAARLAKEAKSETSGPQIKELTDEEAERLQLEIDQKKDAENHEAQLKNGSLDSPGKQDTEEDEE
EDEKDKGKLPNLGNGADLPNYRWTQTLSELDLAVPFCVNFRLKGKDMVVDIQRRHLRVGLKGQPAIIDGELYNE
VKVEESSWLIEDGKVVTVHLEKINKMEWWSRLVSSDPEINTKKINPENSCLSDLDSETRSMVEKMMYDQRQKSMG
LPTSDEQKKQEILKKFMDQHPMDFSKAKFN

WO 2004/030615

PCT/US2003/028547

128/6881
FIGURE 120

CCTGGTATGATTCCATCCTGAGCGGCTGTTCTCTTGAGCAGCGTTCAATTTATCTCCGTCTGCCTTCTGTCCCACC
TAAGTGTGTGCCGCCACCCAATAGAAAGATTGATGACATGGACATGAGCCCCCTGAGGCCCCAGAACTATCTTT
TCGGTTGTGAACTAAAGGCTGACAAAGATGATCACTTTAAGGTGGATAATGATGAAAATGAGCACCAGTTATCTT
TAAGAACGGTCAGTTTAGGGGCTGGTACAAAGGATGAATTGCACATTGTTGAAGCAGAGGCAATGAATTACAAAG
GCAGTCCAATTAAAGTAACACTGGCAACTTTGAAAATGTCTGCACAGCCAACAGTTTCCCTTGGGGGCTTTGAAA
TAACACCACCAGTGGTCTTAAGATTTAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTG
TGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAACTCTTAAGTATATCTGGAAAGCGGTCTG
CCCCTGGAGGTGGTAGCAAGGTTCCACAGAAAAAGTAAACTTGCTGTTGATGAAGATGATGATGATGATGATG
ATGATGATGATGATGATTTTATGATGATGAGGAAGCTGAAGAAAAAGTGCCAGTGAAGAAAGGACAAGAATCCTTCA
AAACACAGGAAAAAACTCCTAAAACACCAAAAGGATCTAGTTCTGTAGAAGACATTAAAGCAAAAAATGCAAGCAA
GTATAGAAAAAGGGGGTTCTCTTCCCAAAGTGGAAGCCGAGTTCATCAATTTTGTGAAGAATTGCTTCTGGATGA
CTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCCTTAAGAAAAATAGTTTCAACAATTTGTTAA
AAATTTCCATCATATTTTCAATTTCTGTAAACAGTTGATATCTGGCTGTCCTTTTTATAATGCAGAGTGAGAACTTT
CCCTACCGTGTTTGATAAATGTTGTCCAGGTTCCATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTTTTT
AAAGATGGAACACCCCTTTGCTTGGTTTTAAATATGTATGGAATGTTATGATAGGACATAGTAGTAGCGGTGGT
CAGACATGGAATTTGTGGGAAGACAAAAATATGCCTGTGAAATAAACTCAATATTTTAATAAAGTAAAAAAA
AAAAAA

WO 2004/030615

PCT/US2003/028547

129/6881
FIGURE 121

MDMDMSPLRPQNYLFGCELKADKDDHFKVDNDENEHQLSLRTVSLGAGTKDELHIVEAEAMNYKGSP IKVTLATL
KMSAQPTVSLGGFEITPPVVLRFKCGSGPVHISGQHLVAVEEDAEESEDEEEEDVKLLSISGKRSAPGGGSKVPQK
KVKLAVDEDDDDDDDDDDDDDFDDEEAEEKVPVKKGQESFKTQEKTPKTPKGSSSVEDIKAKMQASIEKGGS LPKV
EAEF INFVKNCFWMTDQEAIQDLWQWRKSP

WO 2004/030615

PCT/US2003/028547

130/6881
FIGURE 122

AGCTGCTGGCTGGGCTGCCTGTTGAGTCAGCCTTCTTCCCTCACGGCTCTTCTCCCGGTCCCTGAAACTCGGCTG
CCAGGGGAGCTGGAGCCACCTGCGAAGGTGTCTCCCTACTGGACCCCTACAGGAAGCTCCGTGTGCCCAGCTG
GGGCACAGCCCCAGCTGATGCCCCAGAGGGGGCCACCCATCGCAAGAGGGGCTTTGGGCTCTGCCCTCCCTCCCCA
TGGCGCATGGGCCAAAGCCTGAGACTGAAGGACTGTTGGACCTCAGCTTCCTGACAGAGGAGGAGCAGGAGGCCA
TTGCTGGCGTCTCTCAACGAGATGCCCCGCTGCGCCAGCTGGAGGAGGGGCGGGTCAGCAAGCTCCGGGCCTCAG
TGGCAGACCCTGGGCAGCTGAAGATCCTGACAGGGGACTGGTTCCAGGAAGCACGCTCCCAGCGGCACCACAATG
CCCCTTCGGCTCTGACCTTGTCCGAGCGTCTATGCGCAGGAAGAAGAGCACCAGGGGAGACCAGGCTCCAGGCC
ACGACAGGGAGGCTGAGGCTGCTGTGAAAGAGAAGGAAGAGGGGGCCAGAGCCCAGGCTCACCATTGATGAGGCCC
CTCAGGAGAGGCTCAGGGAGACTGAGGCTTCAGATCCTGAGGAGGCGTCCCAGGCCAGGAAGATCCTGGCCAAG
GAGACCAACAGGTCTGTGCCGAGGAGGCTGACCCGGAGCTGGAGCCCGCTCGGGGGGAGAGCAGGAGCCGCGGC
CCCAGCAAGCCCAGACCAAGGCCGCGTCCCAGATCCTGGAGAATGGGGAGGAGGCCCCGGGGCCCCGACCCCTCTC
TCGACCGCATGCTCAGCAGCAGCTCCTCGGTGTCCAGCCTTAACCTCCTCCACGCTGAGCGGCAGCCAGATGAGCC
TGTCAGGCGACGCGGAGGCGGTGCAGGTCCGCGGCTCCGTGCACCTTCGCGCTGCACTACGAGCCGGGCGCCGCCG
AGCTGCGCGTGACGTGATCCAGTGCCAGGGCCTGGCCGCCGCCCGGCGCCGCCGCTCGGACCCCTACGTCAAAA
GCTACCTCCTCCCGGATAAGCAGAGCAAGCGCAAGACGGCGGTGAAGAAACGGAATCTGAATCCGGTTTTCAACG
AGACTCTCCGGTACTCCGTCCCGCAGGCCGAGCTTCAGGGCCGCGTGTGAGCCTGTCTGTGTGGCACCGCGAAA
GCCTGGGTGCAACATCTTTCTGGGCGAAGTTGAAGTGCCCCGGACACGTGGGACTGGGGCTCTGAGCCACCT
GGCTCCCCCTGCAGCCCCGGGTCCCACCCTCTCCCAGACGACCTTCCGAGCCGCGGGTTACTCGCCCTGTCCCTCA
AGTACGTCCCCGCGGCTCCGAGGGCGCAGGACTGCCCCGAGCGGGGAGCTGCACTTCTGGGTGAAGGAGGCTC
GGGACCTCCTGCCGCTGCGGGCAGGATCCCTGGACACTTACGTACAATGCTTCGTGCTGCCTGATGACAGCCAGG
CCAGCCGCCAGCGTACAAGGGTTGTGCGACGCAGCCTCAGCCCTGTGTTCAATCACACCATGGTGTACGATGGCT
TTGGGCCTGCTGACCTGCGCCAGGCTTGTGCCGAGCTCTCCCTCTGGGACCATGGGGCCCTGGCCAACCGCCAGC
TGGGGGGCACACGCTCAGCCTGGGCACCGGCAGCAGCTATGGGCTGCAGGTGCCCTGGATGGATTCCACACCTG
AGGAGAAGCAGCTGTGGCAAGCCCTCCTGGAGCAGCCGTGCGAATGGGTGGATGGCCTTCTACCCCTCAGAACCA
ACCTGGCCCCCAGGACGTAGCCCCACCAAGCCTCTCTCTTGACCCCCATCTCAGGGCCTGCCCTTGGCTAAAG
TCAATAAAGTCTATTCTAAGAGC

WO 2004/030615

PCT/US2003/028547

131/6881
FIGURE 123

MPQRGHPSQEGWLWALPSLPMAHGPKPETEGLLDLSFLTEEEQEAIAGVLQRDARLRQLEEGRVSKLRASVADPGQ
LKILTGDWFQEARQRHHNAHFGSDLVRASMRRKKSTRGDQAPGHDREAEAAVKEKEEGPEPRLTIDEAPQERLR
ETEASDP EEASQAQEDPGQGDQQVCAEEADPELEPASGGEQEPRPQQAQTKAASQILENGEEAPGPDPSLDRMLS
SSSSVSSLNSSTLSGSQMSLSGDAEAVQVRGSVHFALHYEPGAAELRVHVIQCQGLAAARRRRSDPYVKSYPD
KQSKRKTAVKKRNLPVFNETHRYSVPAELQGRVLSLSVWHRESLGRNIFLGEVEVPLDTWDWGSEPTWLP LQP
RVFPSPDDLPSRGLLALSILKYVPAGSEGAGLPPSGELHFWVKEARDLLPLRAGSLDTYVQCFVLPDDSQASRQRT
RVVRRSLSPVFNHTMVYDGF PADLRQACAELSLWDHGALANRQLGGTRLSLGTGSSYGLQVPWMDSTPEEKQLW
QALLEQPCEWVDGLLPLRTNLAPRT

WO 2004/030615

PCT/US2003/028547

132/6881
FIGURE 124

ATGCCGTTAGTAACGAGGAACATCGAGCCAAGGCACCTGTGCCGTCAGACGTTGCCTAGCGTTAGAAGCGAGCTG
GAATGCGTGACCAACATCACCTTGGCAAATGTCATCCGACAGCTGGGCAGCCTGAGTAAATATGCAGAGGACATT
TTTGGAGAGCTCTTTACTCAGGCAAATACCTTTGCCTCTCGGGTAAGCTCCCTTGCTGAGAGGGTCGACCGACTA
CAGGTTAAAGTCACTCAGCTGGATCCCAAGGAAGAAGAAGTGTCACTGCAAGGAATCAACACCCGAAAAGCCTTC
AGAAGTTCCACCATTC AAGACCAGAAGCTTTTTGACAGAACTCTCTCCAGTGCCTGTCTTAGAAACATACAAT
ACCTGTGATACTCCTCCCCCTCTCAACAATCTTACCCCTTACAGGGACGATGGAAAAGAGGCACTCAAATTCTAC
ACAGACCCCTTCATACTTCTTTGATCTTTGGAAGGAGAAGATGCTGCAGGACACCAAGGATATCATGAAAGAGAAG
AGAAAGCACAGGAAAGAAAAGAAAGATAATCCAAATCGAGGGAATGTAAACCCACGTAAAATCAAGACACGTAAG
GAAGAGTGGGAGAAAATGAAGATGGGGCAAGAATTTGTGGAGTCCAAAGAAAAGCTGGGGACTTCTGGGTATCCA
CCCACTTTGGTGTACCAGAATGGCAGCATTGGCTGTGTTGAAAACGTGGATGCAAGTAGCTATCCGCCACCACCA
CAGTCAGACTCTGCTTCTTACCTTCTCCTTCTCCTTCTCCGAGGACA ACTTGCCTCCTCCACCAGCAGAATTCAGT
TACCCAGTGGACAACCAAAGAGGATCTGGTTTGGCTGGACCCAAAAGATCCAGTGTGGTCAGCCCAAGCCATCCA
CCACCAGCTCCTCCTCTAGGCTCTCCACCAGGCCCTAAACCCGGGTTTGCTCCACCACCTGCCCCCTCCGCCACCT
CCGCCCTCAATGATAGGCATCCCACCTCCACCACCGCCTGTAGGATTTGGGTCTCCAGGGACGCCTCCACCACCC
TCACCCCATCTTTCCACCTCACCTGATTTTGCTGCCCTCCACCTCCTCCTCCACCACCAGCAGCTGACTAC
CCAACTCTGCCACCACCTCCCTTGTCCCAGCCAACAGGAGGAGCACCTCCTCCTCCCCCTCCTCCTCCTCCTCCG
GGGCCCCCTCCTCCCCCTTCACTGGTGCAGATGGCCAGCCTGCTATACCACCACCGCTTTCTGATACCACCAAG
CCCAAGTCCTCCTTGCTGCGGTGAGCGATGCCCGTAGCGACCTGCTTTTCAGCCATCCGTCAAGGTTTTTCAGCTG
CGCAGGGTTGAGGAGCAGCGGGAACAAGAGAAGCGGGATGTTGTGGGCAATGACGTGGCCACCATCTTGTCTCGT
CGCATTGCTGTTGAGTACAGTGACTCAGAAGATGACTCCTCTGAATTTGATGAGGACGACTGGTCCGATTAA

WO 2004/030615

PCT/US2003/028547

133/6881
FIGURE 125

MPLVTRNIEPRHLCRQTLPSVRSELECVTNITLANVIRQLGSLSKYAEDIFGELFTQANTFASRVSSLAERVDRL
QVKVTQLDPKEEEVSLQGINTRKAFRSSTIQDQKLFDRNSLPVPVLETYNTCDTPPPLNNLTPYRDDGKEALKFY
TDPsyFFDLWKEKMLQDTKDIMKEKRKHKRKEKKDNPNGNVNPRKIKTRKEEWEKMKMGQEFVESKEKLGTS GYP
PTLVYQNGSIGCVENV DASSYPPPPQSDSASSPSPSFS EDNLPPPPAEFSYPVDNQRGSGLAGPKRSSVVSHP
PPAPPLGSPPGPKPGFAPPPAPPPPPPPMIGIPPPPPVGFSGPTPPPPSPPSFPHPDFAAPPPPPPPAADY
PTLPPPPLSQPTGGAPPPPPPPPPGPPPPFTGADGQPAIPPLSDTTKPKSSLPAVSDARSDDL SAI RQGFQL
RRVEEQREQEKRDVVGN DVATILSRRIAVEYSDSEDD SFEDEDDWSD

WO 2004/030615

PCT/US2003/028547

134/6881
FIGURE 126

GCAGCACCCCAGTTCTCCCCGCACGCCGGCACTCGCGGCTGCTGGAGCCCCGGCTGGCTCACCCCAGGGGCCGGG
AGAATTGGGCTCCAGGTCTCTGACCCCTCCCAAGGATCATGCCGCAGCCCCACTGACCCAGGAGTAGGGGCCTAA
GGGCAGGGAACCTGGAATGGGCTGTGTGTTCTGCAAGAAATTGGAGCCGGTGGCCACGGCCAAGGAGGATGCTGG
CCTGGAAGGGGACTTCAGAAGCTACGGGGCAGCAGACCCTATGGGCCTGACCCCACTAAGGCCCGGCTGCATC
CTCATTGCCCCACATCCCCAACTACAGCAACTTCTCCTCTCAGGCCATCAACCCTGGCTTCCTTGATAGTGGCAC
CATCAGGGGTGTGTGAGGGATTGGGGTGACCTGTTCATTGCCCTGTATGACTATGAGGCTCGAACTGAGGATGA
CCTCACCTTCACCAAGGGCGAGAAGTTCACATCCTGAACAATACTGAAGGTGACTGGTGGGAGGCTCGGTCTCT
CAGCTCCGGAAAACTGGCTGCATTCCAGCAACTACGTGGCCCTGTGACTCAATCCAAGCTGAAGAGTGGTA
CTTTGGAAAGATTGGGAGAAAGGATGCAGAGAGGCAGCTGCTTTCACAGGCAACCCCCAGGGGGCCTTTCTCAT
TCGGGAAAGCGAGACCACCAAAGGTGCCTACTCCCTGTCCATCCGGGACTGGGATCAGACCAGAGGCGATCATGT
GAAGCATTACAAGATCCGCAAACCTGGACATGGGCGGCTACTACATCACCACACGGGTTCAAGTTCAGGTGCA
GGAGCTGGTGCAGCACTACATGGAGGTGAATGACGGGCTGTGCAACCTGCTCATCGCGCCCTGCACCATCATGAA
GCCGCAGACGCTGGGCTGGCCAAGGACGCCTGGGAGATCAGCCGCAGCTCCATCACGCTGGAGCGCCGGCTGGG
CACCGGCTGCTTCGGGGATGTGTGGCTGGGCACGTGGAACGGCAGCACTAAGGTGGCGGTGAAGACGCTGAAGCC
GGGCACCATGTCCCCGAAGGCCTTCCTGGAGGAGGCGCAGGTATGAAGCTGCTGCGGCACGACAAGCTGGTGCA
GCTGTACGCCGTGGTGTGCGAGGAGCCCATCTACATCGTGACCGAGTTTATGTGTACGGCAGCTTGTGGATT
TCTCAAGAACCCAGAGGGCCAGGATTTGAGGCTGCCCAATTGGTGGACATGGCAGCCAGGTAGCTGAGGGCAT
GGCCTACATGGAACGCATGAACTACATTACCGCGACCTGAGGGCAGCCAACATCCTGGTTGGGAGCGGCTGGC
GTGCAAGATCGCAGACTTTGGCTTGGCGCGTCTCATCAAGGACGATGAGTACAACCCCTGCCAAGGTTCCAAGTT
CCCCATCAAGTGGACAGCCCCAGAAGCTGCCCTCTTTGGCAGATTCACCATCAAGTCAGACGTGTGGTCCTTTGG
GATCCTGCTCACTGAGCTCATCACCAGGGCCGAATCCCCTACCCAGGCATGAATAAACGGGAAGTGTGGAACA
GGTGGAGCAGGGCTACCACATGCCGTGCCCTCCAGGCTGCCAGCATCCCTGTACGAGGCCATGGAACAGACCTG
GCGTCTGGACCCGGAGGAGAGGCCTACCTTCGAGTACCTGCAGTCTTCTTGGAGGACTACTTCACCTCCGCTGA
ACCACAGTACCAGCCCGGGGATCAGACATAGCCTGTCCGGGCATCAACCCTCTCTGGCGGTGGCCACCAAGTCCT
GCCAATCCCCAGAGCTGTTCTTCCAAAGCCCCAGGCTGGCTTAGAACCCCATAGAGTCTTAGCATCACCAGGA
CGTGGCTGCTCTGACACCACCTAGGGCAACCTACTTGTTTTACAGATGGGGCAAAGGAGGCCAGAGCTGATCT
CTCATCCGCTCTGGCCCCAAGCACTATTTCTTCTTTTCCACTTAGGCCCTACATGCCCTGTAGCCTTTCTCACT
CCATCCCCACCCAAAGTGCTCAGACCTTGTCTAGTTATTTATAAACTGTATGTACCTCCCTCACTTCTCTCCTA
TCACTGCTTTCTACTCTCCTTTTATCTCACTCTAGTCCAGGTGCCAAGAATTTCCCTTCTACCTCTATTCTCT
TGTGTCTGTAAGTTACAAAGTCAGGAAAAGTCTTGGCTGGACCCCTTTCTGCTGGGTGGATGCAGTGGTCCAGG
ACTGGGGTCTGGGCCCAGGTTTGAGGGAGAAGGTTGCAGAGCACTCCACCTCTCTGAATAGTGTGTATGTGTT
GGTTTATTGATTCTGTAAATAAGTAAAATGACAATATGAATCCTC

WO 2004/030615

PCT/US2003/028547

135/6881
FIGURE 127

GGCACGAGGCTTCGTAAAGATGGCCGCGGAGGCTTTTGGAGCCAAC TGGGAGCGCAGTACGCGTTTTCTGGAGCA
TGGGCAGAGGAGACAGGAACAAGCGTAGCATCCGTGAGCACCGATTGGCTGAAGCGAGCACCCCGGGAGCTGACT
GGCTCCGCCATTTCGCGGGAAGGCGTTTGTGGTGCCAGAGAAAAGTAGCCAGAGCGGCGCAGTGGCGGCCGCGTTC
TGTTGGTTTTCCGCTATTCCCCCAGACCCGCACCTTCTCGGCCTCTTTGCGGAGAATCGTGACCAAGATGTGGAAC
AGTGGATTTCGAAAGCTATGGCAGCTCCTCATACGGGGGAGCCGGCGGCTACACGCAGTCCCCGGGGGGCTTTGGA
TCGCCCCGCACCTTCTCAAGCCGAAAAGAAATCAAGAGCCCGAGCCAGCACATTGTGCCCTGTACTATATCTCAG
CTGCTTTCTGCCACTTTGGTTGATGAAGTGTTTCAAGATTGGGAATGTTGAGATTTCACAGGTCACATTTGTGGGG
ATCATCAGACATGCAGAGAAGGCTCCAACCAACATTGTTTACAAAATAGATGACATGACAGCTGCACCCATGGAC
GTTTCGCCAGTGGGTTGACACAGATGACACCAGCAGTGAACCACTGTGGTTCCTCCAGAAACATATGTGAAAGTG
GCAGGCCACCTGAGATCTTTTTCAGAACAAAAGAGCCTGGTAGCCTTTAAGATCATGCCCCCTGGAGGATATGAAT
GAGTTACACACATATTCTGGAAGTGATCAATGCACACATGGTACTAAGCAAAGCCAACAGCCAGCCCTCAGCA
GGGAGAGCACCTATCAGCAATCCAGGAATGAGTGAAGCAGGGAACTTTGGTGGGAATAGCTTCATGCCAGCAAAT
GGCCTCACTGTGGCCCAAACAGGTGTTGAATTTGATTAAAGGCTTGTTCCAAAGACCTGAAGGGTTGAACTTTAG
GATCTCAAGAACCAGCTGAAACACATGTCTGTATCCTCAATCAAGCAAGCTGTGGATTTTCTGAGCAATGAGGGG
CACATCTATTCTACTGTGGATGATGACCATTTTAAATCCACAGATGCAGAAATAACTGGATCTAACTGGGTACCTG
AGATATTTTACAGCTGGACCTAGTTTACAACTCTGTTGTCTCCAGCTCTGCATATGTCTGGCCAGGGGGCTTCTA
GGAAGTAGGTTTCATCTATCAATGTCTCCTCTGACTTCCTTTTGAAACTTACTGCTCTTCTGTTTTATTTTGT
TTGTTTGAAGCTCAGAGGGAGATGGGCAATTGACAGGGATGCAATCCAGGGTGGGATTTCTTGAGGAAGTTACAA
ATAAGCTTGTTACAACATCAAGATAGATGGAATTGGAAGGATGCTACCAGGAGAGTACTTACATAGTGCTCAGGA
GTTTCTCTTCTTAAATGTTTACTGCTGAAAGATGAGCAGGACCAGGGCGTTATAGGCAGAGCCCTAGCCGAGAA
ACCTGCTGGCCTCTGCCTGTTTTCAATTTCCCACTTTGGTTGTGTGGCATTACTTTTCAAGATTGCACTTTCTGCT
TGTCATGACTTTTTGACACACTTGCCATGACGTGTGTTTCTGTGAACATGAAGTTCTGCGGTAGTGCTCCAGGG
GCAGAGGAAAAGAAGAAGTGTTACTGCGTTTTGTACAAAATAAATACAGTCATATGTTTAAATAAACAGTTCTAT
TGTA

WO 2004/030615

PCT/US2003/028547

136/6881
FIGURE 128

MWNSGFESYGSSSYGGAGGYTQSPGGFGSPAPSQAEKKSRARAHIVPCTISQLLSATLVDEVFRIGNVEISQVT
IVGIIIRHAEKAPTNIYKIDDMTAAPMDVRQWVDTDDTSSSENTVVPPETYVKVAGHLRSFQNKKS LVAFKIMPLE
DMNEFTTHILEVINAHMVLSKANSQPSAGRAPISNPGMSEAGNFGGNSFMPANGLTVAQNQVLNLIKACPRPEGL
NFQDLKNQLKHMSVSSIKQAVDFLSNEGHIYSTVDDDDHFKSTDAE

WO 2004/030615

PCT/US2003/028547

137/6881
FIGURE 129

GGAGGGAGACGCAGAGGCGGACAAGATGGCGGCGGCAGCTGTACAGGGCGAGAGAAGCGGTGGTAGCGGAGGCTG
TAGTGGGGCTGGTGGTGCTTCCAAGTGCAGGACAGGGAGTGGCCGTAGCGGCTTGTTGGATAAGTGGAGATAGA
TGATAAGCCTGTAAAAATTGACAAGTGGGATGGATCAGCTGTGAAAACTCTTTGGATGATTCTGCCAAAAAGGA
GAAGAGCATCTTTCTCGTGGCCACAGGAAAGATCCTACAGGAATGGATCCTGATGATATTGGCAGCTGTCCTC
CAGTCTTAAAGGGTTTGATGACAAATACACCTTGAAGCTGACCTTCATCAGTGGGAGAACAAAGCAGCAGCGGGA
AGCCGAGTTCACAAAGTCCATTGCTAAGTTTTTTGACCACAGTGGGACACTGGTCATGGATGCATATGAGCCTGA
AATATCCAGGCTCCATGACAGTCTTGCCATAGAAAGAAAAATAAAGTAGCCAATTCTAAAAGTAGCCCTCTTCT
CCTGGATCTTGCTGAATTAGTGGCTTGGGGGTGGGGGAGATAAAAAGAACTTAAATGGGTAAAGTAAGAAATG
TTAAAAAG

WO 2004/030615

PCT/US2003/028547

138/6881
FIGURE 130

CTGGGCCGGGGAAATGGCGGCTTCAGGAGAGAGCGGGACTTCAGGCGGCGGAGGCAGCACCGAGGAAGCATTAT
GACCTTCTACAGTGAGGTGAAACAAATAGAGAAGAGAGACTCGGTTCTAACTTCGAAAAATCAGATTGAAAGACT
GACCCGTCTCGGTTCTTCTTCAATTTGAACCCATTTGAGGTTCTTCAGATAGATCCTGAAGTTACAGATGA
AGAAATAAAAAAGAGGTTTCGGCAGTTATCCATCTTGGTGCATCCTGACAAAAATCAAGATGATGCTGACAGAGC
ACAAAAGGCTTTTGAAGCTGTGGACAAAGCTTACAAGTTGCTACTGGATCAGGAGCAAAAGAAGAGGGCCCTGGA
TGTAATTCAGGCAGGAAAAGAATACGTGGAACACACTGTGAAAGAGCGAAAAAACAATTAAAGAAGGAAGGAAA
ACCTACAATTGTAGAGGAGGATGATCCTGAGCTGGAAACGACAAAGGGAAGAAGAGATTGAAGCTCAAGAAAAAG
CCAAACGGGAAAGAGAGTGGCAGAAAACTTTGAGG

PCT/US2003/028547

TCCAGACGACAAAGACCGCGTGTCTCGGATTCCTCGGAGCGTTCCTGGAGCCCCGAGAGACGCCCCGGGGTCTTAGAAGC
TCCCCGCCGCGCGCCAGTCCCGGCTTCATTTCGGGCGTCCCTCCGAAACCCACTCGGGTGCACGGGTCGTTCGGCGA
GCCGCGACCGGGTCTCTGGCGCGCACCATGATCGTGGCGGACTCCGAGTGCCGCGCAGAGCTCAAGGACTACCTGCG
GGTTCGCCCCGGGCGGGCGTTCGGCGACTTCGGGCCCGGAGAGGAGCAGAGGGAGAGCCGGGCTCGGCGAGGCCCTC
GAGGGCCAGCGCCTTCATCCCCGTGGAGGAGGTCTTCGGGAGGGGGCTGAGAGCCTCGAGCAGCACCTGGGGC
TGGAGGCACTGATGTCTCTGGGCGAGTAGACAACCTGGCAGTGGTGATGGGCTGCACCCTGACTACTTTACCA
GCTTCTGGCGCCTGCACTACCTGCTGCTGCACACGGATGGTCCCTTGGCCAGCTCCTGGCGCCACTACATTGCCA
TCATGGCTGCGCGCCGCCATCAGTGTTCTTACCTGGTAGGCTCCACATGGCCGAGTTTCTGCAGACTGGTGGT
ACCCTGAGTGGCTGCTGGGCTCCACCAGGGCCCCGAGAAGCTGCGCAAACCTCAGCGAGATCAACAAGTTGCTGG
CGCATCGGCCATGGCTCATCACCAAGGAACACATCCAGGCCCTTGTGAAGACCGGCGAGCACACTTGGTCCCTGG
CCGAGCTCATTAGGCTCTGGTCTGCTCACCCTGCGACTCGCTCTCCTCCTCGTGTTTGGCTGTGGCATCC
TCCCTGAGGGGGATGCAGATGGCAGCCCTGCCCCCAGGCACCTACACCCCTAGTGAACAGAGCAGCCCCCAA
GCAGGGACCCGTTGAACAACCTCTGGGGGCTTTGAGTCTGCCCGCGACGTGGAGGCGCTGATGGAGCGCATGCAG
AGCTGCAGGAGAGCCTGCTGCGGGATGAGGGGACGTCCAGGAGGAGATGGAGAGCCGCTTTGAGCTGGAGAAGT
CAGAGAGCCTGCTGGTGACCCCTCAGCTGACATCCTGGAGCCCTCTCCACACCCAGACATGCTGTGCTTTGTGG
AAGACCCTACTTTTCGGATATGAGGACTTCACTCGGAGAGGGGCTCAGGCACCCCTACCTTCCGGGCCAGGATT
ATACCTGGGAAGACCATGGCTACTCGCTGATCCAGCGGCTTTACCCTGAGGGTGGGCAGCTGCTGGATGAGAAGT
TCCAGGCAGCCTATAGCCTCACCTACAATACCATCGCCATGCACAGTGGTGTGGACACCTCCGTGCTCCGCAGGG
CCATCTGGAACATATACCTGCGTCTTTGGCATCAGATATGATGACTATGATTATGGGGAGGTGAACCAGCTCC
TGGAGCGGAACCTCAAGGTCTATATCAAGACAGTGGCCTGCTACCCAGAGAAGACCACCCGAAGATGTACAACC
TCTTCTGGAGGCACTTCCGCCACTCAGAGAAGGTCCACGTGAACCTTGCTGCTCCTGGAGGCGCGCATGCAAGCCG
CTCTGCTGTACGCCCTCCGTGCCATCACCCGCTACATGACCTGACTCCTGAGCAGGACCTGGGCCCCGGTTCAGCT
CCCCACAAGGACTTCTCTGTCTGGAGACAGCCCCAGACCCTTTTGTGTCCCATGCCACCCCTCCCCACGCTGCAG
TGGGCTTGTGTGTGATGTGCAGTCCCGAAGCCACACCCCTCCCTTTTCCCTCACTGGAATGGACAGTTTATTGCACT
GACTCTGGGATCTCAGCCCTGCTCCTGGGAGCTGGAAGAGCACTTGGAGATCCTAAGGGACCACACCCCTCCTCC
TTCCCCTGCCACAGAGGCAGAGGGCACAGGAAAGAAGCCGGGCCAAGCTCGGAATTAATGTGCCACAAGTGTG
TGGCCTTCTGAACTGGGAAGTCCCTGGCTGGCCCCCGGGGGAGAGGGGCAAATGCCCTCCGGGACTGACACTCCA
GGCAGCTTTGCCTTCTCTCCCCTGTCAATTTCCAGATTTTATTACCTCCTACTTGCCATTACCCATCAATGTGAA
AGTCAGGGTCACAGCTGGTCTGTGTGTCCAGTTCCCTAAAAGCCTGTTCTGTGGGCAGCCTGAGGCTGTTGCC
GAATCCTAGTTTCAGTTTTTTGACTTCCTTTGCCCTTTTTCCCTTTTCTCCATGCTTAATGGTGTGAGGCGTCAGG
AGAGAGGCCAAGTACATAAAAAAAAAAAAAAGCAGATTATCTCTAGAGAGTTTGGCCCTTGTGGTACATTGCG
CTTCTGAAGAGGAGGGAGTATTAGATTATAAATCCTCTTTATTTTGGTCCCTTATGCTTGAGGTTCCAACCTGGA
GCCACAGTGTGTGAGAGGAGGAGGAGAGGGAGAATTCTGTTCTCCAGAGCTGCACCTGCCATCGCAGAGGCCAGC
ACCCCACTCTCCTGCCCTCAGTGGCCCTGCCGCAGATGTCTCCAAAAAGTTGAGCCTTTCTAGATGGCTTAGGT
GGCACCATGGCTCAGCAGGAGGGGCGGGAGGCACAGGGTCTTGTGTTGGACCTGCCCTGGGCCATGGCCAGG
TGACCATGGCTACATTGCCAAACCTCTGACTGCCACAGCTGCAGACTGAGAGGAGGAGGTTCTGAGTCCCCACAATG
TCTGAAGCTGCCCTGGGATTCTCAGGCCAACCTGCCAACAGCAAGCGATTCTTCTGCAAGATCAGGGACCCCA
TTTCTGCAGCCAGTGTCTCCTGGTGCCTCTGAGGACTCCACCCCCATCCAGTATCTCATCTGTCCCCTCTC
CTGGGGCTTAAGTGGGTGCTTCCAGGCAGAAGCAGCCAAGGACCATTCCAGGCACCTTCTGTAGCAAAATGACT
GTGAATTACGACTTCTCTGCCCCTCTCTAGCAGTCTGTGCCCTCCTCTCTGACCAGTTTGGAGGGCACTGAAGA
AAGCAAGGGCGCTGCTGCTGCTGGGCGGGGCGAGGAGAGGAGCCTGGCCAGTGTGCCACATTAAATACCCGTGCA
GGCGCGGAGAAGCAACCGGCACCCCTTCCGGCCTGAAAGCCCTCCCTGCAAGAAGGTGTGCAGGAGAGAAGAGG
CCCCGGCATGGGGATCTGGGTTCTAGAGGGCATGTGATGACTGTAAATGTTCACTGGGTGGGTAGGGAGTGGTAT
CCAGTGTTCAAGTGCAGAAATCTTTGGCTTTGCTACCAGTTCCATATGATGAGAAATAAACGTTTCGTGAGGTTT
TGTTTCATAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

140/6881
FIGURE 132

MIVADSECRAELKDYLRFAPGGVGDSGPGEEQRESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGR
VDNLAVVMGLHPDYFTSFWRLLHYLLHTDGPLASSWRHYIAIMAAARHQCSYLVGSHMAEFLQTGGDFEWLLGLH
RAPEKLRKLSEINKLLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLSSFVFGCGILPEGDADGS
PAPQAPTTPSEQSSPPSRDPLNNSGGFESARDVEALMERMQQQLQESLLRDEGTSQEEMESRFELEKSESLLVTPS
ADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQDYTWEDHGYSLIQRLYPEGGQLLDEKFQAAAYSLTY
NTIAMHSGVDTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTVACYPEKTTRMYNLFWRHFRHS
EKVHVNLLLLLEARMQAALLYALRAITRYMT

WO 2004/030615

PCT/US2003/028547

141/6881
FIGURE 133

GAGACGTCGGCTTCCGACCGGAAGTGAGAAGAGGAGGAAGTTGGCTGGTTGCACCGATCTGGGGGCTTCCCGGGC
TCGGGTAACCGGAGTGCTGGTATCTAATCGTCGCTCAAAAGCTCCTAGGTATATCCCGTGCCCTTACCTGACTGGG
GGCTCTGAGTCCAGTTGTGTTGTCTTCAACTTAGACACCATGGAGGCACCTCCAGTCACCATGATGCCTGTCACT
GGGGGCACCATTAACATGATGGAGTACCTGTTGCAGGGAAGTGTTTTAGATCACAGTTTGGAAAGCCTCATCCAC
CGCCTTCGTGGTTTGTGTGACAACATGGAACCTGAGACTTTCCTTGACCATGAGATGGTATTCCTCCTTAAGGGC
CAGCAAGCCAGCCCATTGTCTCAGGGCCCGACGCTCTATGGACAGGGCAGGGGCACCCTGGCATCTGCGCTAC
CTGGGACAGCCAGAAATGGGAGACAAGAACCGCCATGCCCTGGTGCGAAACTGCGTGGAACATTGCCACATCTGAG
AACCTCACCGACTTCTTGATGGAAATGGGCTTCCGCATGGACCATGAGTTTGTGCTAAGGGACATTTGTTCCGT
AAGGGCATCATGAAGATTATGGTGTACAAGATTTCCGCATCCTGGTGCCAGGGAACACAGACAGCACTGAGGCC
TTGTCACTCTCCTATCTCGTGGAATTAAGTGTGGTAGCACCCGCTGGGCAGGACATGGTCTCTGATGACATGAAG
AACTTCGCAGAACAGCTAAAACCTCTGGTTCACCTAGAGAAAAATAGACCCCAAGAGGCTCATGTGACTAAGAGGA
TCTGTCCACATTTGGGGCCTATCCTTACTTGTTTGAAAAAATATGTTTGCTTTTTTGGTTTTTGTGTTTGTGTTG
TTTTTGAGACAGAGTCTCGCTTTGTTTCCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAACCTCTGC
CTCCTGGGTTCAAGCAATTCTCCACCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACATGCCACCATGCTCAG
CTAATTTTTGTATTTTTAGTAGAAATGGGGATTACCATGTTGGTCAGGCTATTCTCGAACTCCTGACCTCGTGA
TCCACCCACCTTGCCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACGCCTGGCCAAAAAAATATGTTTT
AAATGTCCCATTTACCATTTGCCAGGCAGGCATTCTTCCTTCAGGGAGAGGATGGTGAGAATTAATTGGTTCCTT
GCACTGTTCTCCTCATGTGGCGATTTCACTTTCATGACAGCCTTCTATATTAAAGGCTCAGGATGTCACGGAGA
ATCTATCTAATCCCACCTGTATTAAGAGGGGAAACCGGGCCAAGCGCAGTGGCTCACACCTCTAATCCCAGCACTT
TGGGAGGCTGAGGTAGGTGGATCACCCAAGGTCAGGAGTTTGAGACCAGCCTGGCCAAATGGTGAAAACCCCATCT
CTACGAAAAATACAAAATTTAGCCGGGCATGGTAGCAGGCGCTTGTAAATCCCAGCTACTTGGGAGGCTGAGGCTG
GAGAATCGCTTGAACCCAGGAGGTGAAGGTTGCAGTGACCAGAGATGACGCCATTGCACTCCAGCCTGGGTGAGA
AGAGCGAAACTCCGTCTCAAAAAAATAAAAAATGAAGAGGGGAAACCAGAATAAATTATCTTTTGGAAAGGACA
ATTTCTTGTTTGGCCATTTGTGTATAAGGTTGGTAACATTAGAGGCTGTGAGCTTGTGTTACATGGTAATAAAGC
CAATGAAGAG

WO 2004/030615

PCT/US2003/028547

142/6881
FIGURE 134

GGCCGGCCTCTCCCTTCCCGGGGTTCTTCGCGCCGGGCCCCCTTCCGCGTGGGTGAGTGAATGTGAGAGTCAGCGC
TCGCGCCGCGCGCGCCGCCCCGCTCCGCTGTTTCGGCGCTCTGCTTTAGGCGGTGGGGGGCGGGCGCGCGCTAAA
AGCATAGAGACGGGCATTGAGCTCTTGGGCTAGAGCGTCGCCGAGTCGGAGCCGGAGCCTGAGCCGCGCGCTGTG
TCTCCGCTGCGTCCGCCGAGGCCCCGAGTGTTCAGGGACAAAAGCCTCCGCGCTGCTCCCGCAGACGGGGCTCATC
TGCCGCCGCGCGCGCTGAGGAGAGTTTCGCCGCCGTTCGCCGCCGTGAGGATCTGAGAGCCATGTTCGGCCAGCA
GCCTCTTGAGCAGAGACCAAAAGGTCAAGGAAACAAAGTACAAAATGGATCTGTACATCAAAAGGATGGATTAA
ACGATGATGATTTTGAACCTTACTTGAGTCCACAGGCAAGGCCCAATAATGCATATACTGCCATGTTCAGATTCCCT
ACTTACCCAGTTACTACAGTCCCTCCATTGGCTTCTCCTATTCTTTGGGTGAAGCTGCTTGGTCTACGGGGGGTG
ACACAGCCATGCCCTACTTAACTTCTTATGGACAGCTGAGCAACGGAGAGCCCCACTTCCCTACCAGATGCAATGT
TTGGGCAACCAGGAGCCCTAGGTAGCACTCCATTTCTTGGTCAGCATGGTTTTAATTTCTTTCCAGTGGGATTG
ACTTCTCAGCATGGGGAAATAACAGTTCTCAGGGACAGTCTACTCAGAGCTCTGGATATAGTAGCAATTATGCTT
ATGCACCTAGCTCCTTAGGTGGAGCCATGATTGATGGACAGTCAGCTTTTGCCAATGAGACCCTCAATAAGGCTC
CTGGCATGAATACTATAGACCAAGGGATGGCAGCACTGAAGTTGGGTAGCACAGAAGTTGCAAGCAATGTTCCAA
AAGTTGTAGGTTCTGCTGTTGGTAGCGGGTCCATTACTAGTAACATCGTGGCTTCCAATAGTTTGCCTCCAGCCA
CCATTGCTCCTCCAAAACCAGCATCTTGGGCTGATATTGCTAGCAAGCCTGCAAAACAGCAACCTAAACTGAAGA
CCAAGAATGGCATTGCAGGGTCAAGTCTTCCGCCACCCCCGATAAAGCATAACATGGATATTGGAACCTGGGATA
ACAAGGGTCCCGTTGCAAAAGCCCCCTCACAGGCTTTGGTTTCAGAATATAGGTTCAGCCAACCCAGGGGTCTCCTC
AGCCTGTAGGTCAGCAGGCTAACAATAGCCCCACCAAGTGGCTCAGGCATCAGTAGGGCAACAGACACAGCCATTGC
CTCCACCTCCACCACAGCCTGCCAGCTTTAGTCCAGCAACAGGCAGCTCAGCCAACCCGCTGGGTAGCACCTC
GGAACCGTGGCAGTGGGTTCGGTCATAATGGGGTGGATGGTAATGGAGTAGGACAGTCTCAGGCTGGTTCTGGAT
CTACTCCTTCAGAACCCACCCAGTGTGGAGAAGCTTCGGTCCATTAATAACTATAACCCCAAAGATTTTGACT
GGAATCTGAAACATGGCCGGGTTTTTCATCATTAAAGAGCTACTCTGAGGACGATATTCACCGTTCATTAAGTATA
ATATTTGGTGCAGCACAGAGCATGGTAACAAGAGACTGGATGCTGCTTATCGTTCCATGAACGGGAAGGCCCG
TTTACTTACTTTTCAGTGTCAACGGCAGTGGACACTTCTGTGGCGTGGCAGAAATGAAATCTGCTGTGGACTACA
ACACATGTGCAGGTGTGTGGTCCAGGACAAATGGAAGGGTCGTTTTGATGTTCAGGTGGATTTTGTGAAGGACG
TTCCCAATAGCCAACCTGCGACACATTTCGCTTAGAGAACAACGAGAATAAACCAAGTGACCAACTCTAGGGACACTC
AGGAAGTGCTCTGGAAGGCTAAGCAGGTGTTGAAATTATAGCCAGCTACAAGCACACCACTTCCATTTTTG
ATGACTTCTCACACTATGAGAAACGCCAAGAGGAAGAAGAAAGTGTTAAAAGGAACGTCAAGGTCGTGGGAAAT
AAAAGGCAGTTCTACACAGACTGCAGCAACGGTTGCATCTGCATATCCTAAGAGGAAAAATGACCTTCAAGAGA
ATTAGGACTTTTTCTTAATTTCACTGACTTCAGAGACGATTGCAGACTTGCAGTTTAAGTATTGGAATTTTACA
AAAGACATAGGACTTAACTGGAAAAATGAAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
TTTAGGTGAAAAATGTCCCTTTTATTTTGGCTTTGGTTGTGATTTTCAGAGCATAATGCTATGTTTTTTTGTCTTT
TTACTATGTTTTTCGGATTTTTAAGTCCGTAAAGTGCATACAGTTTTCTCTAATTTTTAAACCTTTTCTCTCTCC
ATTTTGACATTTGCACTTGAGAACACTTGAGTTGTGAAGGTTTTGGGCATCCACCCAGAAAGTGGGAATTTGA
TTTTATCCTTCCGAACTGGAAGAACATTTTTATGAAGAATTTTGTCTAGGAGAATATAACAGTGTTACCCAAGG
TTGTGCTTTAAGGGTGGTTTCAATTTCTCTGACCTTTTGTACTCAAAGTAAAGTACTAGGAGTCTTAAGAAATG
TTCTGTTCTTGTACATTATACTGATTAAGTCAGGATTAATTTGATTTCAAAGCTGAGAACAGTGGAATAAACTCG
TTACAGAAATGCATTTTGGAAAGAGAAAAATACTGTAAACGTGTCGTGAATGTTTCTTCAGTTTCTTGTTCAGC
CAATGAGGAAAGGCATTGCCTTTCTTTTACCATTAACTCACTTCTCAATAAACGTGAGATCCTGTTGAGCATC

WO 2004/030615

PCT/US2003/028547

143/6881
FIGURE 135

GTACGTCGCCGGGGTTTCGGCTGCGTCCGTCCCGCCGCCGCCCGTTGCCGCCGCCGCCGCTGCCGCCGTGCTCTC
GCTTTGCCCGCCGCCGCTAAGGGGGGCTGGGGCCGGGGCCAGCCATCACTGCCGTTGCCGGGATGCCGCCGGTG
TACATCGGCCCGCTGAGCTACCAGGCCCGGGAGCGCGATGTGGAGCGCTTCTTTAAGGGCTACGGGAAGATCCTG
GAGGTGGATCTGAAGAACGGATATGGTTTTGTGGAGTTTGATGATCTGCGTGATGCAGATGATGCTGTTTATGAA
CTGAATGGCAAAGACCTTTGTGGTGAGCGAGTAATTGTTGAGCATGCCCGCGGCCACGGCGAGATGGCAGTTAC
GGTTCTGGACGCGAGTGGATATGGTTATAGAAGAAGTGGCCGAGATAAATATGGCCCTCCTACTCGCACAGAGTAC
AGACTTATTGTGGAGAATTTGTCAAGTCGGTGCGAGTGGCAAGACCTAAAGGATTATATGCGTCAGGCAGGAGAA
GTGACTTATGCAGATGCTCACAAGGGACGCAAAAATGAAGGGGTGATTGAATTTGTATCTTATTCTGATATGAAA
AGAGCTTTGGAAAAGTTGGATGGAAGTGAAGTCAATGGGAGAAAAATCAGATTAGTTGAAGACAAGCCAGGTTCC
AGACGACGCCGGTCTACTCCAGAAGCCGGAGTCATTCAAGGTCTCGCTCTCGAAGCAGACATTCCCGTAAGAGC
AGAAGCCGAAGTGGCAGCAGCAAAAGCAGTCATTCTAAGAGTAGATCTCGGTCCAGGTCGGGCTCCCGCTCCCGG
AGCAAGAGCCGGAGCCGGAGCCAGAGTCGGAGCCGGAGCAAGAAAGAGAAAAAGCAGGAGCCCCAGCAAGGAAAAAG
AGCCGCAGCCGCAGCCATAGCGCTGGCAAGAGCCGCAGCAAGAGCAAAAGACCAAGCTGAAGAGAAGATCCAAAAC
AATGACAATGTCCGGAAACCCAAGAGCCGGAGTCCTAGCAGGCATAAAAGTAAGAGCAAAAGTCGGAGCAGGAGT
CAGGAGAGGAGAGTGGAGGAGGAGAAGCGAGGGAGTGTGAGCAGGGGCAGGAGCCAGGAGAAGAGCCTCCGCCAG
AGTCGGAGCCGGAGCAGGAGCAAAAGGGGGCAGCAGGAGCCGGAGCAGGAGCCGCAGCAAGAGCAAGGACAAGAGG
AAGGGCAGGAAGAGAAGCAGAGAGGAGAGCCGAGTCGCAGTCGCAGCCGCAGCAAGAGTGAGAGGAGCAGAAAAG
CGAGGCAGCAAGCGAGACAGCAAGGCGGGCAGCAGCAAGAAGAAGAAGAAGGAAGACACTGACCGCTCCAGTCC
AGATCTCCATCCCGCTCCGTGTCAAAGGAGCGGGAACATGCCAAGTCTGAATCCAGCCAGAGGGAAGGTGAGGA
GAGAGTGAGAATGCTGGCACCAATCAGGAGACCCGGTCCAGGTCCAGATCCAATTCCAAATCGAAACCAAACCTT
CCATCAGAATCACGCTCCAGATCAAAGTCAGCTTCAAAAACCCGATCTCGGTCCAAGTCTAGATCCAGGTCTGCT
TCCAGATCGCCCTCCCGATCTAGATCTAGGTCCCACTCAAGGTCCCTAACTGGCTATGGCCACAGCTGGAACCTACC
CGAGAAGTCTTTTGTACATGTTTGGTAGCCGTAGCACAAAGTGATTGGAGTAGAACATGTCACTGCTGTACATTTT
TAACTCCCCTAATGGTGTGTCTATAATTGTTAAATCTAAGTGCTTCCCTCTCAGTAAAGCCTCCTGGCACCAGGCC
TTCTGCTCGACTGAAAAAAATTTTCTCTTTGAAAATCCCTTTTACTCATGGCCACAGTAGAATATCCAAAAC
GCCTTGGCTTTTCAGGCCTGGCCTTTCCTACAGGGAGCTCAGTAACCTGGACGGCTCTAAGGCTGGAATGACCACA
TAGGTAGGTATGGTGAGTTCAACCATTTTGTCTTTGAATTGATGCCCTTCGATGTATGCCATTTAGTGAAAGTG
CTAAGTCTTAAGTTTCTTACCACTTTGGTTTCATATTTTGGACTTAACAAAGTTGTGAATAGCACAGTCGAGGA
AAATTGATACCTGCAGTAACCCATAGGAAATAAACTGTAGAGTTCCATATTCTGGTATTGTGATTATATTGTTTT
ATATT

WO 2004/030615

PCT/US2003/028547

144/6881
FIGURE 136

AGGGTTCTCTCCCCTTGCCACCATGAGCGAGTCATTTGACTGTGCAAAATGCAACGAGTCCCTGTATGGACGCAA
GTACATCCAGACAGACAGCGGCCCTACTGTGTGCCCTGCTATGACAAATACCTTTGCCAACACCTGTGCTGAGTG
CCAGCAGCTTATCGGGCATGACTCGAGGGAGCTGTTCTATGAAGACCGCCATTTCCACGAGGGCTGCTTCCGCTG
CTGCCGCTGCCAGCGCTCACTAGCCGATGAACCCTTCACCTGCCAGGACAGTGAGCTGCTCTGCAATGACTGCTA
CTGCAGTGCGTTTTCTCGCAGTGCTCCGCTTGTGGGGAGACTGTCATGCCTGGGTCCCGGAAGCTGGAATATGG
AGGCCAGACATGGCATGAGCACTGCTTCTGTGCAGTGGCTGTGAACAGCCACTGGGGTCCCGTTCTTTTGTGCC
CGACAAGGGTGCTCACTACTGCGTGCCCTGCTATGAGAACAAGTTTGCTCCTCGCTGCGCCCGCTGCAGCAAGAC
GCTGACACAGGGTGGAGTGACATACCGTGATCAGCCGTGGCATCGAGAATGTCTGGTCTGTACCGGATGCCAGAC
GCCCCCTGGCAGGGCAGCAGTTACCTCCCGGGATGAAGATCCCTACTGTGTGGCCTGTTTTGGAGAACTCTTTGC
ACCTAAGTGACAGCAGCTGCAAGCGCCCCATCGTAGGACTCGGTGGAGGCAAGTATGTGTCCTTTGAAGACCGACA
CTGGCACCACAACCTGCTTCTCCTGCGCCCGCTGCTCTACCTCCCTGGTGGGCCAGGGCTTCGTACCGGATGGAGA
CCAAGTGCTCTGCCAGGGCTGTAGCCAGGCAGGGCCCTAAGCCAGGGCTCCTGGACCCAGGCTTTCCCATACCAC
GGGCCCAGGACTGTGGCTCCTTTTCTAAACCACCTCTGGGACTCAGCTCCCCCGCCAAAAAAATGGGTCTCCT
TCTGGGCTCCAGGATTGTCTCCCCACTCCAGCATCCCCAACTGGTACTCCCTGACCCAGGGCCCCAAACCTGGG
CTCTTACAGAGCCTCCATGAGTCAAGCCCCCTCCCCACACCTGGACTCCAGAATTCACCCCTCTCCCTGCAGTCT
GGGTTCAGACTGAGTCTCTCCCCAAATCAGGGCTCTAGACCCGAGCCCTCCAAACCTGGACTCTGGGACTTA
GGCCCCCTTAAATCTAGACTTCTCTTTATAGGTTTCAGGTCTCCTATGGGTGCCTGGGAAGTCCTTGAAAGTGGA
CTGTTCTCAGGCTTGACCTGCCCCACCCCATCCCCGCGGTTGAGGCTGTGGGGCAGCAGATCAGGAGCCCACTG
ATAAGGGGCCCTAGGGTACAGGGTGCTGCCAGCAGGTGCCACCGAGTGTCTTCTCATTTTATTTAGCTCCAT
TTTGCCCATAGATGGGCAGAGGGGTGAGATTGGCTCATCCCCCTTCCAGATTCTGCAATAAAGCGGTGTGAGG

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

146/6881
FIGURE 138

MERSEELNKDLNPFPTPLVGIRIPDHAFMQDLAQMFEGLALTSANLSSQASSLNVEEFQDLWPQLSLVIDGGQIG
DGQSPECRLGSTVVDLSVPGKFGIIRPGCALESTTAILQQKYGLLP SHASYL

WO 2004/030615

PCT/US2003/028547

147/6881
FIGURE 139A

AGGCCAGCGCTGGCGCAGTGAGAACTTCGAGAGACCCGTGGACCTGGAGGGCTCTGGGGATGATGACTCCTTTC
CCGATGATGAACTGGATGACCTCTACTCGGGGTCGGGCTCGGGCTGTAAGTACCCCCCTCCCTACCTCTGCCTGG
GGGCAGTGACCAGTCTGTATCCAGCCTCAACTCTGAGAAGCCACGGGGGGCTTGCTTCAGTGAGGCAGGGGGCA
TTCACTGCCTGGGTTCAGGCAAGTTCTTCTTGCTCTGGATCCCCAGAACAAGAAGGGCAGAACATCCTTCTGGGGA
TAGAACAAGACCTGGGAGGACCTCAGGGCCCAAGATGTCCAGGTCTCCAGGGTCCCACGTCTGCATCTTTGTGTG
TGCTATGTGGCTTTCTCTGCAGACCTTGCTTGGTTCCGGTGGTCCCGTCAGGTGCAATAAGCTGTGGCCAATGGT
GGGGTTAGGGCAGTGATGACACAGGGCAGGTGCTTCAAGTGGTGCCTGGGATGGCCCCGCCCTGGGGAAGGGGAG
CCAGGTTCAGCTGGGTCTAGCAGAATCTCGGGAGAGAAGGGCACCGCGAACCCCACTCTGCCATGTAGCAACTGTG
TGCCCCCTCGGTGCTCCCCCTCCCTGAATCCCTGTATTTTACCTGTGGATGGTGAGAAAACGACTTCTTCTCAG
TGCTCTAGGAGGGTTTGGGATAGGAAGCTGGGGTCTGGCACAGAGGAGGAGCTCTCAAAATGGTAGCAAAAAGA
AGGCAGCTGAGACTGGGCCAGTGAGGGCACGGGCTGGCATCTGAGGAGATGGTACGGGGTCTGCACGCCACAGA
GCTGGCTCCCCACAGCCCTCGCCTCTGGTCTCCCCCTCCTTAGCCAAGTCTTTGAGCCTCTTTCAAAATTAATCTT
TGTA AAAACCCGTTTATATTGGGTACATCTCTATTGCAAAGTTCCTGGCTCCCCCTCCCTCCTGCCTGGTTCCG
AGCCCAGGAGCTGGCTGTGGCTTCTCCCTCCCCCATCCCTACTCCCCATCTCATTTCTCCCAAGTTCCCTTAC
TGTCGGGCTTTGCGTCAGCCAGATTGCTCAAGCAGTTCCTTCGCTCAAGGGCTTCTTTTCCCTTTTACCCTCC
GCCTCTGCCTCTGGGGGAAGCCCTTAGTGTACCACCCCTGCCTTGAGCTTGTTGGTAGGGGTGCCTTTGGGGTCTG
ACTCTTCCCAAGATGCCACTCCTGTGTTCCTTCGCAAGCCCCAGCAAGTTTTCAGCCAGTAGCGCCTCAGTTGC
TGCTGCCTGGATTCAACCTCATAGAACTGTAGGCTGGGTGGGCAGGAATAGTCAAGGAAGGCTTCCCGGGAGAG
GCGGCCCCCAGAATTTTGACTTGGCAGAGAGAAGTTGGGGAACATCAGCAACTGACCACCTTTAGCTGGGCTGT
GCCTTCTCCTTTCTCTCATCTTTTCTGGGAAAATTGGGTAAAGAGAGGGGGTTGGGAGACCTAATCTTGATGGC
CATTGCTTACCTGGGATCCTCATGCCCCTCACAACCACCCAGCTCCCTAGCTCTCTCCCTCTCCCCACCCCTC
AGACTTCGAGCAGGAGTCGGGCATTGAGACAGCCATGCGCTTCAGCCAGATGTAGCCCTGGCGGTGTCCACCAC
ACCTGCGGTGCTGCCACCCACGAACATCCAGCCTGTGGGCACACCATTGAAGAGCTCCCTCTGAGCGUCCAC
CCTGGAGCCAGCCACCAGCCCCCTGGTGGTGACAGAAGTCCCGGAAGAGCCAGCCAGAGAGCCACCACCGTCTC
CACTACCATGGCTACCACTGCTGCCACAAGCACAGGGGACCCGACTGTGGCCACAGTGCCCTGCCACAGTGGCCAC
CGCCACCCCCAGCACCCCTGCAGCACCCCTTTTACGGCCACCACTGCTGTTATAAGGACCACTGGCGTACGGAG
GCTTCTGCCTCTCCCACTGACCACAGTGGCTACGGCACGGGCCACTACCCCGAGGCGCCCTCCCCGCCACCA
GGCGGCTGTCTTGACACCGAGGCCCAACACCCAGGCTGGTCAGCACAGCTACCTCCCGGCCAAGAGCCCTTCC
CAGGCCGGCCACCACCCAGGAGCCTGACATCCCTGAGAGGAGCACCCCTGCCCTGGGGACCACTGCCCCCTGGACC
CACAGAGGTGGCTCAGACCCCAACTCCAGAGACCTTCTGACCACAATCCGGGATGAGCCAGAGGTTCGGGTGAG
TGGGGGGCCAGTGGAGACTTCGAGCTGCCAGAAGAAGAGACCAACAACCAGACACAGCCAATGAGGTGGTATG
TGTGGGAGGGGCTGCGGCCAAGGCATCATCTCCACTGGGACACTGCCCAAGGGTGCCCGCCCGCCCTGGCCT
CCTGGACAATGCCATGACTCGGGCAGCTCAGCTGCTCAGCTGCCTCAGAAGAGTATCCTTGAGCGGAAGGAGGT
GCTCGTAGCTGTGATTGTGGGCGGGGTGGTGGGCGCCCTCTTTGCTGCCTTCTTGGTCAACTGCTCATCTATCG
TATGAAGAAAAAGGATGAGGGCAGCTACACGCTGGAGGAACCCAAGCAGGCGAGCGTACATACCAGAAGCCTGA
CAAGCAGGAGGAGTTCTATGCCTAGTGGAGCCACAGTGCCTCCCTGCAGCCTCAACACCACCCCTGCTGTCCAGTC
CCCAGCCTGGCCCCACCAGCCCAAGCCTGGGACTGGGCTGGAACCTGGCCCCAGTTCTTCTCTGCCCTCTCTCC
CAAGGTCTGCCAGGCTGCCAGCCTCACACAGATCTTCCCCGAGGAAGAGGGGCTGCTGCCATCTGCCCCAGACT
GTGCCCTTACGAGCTCATCTCTTGTTCCTCATCCCTGCCACCAGTCTGGGGCTTCAGGACCTCATGTTCAGATG
GATGGGAGGAAGAAAGCTCCTGATTGGCTGGTGGTGGAAAGAAAGGGTGGGGCTTGAGATGAGCCTGAGCCCTGAC
TTGGCACCCACAGTGCTCACTGAGATCTCCTTTTTGGGGCAGAGAGGCACTCAGGCTGGTTTTCCAGGACAAACAT
TTGGTAAACACAGCCCTTGAAATCATCTAGACACTGCAACCTCTTGCTCGTATCCAGGGCCTCTCTCTAGCTGG
GTGAGAGGGTGTCCCTTGTACCCAGCCTGTTTTGTCTGGTCTCTCTGGGGTGTGTAATCTCTCCTCTGCCTG
CCAAGTACACATGTACCCAGACTTCATTTCTTTCTGCATCTTCCCCAAGAAACAGCTTCTGAGGGTGTGGGG
CAGCCACTGGTGAGGAGGGGCTGCTCTGATGTCCCTCCTATGAGGGGACTCTGCACAGACACCATTGCCACACT
ATCACCATATTTTCACTCAGTCACACACAAGACAAAAGCATGCAATGACAAAACCATACGCAATCCTGACCGCCC
AGCCAATCAAGACATATCACAGAACACACGCGTCTTCCAAGAATGTTTATCCTCATGCATCACTTACACACCCC
CAGACACGTACTGCAATGCAAGTCACTAGTCATGGTCACATGACAGTGACAGTGTGGCCTCCTCCTACCCCAAAT

WO 2004/030615

PCT/US2003/028547

148/6881
FIGURE 139B

ACACCCACACTCTGGCACCACACACATTGTCTCCAGCTTTTCAGGCTTACTGGGGAGGGTGGAAATCGAGCCAGAAC
AATCAGCCCATATTGGGTCCCCCTAAGTTGCCCCGTCATACTCAGTCCCATGCCATGGTGGCCACACCAACCATG
CAGCCGCCAACCCAGCCAGTGTGACACACAATCCCATGTGGATGCACAGTCTCACTCCACATGACCTGCTCTCA
ATGCTGGAGGGAAACAGGCAGGCCCTTGCCCTTCTCGGAAAAAGTGTGGGGCCACAGCCCTTTTAGGGCATTGCA
TGCAGGTGGGCCTGGCTTCACCCCTACCTGCTTCCCTCCCAACCGCAGCTGGCAGAGGGGGAGGTTTGGGGCCAGA
CCCCACTAGCTGGGAGCCTGGGGGCTCCTCTAAGGCTGAGGAAGGAAATTTGGCCCCAGGTTGTGGGGGGTCT
TGGGTCTCCCAGGACGGAAGGCCAGGGCAGGGAGGGGGCATGTGGTTGGGCTCCTTTATCTCCCTGTGTCCCT
TCCTGCTTTGAGCTAGGGGGCTGACTCTGCCTCCCAAGACACAAGTCTCCAAAGTGCCTGTGAGGGCGGGCCCTC
CGCACCCCTCTGCCCTCTGCCTGGCAGGCCAACCTCAGCCACCTGCCAGAGGCCCTCCCTGTGGACACCCCTC
ACCTATTTGGCCAAACAATTCTGGCTGCAGCTTCAGGGGCCATGGCTGGAAGCAGCCCCCTGCAGATCCCTCAGGC
CCCGAGGTGAGGTTTGTAGGGATGAGACCAGGTGATAGTGGGGGAGGGGTACTTCCCTTTGTTACCTAGCAAGTA
GGGCTATTTCCATCGGTATTTTAAATGTGGGGTCACAGATCTTTTGGGGAGGGTGTGCTTGGCAGGGGGCTCTT
GGAGCCAAAGGGATGTGGTGTGAGTTGCGATTGGCTGGCACTCACACCCCCACCCCTCACCCACATCCCAGATTC
AAGTCAGGAAGGCAGGTTTTATTTCAGGGCCCTTTTCAAGATGCCCTGGCAGCAGATTTCTGCAGGATGAGGGGT
AGCGGTGTGTAGGCAGTGAGGGGGAGGTTCCAGGGGCTGTCCACAGCCTGTCTTTTCCAGGCTGGGCTCCATCT
TCCAGTCCCAAAACCCTCCTTCACAGGGCCAGAGGCTTGTGAGGAAGCCAGGTGGACCCAGCCTTAGAAGAGTG
GGCATGGGGGGCCCCCTGATATCTGGAGGGGGCGGGTTGGCCTCAGTCATCTTTGGAGCAGAAGGGCTGGGTCTCTG
GGGCCACAGACCACAAGGCTCAGCCTCCCTACCTGCTCCCTGGGGTGCTGCTGTCTTGGAGAGCACAGCTCTGG
TGAGACGGCCTGGGCAGGCCGAGGCTGAGAAACCAGGGAGGATAGAGGAGAAAAGGGCTTGGGGCCCCAGCCCCA
GAAGATGCTGGACCCAGGTGGGAGACCCAACAGTGGGTGCAGTTTCTCAGTAGGGCTGGAGCCAATGGTGGGGG
TGGCCCCGGCAGGCCCTGGCTCCTCACATCCCAGGGGTTGGCTTCTGATTTGGGGCTTGGGCTCCAGGCACTGGCT
TCTCTTCTCTGTGTCCTTAGCATTTGAGAGAAGAGGCCAGGGGGCTTGTTCATGGATCCCTGGACCCAAGGCAGA
TGTCAGGCTTTATCCTCCTGAGGATGAGGAGTCTGACCAGCCCAAACTGTGCCCTGGCCGGCCTGACCGGGCAA
GGCAGTCCAAGAGAGTTCAGTGAGGACCAGCTAGGCTCTCCAGGTGCAATGTGGGTGCAGGGCCCTCATGTCCC
CCTACCCCTGCCTGTGATGGAGTGTCTGAGGGGCTTTGGCATTGTCTGGAAGCACAGGGAGTTCCAAATGAGAG
GGAGCTTCTGTGGCTTGAGAGCCTCTGGGGCCTTGGCTGCCAGAGCACGAGGCAGGCCAGGACCTGGAGAGCCCA
GACCCTGTCTCCAGGAGGCCAGGAGGCCAGATGGGGGCTTGCCTGAAAGACTGGTCCCCTTGATCGCTGGAGGC
ATGTGGGTGGCAACCAGGGCTGGGCAGGGCTTAGGGTGTGTGGGCCAAACCCCCCTGGGGTTGGCAAAGCCGCCT
GTCAGGCCTCCTGGTGGGGGGCCCCCTGGACACAGGGAGCAGACCCTCTGCCTCATGGGGTAGGAGTGGCTGCCTCC
TGTGTTCTCTGGATTTCTTCTCCCAACAACACTACAACCCTGGACTTGCCTCCCCAGGCCTCTTGCTGTAAATAGA
AGCCCGCAAACCTGTACAGATTTACAGAGGCATCGAGACTGGGCCCTGGGAGTTGCCATCTGAGAGCCGATGGCCC
CAGCATCCCCAGGTGCCTGCCTGGCACCACAGTGACCCTGGCCTCAGCGTGGCAAATGCATGTAAATATTTTTC
GTAGGCAGCGTGGCTCCAGAGAGCCCCCTGAAGACAGTGTCCCTCCCTCCTGTGAGTCCTTTCTCCTGTACAGAA
CCTGCCTGGGGTGGGTGGGGGTCTGCCATTCCCTCCCCAGGCCTTCCCTGCCCCTTCTCTCCCCTGTAACTGT
TTATTAACCATACCTGTCTGAGTTTCATGGCCAAAACCTTAAATAAGAAAAACAAAAGAAAAAGACAGTGAAAA
AAGAGACCAAGGCGCCTGCCCCACTGCGGGTACTCTCCTGTTCCAGCCTTGTGAAGGAAGTGGTTTTGTTTTTGT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAACACTTCTGTGCTGTGCCCATTTATAAGAGGAA
ATAAAATTAAGCTGAAATG

WO 2004/030615

PCT/US2003/028547

149/6881
FIGURE 140

AGCCATGCCCTTTCTTGGACATCCAGAAAAGGTTTCGGCCTTAACATAGATCGATGGTTGACAATCCAGAGTGGTGA
ACAGCCCTACAAGATGGCTGGTCGATGCCATGCTTTTGAAAAAGAATGGATAGAATGTGCACATGGAATCGGTTA
TACTCGGGCAGAGAAAGAGTGCAAGATAGAATATGATGATTTTCGTAGAGTGTTTGCTTCGGCAGAAAACGATGAG
ACGTGCAGGTACCATCAGGAAGCAGCGGGATAAGCTGATAAAGGAAGGAAAGTACACCCCTCCACCTCACCACAT
TGGCAAGGGGGAGCCTCGGCCCTGAACAGAGCAGCTGCTGATGTCTGGAGGCTGATTTTCCTGTTCTCTGTTCTC
CACTGGAAAGGTTGTTTACGACAAACCTCCTTGTCAAAGTGTGTAAAAATAAAGGATTGCTCCATCCT

WO 2004/030615

PCT/US2003/028547

150/6881
FIGURE 141

GCTGAGCGGGCTTTGGACACCATGAACTTTGATGTGATTAAGGGAAAGCCAATCCGCATCATGTGGTCTCAGAGG
GATCCCTCTTTGAGAAAATCTGGTGTGGGAAACGTCTTCATCAAGAACCTGGACAAATCTATAGATAACAAGGCA
CTTTATGATACTTTTTCTGCTTTTGGAAACATACTGTCCTGCAAGGTGGTGTGTGATGAGAACGGCTCTAAGGGT
TATGCCTTTGTCCACTTCGAGACCCAAGAGGCTGCCGACAAGGCCATCGAGAAGATGAATGGCATGCTCCTCAAT
GACCGCAAAGTATTTGTGGGCAGATTCAAGTCTCGCAAAGAGCGGAAGCTGAGCTTGGAGCCAAAGCCAAGGAA
TTCACCAATGTTTATATCAAAAACCTTTGGGGAAGAGGTGGATGATGAGAGTCTGAAAGAGCTATTAGTCAGTTT
GGTAAGACCCTAAGTGTCAAGGTGATGAGAGATCCCAATGGGAAATCCAAAGGCTTTGGCTTTGTGAGTTACGAA
AAACACGAGGATGCCAATAAGGCTGTGGAAGAGATGAATGGAAAAGAAATAAGTGGTAAATCATATTTGTAGGC
CGTGACAAAAGAAAGTAGAACGGCAGGCAGAGTTAAACGGAAATTTGAACAGTTGAAACAGGAGAGAATTAGT
CGATATCAGGGGGTGAATCTCTACATTAAGAACTTGGATGACACTATTGATGATGAGAAATTAAGGAAAGAATTT
TCTCCTTTTGGATCAATTACCAGTGCTAAGGTAATGCTGGAGGATGGAAGAAGCAAAGGGTTTGGCTTCGTCTGC
TTCTCATCTCCTGAAGAAGCAACCAAAGCAGTCACGTAGATGAATGGACGCATTGTGGGCTCCAAGCCACTATAT
GTTGCCCTGGCCCAGAGGAAGGAAGAGAGAAAGGCTACCTGACCAACCAGTATATGCAACGAGTGGCTGGAATG
AGAGCACTTCCTGCCAATGCCATCTTAAATCAGTTCCAGCCTGCAGCGGGTGGCTACTTTGTGCCAGCAGTCCCA
CAGGCTCAGGGAAGGCCTCCATATTATACACCTAACCAAGTTAGCACAGATGAGGCCTAATCCACGCTGGCAGCAA
GGTGGGAGACCTCAAGGCTTCCAAGGAATGCCAAGTGCTATACGCCAGTCTGGGCCTCGTCCAACCTCTTCGCCAT
CTGGCTCCAACCTGGTAATGCTCCGGCCTCTCGTGGCCTCCCTACTACCACTCAGAGAGTCGGGTCTGAGTGCCCG
GACCGCTTGGCTATGGACTTTGGTGGGGCTGGTGCCGCCAGCAAGGGCTGACTGACAGCTGCCAGTCTGGAGGC
GTTCCACAGCTGTGCAGAACTTAGCGCCACGCGCTGCTGTTGCTGCTGCTGCTCCCCGGGCTGTTGCCCCCTAC
AAATACGCCCTCCAGTGTCGCGAGCCCTCATCCTGCCATACAGCCTCTGCAGGCACCCAGCCTGCGGTCCATGTG
CAGGGGCAGGAGCCACTGACTGCCTCCATGCTGGCTGCAGCACCCCCCAGGAACAGAAGCAGATGCTGGGAGAA
CGCTTGTTCCCACTCATCCAAACAATGCATTCAAATCTGGCTGGGAAGATCACGGGAATGCTGCTGGAGATAGAC
AACTCTGAGCTGCTGCACATGTTAGAGTCCCCCGAGTCTCTCCGCTCCAAGGTGGATGAAGCTGTAGCAGTICTA
CAGGCTCATCATGCCAAGAAAGAGCTGCCCAGAAGGATTCAAAGCCAAATAACCCCTTATGGAATTCAACTCA
AGGTTTGAAGACTTCTAGCTTGTCCTATGGACCTCAACACCAAGGATTACAAATTGCAAATTTAATAGGTCATT
TTGTATCAAAAGGTCAATTATGAAGCACCTAGAATTTTTCAATTATACGAATATGTTCTTTGGGTTCTGCTGTGG
CCCAGACAGTGTTAACTTTTTTTTTTATTGTGGGTTTTGATTTTTTCCCCCAGAAATTGGTTTTATTGTGTACC
CAAGTCTTACGTTTCCCAATAAAGAAAAAAAATCTCCAT

PCT/US2003/028547

ACCAGGCAGCCTGCGTTTCGCCATGAAGCGACCCAAAGGAGCGAGCGGCTCCGACGGGAGTCCGACGGACCCATC
GACGTGGGCCAAGAGGGGCCAGCTGAGCCAGATGGCCAGGCCGCTGTCCACCCCCAGCTCTTTCGAGATGCAAGCC
AGGAAGAAACGCAGAGGGATCATAGAAACGGCGTTCGAGACCGCATCAACAGTAGCCTTTCTGAATTGCGACGC
TTGGTCCCCACTGCCTTTGAGAAACAGGGCTCTTCCAAGCTGGAGAAAGCCGAGGTCTTGAGATGACGGTGGAT
CACTTGAAAATGCTCCATGCCACTGGTGGGACAGGATTCTTTGATGCCCGAGCCCTGGCAGTTGACTTCCGGAGC
ATTGGTTTTTCGGGAGTGCCTCACTGAGGTACATCAGGTACCTGGGGGTCTTGAAGGGCCCAGCAGCCGTGCAGAC
CCCGTCCGGATTTCGCTTCTCTCCACCTCAACAGCTACGCAGCCGAGATGGAGCCTTCGCCCACGCCCCTGGC
CCTTTGGCCTTCCCTGCTTGGCCCTGGTCTTTCTTCCATAGCTGTCCAGGGCTGCCAGCCCTGAGCAACCAGCTC
GCCATCCTGGGAAGAGTGCCAGCCCTGTCTCCCCGGTGTCTCCTCTCCTGCTTACCCCATCCCAGCCCTCCGA
ACCGCTCCCCCTTCGCAGAGCCACAGGCATCATCTGCCAGCCCGGAGGAATGTGCTGCCAGTCGAGGGGCATCT
TCCACCCGGAGGGCCCCGCCCTAGAGAGGCCAGCCCTGTGCCTGTGCCCCCAGCAGCAGGGCTGCCAGG
AGCAGCCACATCGTCCCCCTCCTGCAGTCTTCTCTCCCCAACACCCCCCTGGTCTACAGGGTGGCTGCTTACGTG
GCTGTTCCACCCCCAACTCATCTCCCCAGGGCCAGCTGGGAGGCCAGCGGGAGCCATGCTCTACCACTCCTGG
GTCTCTGAAATCACTGAAATCGGGGCTTTCTGAGCTGCCCTTACCACCCCCGCCCCAAGGAATAAGGAAGGTTT
TTTTACCAGGAGCCCCAAAAAGGGCACTGCCTTTTTCTGCTTGTCTCGTGGAAGTGGCTCATATGTGAAGGCACGT
TCTCCAGCCATCAGAGGCCCTCTCTCTCCAAACCATCTCTCCTTCTCACTGTTATCCCAGCTTATCCACCCAG
CTCTCCTGGAGCTGTTCTGGTCTCAGAGGCTTGGTTCCATTTCTCACTGAAACAGATGAGTCTGGGAGAGACCC
TCAGAGATCCGCCAGGACCCCTCTCCTGCCCTCTGCACACCAGCAGCAGGCATGAACCTTGGGTCTGGGAAAAAG
CTTTAACCTGCAGGACACCAGGACCCAAGGCAGGCTGTTCTTGGGGCGGTGAGCCCCAGTCAGGAGCAATGAC
TGACTGGCTGCAGCCTTCCACGCCAAGAGGCTGGAACATAGTGTCTGCCTCGCTTCTGGAGATAGTAACTGAG
CAGGGGCTACAAAGAGGTCTCCTGGGAACCTGTCTGCCCTTCCACCTGTCTTGGGCCACACCATCACACTG
AACCACAGGACAGACCCTTTCTCCACCACAGCCAAGGCCTGGAGACTGGGGGCCAGCAGAGCCTGCTCCCACCC
TCTCCAGCAGCAGACACCCACCCTCTCACTGACTAACAGGTCCCTGCACACAGCTGGCCTGGTAAACCCAGCT
GGGAGGTTTCTAGGCAGCAGCAAACTCTGTGACAGGGTGTCTCACACCAGGCCTTGGACAGCTCTCCCAGACA
GGAGCAGGGTTGAGCAATGGAGAGCCAGCCCCACGTCTTACAGTCGCCATCTCCAGGCGTGTGGTCCCTCC
CCATTGGGTGCACAGTGCAGAGGGGCCGTGGCCCCATGTGATGGTGCAGAGAGGAACCTCTTGGGATTCAGCA
CCAGACGTCTGTGCTGCCTGGTTTGATCCGGCTCACAGAGCCAGACTGCTGGAACAGCCAAGGACTGTCAGGC
TGGACAAAAATAACTGCAAGGAGGGGCAAGAGAAAGGATGATTGAGGCACCTTGGCCCTTCAAGGTGATGCAGT
GGGTGAGCGCCTGAGATCCTGTTTACCAGGACTCCACAGAGCTGGCTCTGCTCAGAAGCCATTTCATTCCCCGG
CTCCACCCTAGGCCACTTTTTCTAACAGAGGAAACAAATGGTCCAGCAGTCGTTCCACAGCAGAACAGCGGAGCCT
GGACTGACACCCAGTGGGACCAGTGTGGCCACACCAGTTGATAAAATGCAGAAACCTTCTGTACTCGTTGGTAA
ATATCTACTCCCCAAGTGACTCCAGGTGCCCCCACCAGCCTGGCACTTCCCCAGGACTCCTACGATCTGGTTA
CTGCCTGGCCGATCCAAGGCTGTGGAGTCCCAGAGCCAGCAGTTCACTGGTGCTCATTCCCACTGGTTAGATAC
TTCAGTTGTACCCCTGGGAAGATTCTCCACCTCCTCCCTTTGATGGAACACCCCTCCCAGAGGCTGCATTGA
GGAGACTCCACAGACTGAAAAGTGAGTTTGAGAAACCTTGGGGAAAAGGGCCCTTTCAAAGAAGTGGAAGAG
GGAGGAGATCATTGAGTGACCCAGAAAGCTCTTTTGAAAAGACAGACTCCTCAAGGAGAGATAAAGAGGAAAGCA
CCTCTTTTCATTTTTTAGTGTGAGCTAATTCCATCAGACTGCTGTCTCCTTGGACCCATCTGAGATGTGCAGTAGC
AAGGAGAGGGGGGATCATTTTAGAGAGTGGGTCACTGGCAGGGAGTGCTCCGGAGGGAGGCAGAGGGGAGACTGT
GGTAGAAGGAAGACAGAACTCACACATGCTCCCAGGATTGGGGACAGGGACAGAGGAGGTAACAGAAGGCAAAGG
CCAGTTTTCCCGTTATCATGAAGGGGCCACTCAGGACAGGAACAAGGACAACCTCCTCCTCCTCCTCCTCCTC
CTGCTGCTCCTGGGATACCAGGTGAGTGTAGTCTTGAGTTTGGCAACTTCTAGCCTGAGAATCCCTAGTG
GGGCTGTGGGAAACACATTTCCACGTTGCAAGCATGCAACTCCAAGAATCTGTGATGCCACTGAAATGAGATGG
GAATGATCCAGCTCTTTAGCATCTTGGTTGAACTTGCTTTTCAATTGTCCCTGGGATATTGTGGAAGGAAAGGTGA
CTGTGTGATCTGATTCTGTGGTCAAGGACTTGATCTTGTGTTTCTATCCCCAAGCCTTCTGGTGTCTCCAAC
CCTACCCCATTCATGGGTTGTTGCGGACATCCAATAAGATTTTTTTAGTGCTTCTGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAC

WO 2004/030615

PCT/US2003/028547

152/6881
FIGURE 143

MKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQMQARKKRRGIIEKRRRDRINSSLSELRRLLVPTAFE
KQGSSKLEKAEVLQMTVDHLKMLHATGGTGFFDARALAVDFRSIGFRECLTEVIRYLGVLGEPSSRADPVRI RLL
SHLNSYAAEMEPSPTPTGFLAFFAWPWSFFHSCPGLPALSNQLAILGRVPSVLPGVSSPAYPIPALRTAPL RRA
TGIILPARRNVLP SRGASSTRRARPLERPATVPVPVAPSSRAARSSHIAPLLQSSSPTPPGPTGSAAYVAVPTPNS
SSPGPAGRPAGAMLYHSWVSEITEIGAF

WO 2004/030615

PCT/US2003/028547

153/6881
FIGURE 144

GATCCTAAATTGCAGCAAGGCTACAATGCTATGGGATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAG
AGATGCCCTTCACCTCCCATGATCAATCTGATCTCGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGA
TGCCCAGGAGAGAGCTCTCACATCTGTGACTTCATCCGAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTT
CAGGAACGCCTCGTGCAAGCCGAATACTGGCATGACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTC
TTGGCAGATATAAATCAGGAGCGGGGTATCAATGAGTCTTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTG
ATGGTGAAAATTCCTCAATGATTCCATTGTGGACCCTGTAGATTGCGAGTGGTTTGGATTTTACAGAAGTGGCCAA
GCCAAGGAAAACCATTCCTTACAGGAGACCTCCCTGTACACACAGGACCGCCTGGGGCTAAAGGAAATGGACAAT
GCAGGACAGCTAGTGTCTTGGCTACAGAAGGGGACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCCACATC
ATACCATTCCCTTGGATGAAACCCGTATAGTTCACAATAGAGCTCAGGGAGCCCCTAACTCTTCCAAACCACATGG
GAGACAGTTTCCTTCATGCCCAAGCCTGAGCTCAGATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCC
TACTTGGAAGATCTAAGATCTGAATCTTATCCTTTGCCATCTTCTGTTACCATATGGTGTGGAATGCAAGTTTA
ATTACCATGGAGATTGTTTTACAACTTTTGATGTGGTCAAGTTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATC
AGTGCCAGAACTGTGCCCAGGCCCAAAGGAGACAATACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTT
TTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTGCCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGG
TGATTTAACCAAGTGCTTGGAATACTTGCTTGGCTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAG
TACGTTGCCCTCTGTGCTATCATCTTATCATCAATTATTAGACAAATCCCACTGGCCTACAGTCTTGCTTCTGCA
GCACCCACTTTGTCTCCTCAGGTAGTGATGAATTAGTTGCTGTGCACAAAAGGAGGGAAGTAGCACCCAAATTAAG
TTGCTTAAGAGAGGAAATGTACATCTTGATAACTTAGGGAGCGAAGAAAATGTAGGCGCGAAAGTGAAAAGTGA
GGCAGCTAGTTCTTCCTATTCCATTCTCGACCAACCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAG
TCAACTTACTCTGTTGCTGGCTTTAGCAGAGAATAGGAGGAACCATATGAAAAAGATCAGGCTTTCTGACTTCCA
TCCCCAAAACACATTTACCAGCATACTCCAACTGTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAA
AAGCTTGGAATACTACACACTCCCTTTCTCCTTCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGA
GAATTCCTGTTACAGTAAACAAAATAACGTAATCTACCATTTCTTACACTATTTGAGCATGGAAATCATAGTCC
CCACTCTGTGAAAACCTAACGCTTTTGGAAAGACATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGC
CTTGATGAAAGAACCGTGTGGTGCTGCTAAGTTTAGCCATTATGGTTTTCTTTCTCTCTTAAAGCCTTATT
CTTCAACTAAAAGATGAGGATTAAGAGCAAGAAGTTGGGGGGGATGTGAAAATAATTTTATGAGGTGTCTAAAA
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WO 2004/030615

PCT/US2003/028547

154/6881
FIGURE 145

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCTCCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCGCCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCCCTTCAAAAGCAGGAGCAGCTCCATATGTGCAGGCATTTG
ACTCGCTGCTTGCTGGTCTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTCCGGGAGAAGAACC
GAGGCAGCAAGTTGTTTAAATCACCTGTCTGAGCTGTCTCAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCTCAAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCAACCGGACTGGCCTGGAGCAAACGGGGCCTGTGGCAAAGAACTGAGCGGACTGCCATCTG
GACCTCTGCCGGATCAGGTCTCTCTCCCTCCACCATGCCCTCTCTCTCCCTCAGTCTCTACCAAGTTTCATGCT
CATATGAGTCTGCTTCCCGCTCAGCACTGTTTCGCGCAGATTAATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAGAACCCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACAGCCCATCCCCAAACGAGCCACAAAGAAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAATCAAGGGCAAATTAACCTCATTACAGTAG
ATAACTGTAAGAACTTGGCCTGGTATTTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTCAGGTAATGGGTAAAGTGCCAACCATATCCATCAACAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCTGGATTGTGAAATAGTCAGTGCCAAATCTTCCGAGATGAATGTCCTCATTCTACAGAAGGCGGTGACT
TTAATGAATTCCAGTTCCTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCAACACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTCTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTCTAGATTTCTCTACCTTTTGTCTCTTAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTCAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAAGTCCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGTTATTCTACCAACAAACAGTCCATTGGAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTACACTGGTTAATCTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAACTAATTTTTCTACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAGGCTGAGGCTTGCCATC
TAGCATTCCATACAAAATGTTTCTATAAGCATTCCTTTTATTCTCTATTCTATCCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGCCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCAGCACCTTCCTATAGAGATGACTTTAAAAGGAAAAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCTGAATCCTTCTTCCCTGCCAGGTGCCTGTCACTGTCTTCACTGCC
TCCTTTTCCCTGTCTATGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGACAGCACTGCTAATGTAAATTTAGTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTGGTGGGAAGAGAGATTGTCTGTGATTTCTACCCATT
TCCTGAGGCCTGTGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAAATAGAATAAAGTTAATACCAAACTT
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WO 2004/030615

PCT/US2003/028547

155/6881
FIGURE 146

GGCTTCGGTTCGCTACCGCTCCCGCTCTGCCACCCCCGCCAACCGCCGCTCGGGCCTCCGTTCGCTGCCGCGTCGCT
TTCTCGCTCCTTGGATCGCAATCCTCCCAGATGCAGCGCCGGGACGACCCGCGCGCATGAGCCGGTCTTC
GGGCCGTAGCGGTCCATGGACCCCTCCGGTGCCACCCCTCGGTGCGTCAGACGCCGTCTCGGCAGCCGCCGCT
GCCTCACCGGTCCCGGGGAGGCGGAGGGGGATCCCGCGGGGGCGCCCGGGCCTCGCCCGCCACGCAGCCGCCACC
GCTGCTGCCGCCCTCGGCCACGGGTCCCGACGCGACAGTGGGCGGGCCAGCGCCGACCCCGCTGCTGCCCCCTC
GGCCACAGCCTCGGTCAAGATGGAGCCAGAGAACAAGTACCTGCCCGAATCATGGCCGAGAAGGACTCGCTCGA
CCCGTCTTCACTCACGCCATGCAGCTGCTGACGGCAGAAATTGAGAAGATTGAGAAAGGAGACTCAAAAAGGA
TGATGAGGAGAATTACTTGGATTTATTTCTCATAAGAACATGAACTGAAAGAGCGAGTGCTGATACCTGTCAA
GCAGTATCCCAAGTTCAATTTTGTGGGGAAGATTCTTGGACCACAAGGGAATACAATCAAAAGACTGCAGGAAGA
GACTGGTGCAAAGATCTCTGTATTGGGAAAGGGCTCAATGAGAGACAAAGCCAAGGAGGAAGAGCTGCGCAAAGG
TGGAGACCCCAAATATGCCCACTTGAATATGGATCTGCATGTCTTTCATTGAAGTCTTTGGACCCCATGTGAGGC
TTATGCTCTTATGGCCCATGCCATGGAGGAAGTCAAGAAATTTCTAGTACCGGATATGATGGATGATATCTGTCA
GGAGCAATTTCTAGAGCTGTCTTACTTGAATGGAGTACCTGAACCCCTCTCGTGACGTGGGGTGCCAGTGAGAGG
CCGGGGAGCTGCACCTCCTCCACCACCTGTTCAGGGGGCCGTGGTGTGGTGGACCACCTCGGGGGGCTTTGGTACG
TGGTACACCAGTAAGGGGAGCCATCACCAGAGGTGCCACTGTGACTCGAGGCGTGCCACCCCACTACTGTGAG
GGGTGCTCCAGCACCAAGAGCACGGACAGCGGCATCCAGAGGATACCTTTGCCTCCACCTCCTGCACCAGAAAC
ATATGAAGAATATGGATATGATGATACATACGACAGAAAGTTACGAAGGCTACGAAGGCTATTACAGCCAGAG
TCAAGGGGACTCAGAATATTATGACTATGGACATGGGGAGGTTCAAGATTCTTATGAAGCTTATGGCCAGGACGA
CTGGAATGGGACCGCCGTGCTGAAGGCCCTCCTGCTAGGCCAGTGAAGGGAGCATAACAGAGAGCACCCATA
TGGACGTTATTAACAAACAAACATGAGGGGAAATATCAGTTATGAGCAAAGTTGTTACTGATTTCTTGTATCTCC
CAGGATTCCTGTTGCTTTACCCACAACAGACAAGTAATGTCTAAGTGTTTTCTTCGTGGTCCCCTTCTTCTCC
CCACCTTATTCATTCTTAACCTCTGCATTCTGGCTTCTGTATGTAGTATTTTAAATGAGTTAAATAGATTTAG
GAATATTGAATTAATTTTTTAAGTGTGTAGATGCTTTTTCTTGTGTTTAAATATAAACAGAGTGTACCTTT
TATAATAAAAAAAGAAGTTGAGTAAAAAACAACACACAAACCTGTTAGTTTCAAAATGACATTGCTTGCT
TAAAGGTTCTGAAGTAAAGGCTTGTTAAGTTTCTCTAGTTTTGATTGAGGCATCCCGTAAAGTTGTAGTTGCA
GAATCCCAAACCTAGGCTACATTTCAAATTCAGGGCTGTTTAAAGATTAAATACAAACATTAACGGCAGTAGG
CACCACCATGTAAAGTGAGCTCAGACGTCTCTAAAAATGTTTCTTTATAAAAGCACATGGCGGTTGAATCTT
AAGGTTAAATTTAATATGAAAGATCCTCATGAATAAATAGTTGATGCAATTTTAAACGTTAATTGATATAAAA
AAAAAACAACAAATTAGGCTTGTAACCTGACTTTTTCATTACGTGGGTTTTGAAATCTAGCCCCAGACATAC
TGTGTTGAGAGATACTTAGAGGGAGGGAGTAGGTTTTGAAGAGGTTGATGGTGGTGGGGAGGGAAGGCCTCCTGA
ATTGAGTTTGATGCAGAGCTTTTAGCCTATGAAGAATCTTCAGTCATAGTACTAATAATTAATTTTCAGTATT
TAAAAAGACAAAGTATTTGTCCATTTGAGATTCTGCACTCCATGAAAAGTTCACTTGGACGCTGGGGCCAAAAG
CTGTTGATTTTCTTAAGTTGACGGTTGTCAATATATCGAACTGTTCCCAAGTTAGTCAAGTATGTCTCAACACTA
GCATGATATAAAAAGGGACACTGCAGCTGAATGAAAAGGAATCAAAATCCACTTTGTACATAAGTTAAAGTCCT
AATTGGATTTGTACCGTCTCCATTTTGTCTCGGAAGATTAAATGCTACATGTGTAAGTCTGCCTAAATAGGT
AGCTTAAACTTATGTCAAAATGTCTGCAGCAGTTGTCAATAAAGTTTAGTCCTTTTTTA

WO 2004/030615

PCT/US2003/028547

156/6881
FIGURE 147

MQRRDDPAARMSRSSGRSGSMDPSGAHPSVRQTPSRQPPLPHRSRGGGGSRGGARASPATQPPPLLPPSATGPD
ATVGGPAPTPLLPPSATASVKMEPENKYLPELMAEKDSLDPSTHAMQLLTAEIEKIQKGD SKKDDEENYLDLFS
HKNMCLKERVLPVKQYPKFNFVGKILGPQGNTIKRLQEETGAKISVLGKGSMRDKAKEEELRKGGDPKYAHLNM
DLHVFIEVFGPPCEAYALMAHAMEEVKKFLVPDMMDDICQEQFLELSYLN GVPEPSRGRGVPVRGRGAAPPPPV
PRGRGVGPPRGALVRGTPVRGAI TRGATVTRGVPPPPTVRGAPAPRARTAGIQRIPLPPPPAPETYEEYGYDDTY
AEQSYEGYEGYYSQSQGDSEYYDYGHGEVQDSYEAYQDDWNGTRPSLKAPPARPVKGAYREHPYGRY

WO 2004/030615

PCT/US2003/028547

157/6881
FIGURE 148

CTCGCGTCACAGCCGGGATGAAGCCGATCCTACTGCAGGGCCATGAGCGGTCCATTACGCAGATTAAGTATAACC
GCGAAGGAGACCTCCTCTTTACTGTGGCCAAGGACCCTATCGTCAATGTATGGTACTCTGTGAATGGTGAGAGGC
TGGGCACCTACATGGGCCATACCGGAGCTGTGTGGTGTGTGGACGCTGACTGGGACACCAAGCATGTCTCTACTG
GCTCAGCTGACAACAGCTGTCTGTCTCTGGGACTGTGAAACAGGAAAGCAGCTGGCCCTTCTCAAGACCAATTCTGG
CTGTCCGGACCTGCGGTTTTGACTTTGGGGGCAACATCATCATGTTCTCCACGGACAAGCAGATGGGCTACCACT
GCTTTGTGAGCTTTTTTGACCTGCGGGATCCGAGCCAGATTGACAACAATGAGCCCTACATGAAGATCCCTTGCA
ATGACTCTAAAATCACCAGTGCTGTTTGGGGACCCCTGGGGGAGTGCAATCATCGCTGGCCATGAGAGTGGAGAGC
TCAACCAGTATAGTGCCAAGTCTGGAGAGGTGTTGGTGAATGTTAAGGAGCACTCCCGGCAGATCAACGACATCC
AGTTATCCAGGGACATGACCATGTTTGTGACCGCGTCCAAGGACAACACAGCCAAGCTTTTTGACTCCACAACCTC
TTGAACATCAGAAGACTTTCCGGACAGAACGTCTGTCAACTCAGCTGCCCTCTCCCCCACTATGACCATGTGG
TCCTGGGCGGTGGTCAGGAAGCCATGGATGTAACCACAACCTCCACCAGGATTGGCAAGTTTGAGGCCAGGTTCT
TCCATTTGGCCTTTGAAGAAGAGTTTGAAGAGTCAAGGGTCACTTTGGACCTATCAACAGTGTTCCTTCCATC
CTGATGGCAAGAGCTACAGCAGCGCGCGCAAGATGGTTACGTCCGTATCCATTACTTCGACCCACAGTACTTTG
AATTTGAGTTTGAGGCTTAAGAAGCTGGATCTCCTGCGGGCGTGTTGGCTCATGCCTGTAATCCCACCACTTT
TTTTTAAAGGCAGGCGGATCACCTGAGGTCAGGAGTTTAAGACCAGCCTGACCAACATGGAGAAACCTCGTCTCT
ACTAAAAATACAAAAATTAGCCAGGCATGGTGGCACACGCCTATAGTCCAGCTACTCAGGAGGCTGAGGCAGGA
GAATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACGTCAATTGCACTCCATCCTGAGCCACAAG
AGCAAAACTCCGTCTCAAAAAAAAAAAGAAGAAGGTGGATCTCCAACCAGGCCAGAGAAGATTCTCACAGAAGG
TTTTGAACCTCTAAGAAATAAATTGGTTTGGTAATAAATGGCTTCTGGTCAGA

WO 2004/030615

PCT/US2003/028547

158/6881
FIGURE 149

MKPIILLQGHERSITQIKYNREGDLLFTVAKDPIVNVWYSVNGERLGTYMGHTGAVWCVDADWDTKHVLTGSADNS
CRLWDCETGKQLALLKTNSAVRTCGFDFGGNIIMFSTDKQMGYQCFVSFFDLRDP SQIDNNEPYMKIPCND SKIT
SAVWGPLGECIIAGHESGELNQYSAKSGEVLVNVKEHSRQINDIQLSRDMTMFVTASKDNTAKLFDSTTLEHQKT
FRTERPVNSAALSPNYDHVVLGGGQEAMDVTTTSTRIGKFEARFFHLAFEEEEFGRVKGHF GPINSVAFHPDGKSY
SSGGEDGYVRIHYFDPQYFEFEFEA

WO 2004/030615

PCT/US2003/028547

159/6881
FIGURE 150

GAGCGGAGCCGCGGGCGGGAGGGCGGACGGACCGACTGACGGTAGGGACGGGAGGCGAGCAAGATGGCGCAGACG
CAGGGCACCCGGAGGAAAGTCTGTTACTACTACGACGGGGATGTTGGAAATTACTATTATGGACAAGGCCACCCA
ATGAAGCCTCACCGAATCCGCATGACTCATAATTTGCTGCTCAACTATGGTCTCTACCGAAAAATGGAAATCTAT
CGCCCTCACAAAGCCAATGCTGAGGAGATGACCAAGTACCACAGCGATGACTACATTAAATTCTTGCGCTCCATC
CGTCCAGATAACATGTCGGAGTACAGCAAGCAGATGCAGAGATTCAACGTTGGTGAGGACTGTCCAGTATTCGAT
GGCCTGTTTGAGTTCTGTCAGTTGTCTACTGGTGGTTCTGTGGCAAGTGCTGTGAAACTTAATAAGCAGCAGACG
GACATCGCTGTGAATTGGGCTGGGGGCTGCACCATGCAAAGAAGTCCGAGGCATCTGGCTTCTGTTACGTCAAT
GATATCGTCTTGCCATCCTGGAAGTATCAACAGAGGGTGTGTACATTGACATTGATATTCACCAT
GGTGACGGCGTGGAAGAGGCCCTTCTACACCACGGACCGGGTCACTGCTGTGCTCTTCATAAGTATGGAGAGTAC
TTCACAGGAAGTGGGACCTACGGGATATCGGGGCTGGCAAAGGCAAGTATTATGCTGTTAACTACCCGCTCCGA
GACGGGATTGATGACGAGTCCATGAGGCCATTTTCAAGCCGGTCACTGTCCAAAGTAATGGAGATGTTCCAGCCT
AGTGCGGTGGTCTTACAGTGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTCAATCTAACTATCAAA
GGACACGCCAAGTGTTGGAATTTGTCAAGAGCTTTAACCTGCCTATGCTGATGCTGGGAGGCGGTGGTTACACC
ATTCGTAACGTTGCCGGTGTCTGGACATATGAGACAGCTGTGGCCCTGGATACGGAGATCCCTAATGAGCTTCCA
TACAATGACTACTTTGAATACTTTGGACCAGATTTCAAGCTCCACATCAGTCCTTCCAATATGACTAACCAGAAC
ACGAATGAGTACCTGGAGAAGATCAAAACAGCGACTGTTTGAGAACCTTAGAATGCTGCCGCACGCACCTGGGGTC
CAAATGCAGGCGATTCTTGAGGACGCCATCCCTGAGGAGAGTGCGGATGAGGACGAAGACGACCCTGACAAGCGC
ATCTCGATCTGCTCCTCTGACAAACGAATTGCTGTGAGGAAGAGTTCTCCGATTCTGAAGAGGAGGGAGAGGGG
GGCCGCAAGAACTCTTCCAACCTCAAAAAAGCCAAGAGAGTCAAAACAGAGGATGAAAAAGAGAAAGACCCAGAG
GAGAAGAAAGAGTCACCGAAGAGGAGAAAACCAAGGAGGAGAAGCCAGAAGCCAAAGGGGTCAAGGAGGAGGTC
AAGTTGGCCTGAATGGACCTCTCCAGCTCTGGCTTCTGTGCTGAGTCCCTCACGTTTCTTCCCCAACCCCTCAGAT
TTTATATTTTCTATTTCTCTGTGTATTTATATAAAAAATTTATTAAATATAAATATCCCCAGGGACAGAAACCAAG
GCCCCGAGCTCAGGGCAGCTGTGCTGGGTGAGCTCTTCCAGGAGCCACCTTGCCACCCATTCTTCCCGTTCTTAA
CTTTGAACCATAAAGGGTGCCAGGTCTGGGTGAAAGGGATACTTTTATGCAACCATAAGACAAACTCCTGAAATG
CCAAGTGCTGCTTAGTAGCTTTGGAAAGGTGCCCTTATTGAACATTCTAGAAGGGGTGGCTGGGTCTTCAAGGA
TCTCCTGTTTTTTTCAGGCTCCTAAAGTAACATCAGCCATTTTATAGATTGGTTCTGTTTTCGTACCTTCCCCTG
GCCTCAAGTGAGCCAAGAAACACTGCCTGCCCTCTGTCTGTCTTCTCCTAATTCTGCAGGTGGAGGTTGCTAGTC
TAGTTTCCTTTTTGAGATACTATTTTCATTTTGTGAGCCTCTTTGTAATAAAATGGTACATTTCT

WO 2004/030615

PCT/US2003/028547

160/6881
FIGURE 151

MAQTQGTRRKVCYYYDGDVGNYYYGQGHMPKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKF
LRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNKQQTDI AVNWAGGLHHAKKSEASGF
CYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVVEAFYTTDRVMTVSFHKYGEYFPGTGDLRDI GAGKGKYYAVN
YPLRDGIDDES YEAI FKPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGG
GGYTIRNVARCWYETAVALDTEIPNELPYNDYFEYFGPDFKLHISP SNMTNQNTNEYLEKIKQRLFENLRMLPH
APGVQMQAIPEDAIPESGDEDEDDPKRISICSSDKRIACEEEFSDSEEEGEGGRKNSSNFKKAKRVKTEDEKE
KDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA

WO 2004/030615

PCT/US2003/028547

161/6881
FIGURE 152

GGCACGAGGGCGCGGAGCGGAGCGGGCGGGCGCGAGCTAGCGGGTCGGCCGCGGAGCGGAGGTGCAGCTCGGCT
TCCCCCGGCACCCCTCCCCCTCGGGCGCCAGCCCCACCCCTCCGCCGGCCGGGCGGACCCCGCCGTACTATCCCC
TGCGGGCGCGAGCCCCGGGGCGGGCTCCAAGCGCCCCCAGCAGACCCCATCATGGGCAGCCAGAGCTCCAAGGCTC
CCCGGGGCGACGTGACCGCCGAGGAGGCAGCAGGCGCTTCCCCCGCGAAGGCCAACGGCCAGGAGAATGGCCACG
TGAAAAGCAATGGAGACTTATCCCCCAAGGGTGAAGGGGAGTCGCCCCCTGTGAACGGAACAGATGAGGCAGCCG
GGGCCACTGGCGATGCCATCGAGCCAGCACCCCTAGCCAGGGTGCTGAGGCCAAGGGGGAGGTCCCCCACAAGG
AGACCCCAAGAAGAAGAAGAAATTCTCTTTCAAGAAGCCTTTCAAATTGAGCGGCCTGTCCTTCAAGAGAAATC
GGAAGGAGGGTGGGGGTGATTCTTCTGCTCCTCACCCACAGAGGAAGAGCAGGAGCAGGGGGAGATCGGTGCCT
GCAGCGACGAGGGCACTGCTCAGGAAGGGAAGGCCGAGCCACCCCTGAGAGCCAGGAACCCCAAGGCCAAGGGGG
CAGAGGCTAGTGACGCTCAGAAGAAGAGGCAGGGCCCCAGGCTACAGAGCCATCCACTCCCTCGGGGCCGAGA
GTGGCCCTACACCAGCCAGCGCTGAGCAGAATGAGTAGCTAGGTAGGGGCAGGTGGGTGATCTCTAAGCTGCAAA
AACTGTGCTGTCTTGTGAGGTCACTGCCTGGACCTGGTGCCCTGGCTGCCTTCTGTGCCAGAAAGGAAGGGG
CTATTGCCTCCTCCCAGCCACGTTCCCTTTCTCCTCTCCCTCCTGTGGATTCTCCCATCAGCCATCTGGTTCTC
CTCTTAAGGCCAGTTGAAGATGGTCCCTTACAGCTTCCCAAGTTAGGTAGTGATGTGAAATGCTCCTGTCCCTG
GCCCTACCTCCTTCCCTGTCCCCACCCCTGCATAAGGCAGTTGTTGGTTTTCTTCCCAATTCTTTTCCAAGTAG
GTTTTGTTTACCCTACTCCCCAAATCCCTGAGCCAGAAGTGGGGTGCTTATACTCCCAAACCTTGAGTGTCCAGC
CTTCCCCTGTTGTTTTTAGTCTCTTGCTGTGCCTAGTGGCACCTGGGCTGGGGAGGACACTGCCCCGTCTAGG
TTTTTATAAATGTCTTACTCAAGTTCAAACCTCCAGCCTGTGAATCAACTGTGTCTCTTTTTTGACTTGGTAAGC
AAGTATTAGGCTTTGGGGTGGGGGGAGGTCTGTAATGTGAAACAACCTTCTGTCTTTTTTCTCCACTGTTGTA
AATAACTTTTAATGGCCAAACCCAGATTTGTACTTTTTTTTTTTTCTAACTGCTAAAACCATTCTCTTCCACCT
GGTTTACTGTAACATTTGGAAAAGGAATAAATGTCGTCCCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

162/6881
FIGURE 153

MGSQSSKAPRGDVTAEAAAGASPAKANGQENGHVKSNGDLSPKGEGESPPVNGTDEAAGATGDAIEPAPPSQGA
AKGEVPPKETPKKKKKFSFKKPKLSGLSFKRNRKEGGDSSASSPTEEEQEQQEIGACSDDEGTAQEGKAAATPE
SQEPQAKGAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE

WO 2004/030615

PCT/US2003/028547

163/6881
FIGURE 154

GCTCCCATTTGGCTGATGTTGGCGCGAAGGTGCGCGAGTCAGCCCTCGCGCTGGGGGCGCAGGAAACAATAGAGGC
CGCGCGCACAGAGCGAGCTCTTGCAGCCTCCCCGCCCCCTCCCGCAACGCTCGACCCCAGGATTCCCCGGCTCGC
CTGCCCCGCATGGCCGACAAGGAAGCAGCCTTCGACGACGCAGTGGAAGAACGAGTGATCAACGAGGAATACAAA
ATATGGAAAAAGAACACCCCTTTTCTTTATGATTTGGTGATGACCCATGCTCTGGAGTGGCCCAGCCTAACTGCC
CAGTGGCTTCCAGATGTAACCAGAATTTGGAGGTTTTGGTTCAGTTAGTGGAAAAATTGAAATAGAAATCAAGAT
CAACCATGAAGGAGAAGTAAACAGGGCCCGTTATATGCCCCAGAACCCTTGATCATCGCAACAAAGACTCCTTC
CAGTGATGTTCTTGTTTTTGACTATACAAAACATCCTTCTAAACCAGATCCTTCTGGAGAGTGCAACCCAGACTT
GCGTCTCCGTGGACATCAGAAGGAAGGCTATGGGCTTTCTTGAACCCAAATCTCAGTGGGCACCTTACTTAGTGC
TTCAGATGACCATAACCATCTGCCTGTGGGACATCAGTGCCGTTCCAAAGGAGGGAAAAGTGGTAGATGCGAAGAC
CATCTTTACAGGGCATAACGGCAGTAGTAGAAGATGTTTCTGGCATCTACTCCATGAGTCTCTGTTTGGGTCAGT
TGCTGATGATCAGAACTTATGATTTGGGATACTCGTTCAAACAATACTTCCAAACCAAGCCACTCAGTTGATGC
TCACACTGCTGAAGTGAAGTGCCTTTCTTTCAATCCTTATAGTGAGTTCATTCTTGCCACAGGATCAGCTGACAA
GACTGTTGCCTTGTGGGATCTGAGAAATCTGAAACTTAAGTTGCATTCTTTGAGTCACATAAGGATGAAATATT
CCAGGTTTCAAGTGGTCACCTCACAATGAGACTATTTTAGCTTCCAGTGGTACTGATCGCAGACTGAATGTCTGGGA
TTTAAGTAAAATTGGAGAGGAACAATCCCCAGAAGATGCAGAAGACGGGCCACCAGAGTTGTTGTTTATTTCATGG
TGGTCATACTGCCAAGATATCTGATTTCTCCTGGAATCCCAATGAACCTTGGGTGATTTGTTCTGTATCAGAAGA
CAATATCATGCAAGTGTGGCAAATGGAGTTAGTCTTGACCACTAGTTTGATGCCATCTCCATTTTGGGTGACCT
GTTTCACCAGCAGGCCTGTTACTCTCCATGACTAACTGTGTAAGTGCTTAAATGGAATAAATTGCTTTTCTACA
TAA

WO 2004/030615

PCT/US2003/028547

164/6881
FIGURE 155A

GGCTCGCATCCCCATAGTGCTGGGTTACAGTGAAGGTACGCCCCGCGCTCTGCTCTGGAGAGGCAGGGTGGGATA
GGGAACGTCTCGAGTGGCGCCCGCAGTCAATGGTGGTGTTTCGTGGCCGCCGCTCCCGGCGCTCCTAGGGCTGTT
TAAGAAGAAGGGCTCTGCCAAGGCTGAGAATGACAAACATCTAAGTGTAGGGCCTGGCCAGGGGCCAGGGTCTGC
AGTGGATGAGCACCAGGACAACGTCTTCTTTCCAGTGGGCGACCCCCCACCCTGGAAGAGCTGCACACTCAGGC
CCAGGAGGGGCTCCGCTCCCTACAACACCAAGAGAAAACAGAACTGAACAAGGGTGGCTGGGACCATGGAGACAC
CCAGAGTATCCAGTCTCCCGGACGGGGCCGGATGAAGACAACATCTCCTTCTGCAGTCAGACCACATCCTACGT
GGCTGAGAGCTCCACAGCAGAGGACGCGCTCTCCATCCGCTCGGAGATGATCCAGCGCAAAGGCTCCACCTTCCG
ACCCCATGACTCATTTCCCAAATCTGGAAAGTCAGGGCGGCGCTCGGCGGGAGCGGCGGGAGCACTGTGCTGGGACT
CCCGCAGCATGTGACAGAAGGAGCTTGGCCTGAGGAATGAGCGTGAGGCACCAGGCACGCCCCGGGCTCCTGGTGC
ACGGGATGCCGTACGCATCCCCACAGTGGACGGCCGCCCGGAGGCACCTCAGGGATGGGGGCCCGGGTGTCCCT
GCAGGCGCTGGAGGCGGAGGCGGAGGCTGGCGCTGAGACAGAGGCCATGCTGCAGCGCCACATTGACCGTGTCTA
CCGGGATGACACCTTTGTTGGCCGGTCCACGGGTACCGGGGCCACCATTGACCGGCCCATGTCCCTAGCAGT
GCCTGGATTGACAGGAGGGGAGGGCCTGCAGAGCCCCTGAGCCCGGCCATGTCCATCTCCCCCAGGCCACCTA
CCTGTGCAAGTTGATTCCACATGCTGTGCTGCCGCTACAGTGGACGTGGTGGCCCTAGGCCGCTGCAGCCTGCG
CACACTAAGCCGCTGCAGCCTGCACTCGGCCAGCCAGCCTCAGTCCGCTCGCTGGGGCGCTTCTCCTCCGTCTC
CAGCCCACAGCCCCGAGCCGCCACCCATCCTCCTCCAGTGACACCTGGAGCCACTCTCAATCCTCCGACACCAT
TGTGTCTGACGGTTCACCCCTCTCCTCTAAGGGTGGCTCTGAGGGCCAGCCGGAGAGCTCTACGGCTAGCAATAG
CGTGGTACCCCTCCCCAGGGAGGCAGTGGGAGGGCTCTCCAGTGGGGGCAGCACTGCTGAGGCCTCAGACAC
ACTCAGCATTCGAGCAGTGGGCAGTTGTCTGGCCGGAGTGTGTCCCTGCGTAAGCTGAAGCGGCCTCCACCCCC
TCCCCGCCGACCCACTCCCTCCATCAGCGGGGCTTAGCAGTGCCATGAGGGCATTAGGGTTGCCCCCTAAGCC
TGAGCGTAAGCAGCAGCCCCAGCTGCCTCGGCCACCCACCACTGGTGGCTCAGAAGGGGCGGGGCGAGCACCCTG
TCCACCCAACCCAGCCAACAGCTGGGTACCTGGCTTGTCTCCGGGTGGTTCCCGGCGCCCCCAGGTTCCCCAGA
ACGGACACTTTCGCCCTCCAGTGGATACTCGAGCCAAAGTGGTACTCCACCCCTCCCTCCCAAGGGCCTGGCAGG
TCCCCCTGCTTCCCCAGGCAAGGCCAGCCCCCTAAACCAGAGCGTGTACGTCTCTTCGCTCCCCCTGGGGCCTC
CGTCTCCTCTTCCCTCAGTCTTTATGTTCTCTCTCTGACCCAGCCCCCTCAGACCGCTCTGGGCCACAGAT
ATTGACCCCCCTGGGTGACAGGTTTGTCTACCTCCTCACCCCAAGGTGCCTGCCCCCTTCTCCCCACCTCCCTC
CAAGCCCAGGAGCCCTAACCAGCTGCCCTGCTCTAGCCGCCCCCTGCTGTGGTTCTTGGGCTGTTTCTACCAC
TGACGCCAGTCTCTAGTCCCTCCCACTCCCCAGACAACCTTGACTCCACTGCAGAGTCTCTGTCTATCTCCAA
AGACCAGTACCCCCACCTTCCCCACCCCATCTTATCATCCACCCCCACCACCCACTAAGAAGCCAGAGGTGGT
TGTGGAGGCACCATCTGCCTCAGAGACTGCTGAGGAGCCCCCTCAAGATCCCAACTGGCCCCCTCCCCACCCCC
TGCCCCCTGAGGAGCAGGACCTGTCCATGGCTGACTTCCCCCACCAGAGGAGGCTTTTTTCTCTGTGGCCAGCCC
TGAGCCTGCAGGCCCTTTCAGGCTCCCCAGAGCTTGTGAGCTCCCCGGCTGCTTCGTCCTCCTCAGCTACTGCTTT
GCAGATTACGCCCCCGGTAGCCCAGACCTCCTCCAGCTCCGCCAGCCCCAGCTCCTGCTAGTTCCGCCCCAGG
GCATGTGGCCAAGCTCCCTCAGAAGGAACCGGTGGGCTGTAGCAAGGGTGGTGGGCCTCCAGGGAGGACGTAGG
TGCGCCCTTGGTCACGCCCTCGCTCCTGCAGATGGTGC GGCTGCGCTCCGTGGGTGCTCCAGGAGGGGCTCCAC
CCCAGCACTGGGGCCATCGGCCCCCAGAAACCACTGCGAAGGGCCCTGTGAGGGCGGGCCAGCCAGTGCCTGC
CCCCTCCTCAGGGCTCCATGCTGCGGTCCGACTCAAGGCCTGCAGCCTGGCCGCCAGTGAAGGCCTCTCAAGTGC
TCAGCCCCAACGGACCGCCTGAGGCAGAGCCACGGCCTCCCCAGTCCCCTGCCTCAACGGCCAGTTTCTCTCTC
CAAGGGCTCTAGGAAGCTGCAGCTGGAGCGGGCCCGTGTCCCCTGAGACCCAGGCTGACCTCCAGCGGAATCTGGT
GGCAGAACTCCGGAGCATCTCAGAGCAGCGGCCACCCAGGCCCCAAAGAAGTACCTAAGGCTCCCCACCTGT
GGCCCCGAAGCCGTCTGTGGGAGTCCCCCACC CGCTCCCCAGTTACCCTCGAGCTGAGCCCTTACTGCTCC
TCCCACCAATGGGCTCCCTCACACCCAGGACAGGACTAAGAGGGAGCTGGCGGAGAATGGAGGTGTCTGCAGCT
GGTGGGCCCAGAGGAGAAGATGGGCCTCCCGGGCTCAGACTCACAGAAAGAGCTGGCCTGACCACCAGGCACCTC
ACTGGCACTGCTGACCCATCCCAGAAACACAATCTCAGGGACCCGAGCAGCTCCAAGGACGAGAGGATACAGCAG
ACACAACCTAATAGAGAGGGCGCCTGCAGCCTTAACCTCCACGGCCTTCGATACTTATGCAAGCCTGGTGTGCT
CCTGTCTCAGAGTCATCTGCGCTCATGCCTTTTCCGAATGGGTTACCTCTGGCAGTTGCCGCTTCACTCTT
GGCCTTAGCCTCATCTTGAAGTGGGTAGCTGGCGGGAGAGGGTGGCTGCGCCCCCTGCTGGCCCTGAGGCTGCAG
AGTTGGGAGCAGGACACCTCACCTGAGTTTCATTTTTTTTCATGTCCAAACCATGCACATACTATAGTCCAGAAT

WO 2004/030615

PCT/US2003/028547

165/6881
FIGURE 155B

CAAAGCACTTTTGAAGTGGCTGCATGGCCATCCTCCAGGGCCCAGGAAGTTGCATTCCAAGGGCCTGTTTACA
TGGCAGCAGAATCCATCCCCGGCAGTCAGCCCATAGCTTGGGACCAGTCTGTGCCCTCCTGCCAGTCCAGTTTA
CTCCTCTTGGTTCCTGAAGGTGGCCAAGTCATTGTGTTCCACAGGCTTCTCTAGGCTGGGGGCAGGTGTGGGGC
TGTGGAATTCAAAGCACAAAAGGTGCAGAGGGGATTGGCCTTCTGTGCCTCAACTCACCACCACCTCCTGC
CTTCCAGTTCTGCCAGGTGCTCCATGCTGGGGACAAGTAGGAGACTGCCAGGGCCCAAAGAAATGGGTGAGCAGT
AGAGTCATCTCGGGGCACTTGGCAGTGTCAAGCACCTGCCCTTGCCTCCTTGACCACACTGGGGTGGGTGGGCC
CCCAGCACTTCAGAGGCAGGAGCCTTTGGGCTGAGCAAGCACTGAGGAGGTGGATGGAAGGGAGCATCTGGAGGG
GGGGAGCTTCCTTGAGCAGTGGGGCCAGGCCTGGCCCTCCACACTTCATTCTCTGACCTTTCTCTCTCCTCATT
CGGTGCATGTCCTTTCTGCAGCTGCCTTTCAGCACAGGTGGTTCCTGAGGGGCAGCTAACGCTGAGTGACAAGG
ATGGGAAGCCACAGGTGCATTTTACTCAAGTCTTCTCTAGTCAATGAGGGGCACCCAGTGCTTCTAGGGCAGGCT
GGGTGGTGGTCCCCTAGGTATCAGCCTCTCTTACTGTACTCTCCGGGAATGTTAACCTTTCTATTTTCAGCCTGT
GCCACCTGTCTAGGCAAGCTGGCTTCCCCATTGGCCCTGTGGGTCCACAGCAGCGTGGCTGCCCCCAGGGCCA
CQGCTTCTTTCTTGATCCTCTTCTTAAACAGTGACTTGGGCTTGAGTCTGGCAAGGAACCTTGCTTTTAGCTTC
ACCACCAAGGAGAGAGGTGACATGACCTCCCCGCCCCCTCACCAAGGCTGGGAACAGAGGGGATGTGGTGAGAG
CCAGGTTCCTCTGGCCCTCTCCAGGGTGTTCCTCACTAGTCACTACTGTCTTCTCCTTGCTAGCTAATCAATCAAT
ATTCTTCCCTTGCTGTGGGCAGTGGAGAGTGTGCTGGGTGTACGCTGCACCTGCCACTGAGTTGGGGAAAGA
GGATAATCAGTGAGCACTGTTCTGCTCAGAGCTCCTGATCTACCCACCCCTAGGATCCAGGACTGGGTCAAAG
CTGCAATGAAACCAGGCCCTGGCAGCAACCTGGGAATGGCTGGAGGTGGGAGAGAACCTGACTTCTCTTCCCTCT
CCCTCCTCCAACATTACTGGAACCTATCCTGTTAGGATCTTCTGAGCTTGTTCCTGCTGGGTGGGACAGAGG
ACAAAGGAGAAGGGAGGGTCTAGAAGAGGCAGCCCTTCTTTGTCCTCTGGGGTAAATGAGCTTGACCTAGAGTAA
ATGGAGAGACCAAAGCCTCTGATTTTTAATTTCCATAAAATGTTAGAAGTATATATATACATATATATATTTCT
TTAAATTTTGTAGTCTTTGATATGTCTAAAAATCCATTCCCTCTGCCCTGAAGCCTGAGTGAGACACATGAAGAA
AACTGTGTTTCATTTAAAGATGTTAATTAAATGATTGAACTTG

WO 2004/030615

PCT/US2003/028547

166/6881
FIGURE 156

MVVFVGRRLPALLGLFKKKGSACAENDKHL SVGPGQGPGSAVDEHQDNVFFPSGRPPHLEELHTQAQEGRLRLQH
QEKQKLNKGGWDHGDTSIQSSRTGPDENISFCSQTTSYVAESSTAEDALSIRSEMIQRKGSTFRPHDSFPKSG
KSGRRRRERRSTVLGLPQHVKELGLRNEREAPGTPRAPGARDAVRIPTVDGRPRGTSGMGARVSLQALEAEAEA
GAETEAMLQRHIDRVYRDDTFVGRSTGTRAPPLTRPMSLAVPGLTGGAGPAEPLSPAMSISPQATYLSKLIPHAV
LPPTVDVVALGRCSLRTLRLSLHSASPASVRSLSGRFSSVSSPQPRSRHPSSSSDTWSHSQSSDTIVSDGSTLSS
KGGSEGQPESSSTASNSVVPPPQGGSGRGSPSGGSTAEASDTLSIRSSGQLSGRSVSLRKLKRP PPPPRRTHSLHQ
RGLAVPDGPLGLPPKPERKQQQLPRPPTTGGSEGAGAAPCPNPANSWVPGLSPGGSRPPRSPERTLSPSSGY
SSQSGTPTLPPKGLAGPPASPGKAQPPKPERVTSLSRPGASVSSSLTSLCSSSSDPAPSDRSGPQILTPLGDRFV
IPPHPKVPAPFSPPP SKPRSPNPAAPALAAPAVVPGPVSTTDASPQSPPTPQTTLTLPQESPVISKDQSPPPSPP
PSYHPPPPPTKKPEVVVEAPSASETAEELQDPNWP PPPPPAPEEQDLSMADFPPPEEAFFSVASPEPAGPSGSP
ELVSSPAASSSSATALQIQPPGSPDPPPPAPPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLL
QMVRLRSVGAPGGAPTPALGPSAPQKPLRRALSGRASVPAPSSGLHAARLKACSLAASEGLSSAQPNGPPEAE
PRFPQSPASTASFIFSKGSRKLQLERPVS PETQADLQRNLVAELRSISEQRPPQAPKKSPKAPPPVARKPSVGVP
PPASPSYPRAEPLTAPPTNGLPHTQDRTKRELAENGGVLQLVGPEEKMGLPGSDSQKELA

WO 2004/030615

PCT/US2003/028547

167/6881
FIGURE 157

ATGGGGGACGCTCCCAGCCCTGAAGAGAACTGCACCTTATCACCCGGAACCTGCAGGAGGTTCTGGGGGAAGAG
AAGCTGAAGGAGATACTGAAGGAGCGGGAACCTTAAATTTACTGGGGAACGGCAACCACGGGCAAACCACATGTG
GCTTACTTTGTGCCCATGTCAAAGATTGCAGACTTCTTAAAGGCAGGGTGTGAGGTAACAATTCTGTTTGCGGAC
CTCCACGCATACCTGGATAACATGAAAGCCCCATGGGAACCTCTAGAACTCCGAGTCAGTTACTATGAGAATGTG
ATCAAAGCAATGCTGGAGAGCATTGGTGTGCCCTTGGAGAAGCTCAAGTTCATCAAAGGCACCTGATTACCAGCTC
AGCAAAGAGTACACACTAGATGTGTACAGACTCTCCTCCGTGGTCACACAGCACGATTCCAAGAAGGCTGGAGCT
GAGGTGGTAAAGCAGGTGGAGCACCTTTTGCTGAGTGGCCTCTTATACCCCGGACTGCAGGCTTTGGATGAAGAG
TATTTAAAGTAGATGCCCAATTTGGAGGCATTGATCAGAGAAAGATTTTCACCTTTGCAGAGAAGTACCTCCCT
GCACCTTGGCTATTCAAACGGGTCCATCTGATGAATCCTATGGTTCAGGATTAACAGGCAGCAAAATGAGCTCT
TCAGAAGAGGAGTCCAAGATTGATCTCCTTGATCGGAAGGAGGATGTGAAGAAAAAACTGAAGAAGGCCTTCTGT
GAGCCAGGAAATGTGGAGAACAATGGGGTTCTGTCTTCATCAAGCATGTCCTTTTCCCTTAAGTCCGAGTTT
GTGATCCTACGAGATGAGAAATGGGGTGGAAACAAACCTACACAGCTTACGTGGACCTGGAAAAGGACTTTGCT
GCTGAGGTTGTACATCCTGGAGACCTGAAGAATTCTGTTGAAGTCGCACTGAACAAGTTGCTGGATCCAATCCGG
GAAAAGTTTAATACCCCTGCCCTGAAAAAACTGGCCAGCGCTGCCTACCCAGATCCCTCAAAGCAGAAGCCAATG
GCCAAAGGCCCTGCCAAGAATTCAGAACCAGAGGAGGTCATCCCATCCCGGCTGGATATCCGTGTGGGGAAAATC
ATCACTGTGGAGAAGCACCCAGATGCAGACAGCCTGTATGTAGAGAAGATTGACGTGGGGGAAGCTGAACCACGG
ACTGTGGTGAGCGGCCTGGTACAGTTCGTGCCCAAGGAGGAACTGCAGGACAGGCTGGTAGTGGTGTGTGCAAC
CTGAAACCCAGAAAGATGAGAGGAGTCGAGTCCCAAGGCATGCTTCTGTGTGCTTCTATAGAAGGGATAAACCGC
CAGGTTGAACCTCTGGACCCTCCGGCAGGCTCTGCTCCTGGTGAGCACGTGTTTGTGAAGGGCTATGAAAAGGGC
CAACCAGATGAGGAGCTCAAGCCCAAGAAGAAAGTCTTCGAGAAGTTGCAGGCTGACTTCAAATTTCTGAGGAG
TGCATCGCACAGTGGAAGCAAACCAACTTCATGACCAAGCTGGGCTCCATTTCTGTAAATCGCTGAAAGGGGGG
AACATTAGCTAGCCAGCCCAGCATCTTCCCCCTTCTTCCACCACTGAGTCATCTGCTGTCTCTTCAGTCTGCTC
CATCCATCACCCATTTACCCATCTCTCAGGACA

WO 2004/030615

PCT/US2003/028547

168/6881
FIGURE 158

MGDAPSPEEKHLHLITRNLQEVLGEEKLKEILKERELKIYWGTTGKPHVAYFVPMSKIADFLKAGCEVTILFAD
LHAYLDNMKAPWELLELRVSYENVIKAMLESIGVPLEKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGA
EVVKQVEHPLLSGLLYPGLQALDEEYLKVDAQFGGIDQRKIFTFAEKYLPALGYSKRVHLMNPMVPGLTGSKMSS
SEESKIDLLDRKEDVKKKLKKAFCPEGNVENNGVLSFIKHVLFPLKSEFVILRDEKWGGNKTYTAYVDLEKDFA
AEVVHPGDLKNSVEVALNKLLDPIREKFNTPALKKLASAAYPDPSKQKPMAGPAKNSEPEEVIPSRLDIRVGKI
ITVEKHDPADSLYVEKIDVGEAEPRTVVSGLVQFVPKEELQDRLVVLCNLKPQKMRGVESQGMLLCASIEGINR
QVEPLDPPAGSAPGEHVFKGYEKGQPDDEELPKKKVFEKLQADFKI SEECIAQWKQTNFMTKLGSISCKSLKGG
NIS

WO 2004/030615

PCT/US2003/028547

169/6881
FIGURE 159

GCGCGAGCAAGATGGCCACCACCAAGCGCGTCTTGTACGTGGGTGGACTGGCAGAGGAAGTGGACGACAAAGTTC
TTCATGCTGCGTTTCATTCTTTTGGAGACATCACAGATATTAGATTCTCTGGATTATGAAACAGAAAAGCACC
GAGGATTTGCTTTTGTGTAATTTGAGTTGGCAGAGGATGCTGCAGCAGCTATCGACAACATGAATGAATCTGAGC
TTTTTGGACGTACAATTCGTGTCAATTTGGCCAAACCAATGAGAATTAAGGAAGGCTCTTCCAGGCCAGTTTGGT
CAGATGATGACTGGTTGAAGAAGTTTTCTGGGAAGACGCTTGAAGAGAATAAAGAGGAAGAAGGGTCAGAGCCTC
CCAAAGCAGAGACCCAGGAGGGAGAGCCCATTGCTAAAAAGGCCCGCTCAAATCCTCAGGTGTACATGGACATCA
AGATTGGGAACAAGCCGGCTGGCCGCATCCAGATGCTCCTGCGTTCTGATGTCGTGCCCATGACAGCAGAGAATT
TCCGCTGCCTGTGCACTCATGAAAAGGGCTTTGGCTTTAAGGGAAGCAGCTTCCACCGCATCATCCCCCAGTTCA
TGTGCCAGGGCGGTGATTTACAAACCACAATGGCACTGGGGGCAAGTCCATCTATGGGAAGAAGTTCGATGATG
AAAACTTTATCCTCAAGCATAACGGGACCAGGTCTACTATCCATGGCCAACCTCTGGCCCAAACACCAATGGCTCTC
AGTTCTTCTGACATGTGACAAGACAGACTGGCTGGATGGCAAGCATGTGGTGTGTTGGAGAGGTCACCGAAGGCC
TAGATGTCTTGC GGCAAATTGAGGCCCAGGGCAGCAAGGACGGGAAGCCAAAGCAGAAGGTGATCATCGCCGACT
GTGGGGAGTACGTGTGAGGCGGCACTCTCTCTGCTTCCCCCTCCGCTCTTGACCCTGCATATCCAGGAAGGAACT
GCCAGCCTCAGAGGAGGCAGCACCGAGGGTGCTGTTTGAAGCAAGCAGCATTGTTGGGATATGTGCCCTTCTCAG
GGTCTGCTTGGAGCAGCTCCTCTGCAGGCACAGCTGGACTATTCCCAGGCACAGCTGTGGGCCCAGGAGCCAGC
TCAGGTGCTCCCCTCCACCATGGGCAGGCTGTGCAAAAAGCCACTGGCTTTTCTCAGCATTGCTGCTGGGCCT
CTCCTGGGACTACCAGTGTGGCTCTTACGTGTTTTCTTTGCTAAAATAAACCCCTAGTTCTTATATTAACCAAAAA
AAAAA

WO 2004/030615

PCT/US2003/028547

170/6881
FIGURE 160

MATTKRVLYVGGLAEVDDKVLHAAFIPFGDITDIQIPLDYETEKHRGFAFVEFELAEDAAAAIDNMNESELFGR
TIRVNLAKPMRIKEGSSRPVWSDDDWLKKFSGKTLEENKEEEGSEPPKAETQEGEPIAKKARSNPQVYMDIKIGN
KPAGRIQMLLRSDVVPMTAENFRCLCTHEKGFGFKGSSFHRIIPQFMCQGGFTNHNGTGGKSIYGKKFDDENFI
LKHTGPGLLSMANS GPNTNGSQFFLTCDKTDWLDGKHVVFGEVTEGLDVLRQIEAQGSKDGPKQKVI IADCGEY
V

WO 2004/030615

PCT/US2003/028547

171/6881
FIGURE 161

TCAAAGCACCTGCAGCCCCAATTTGTGATCCAGCAGCAGCCACAGCCACAACAGCAGCAGCCGCCGCCCCAGCAG
TCACGGCCTGTGCTCCAAGCTGAGCCCCACCCCCAGCTCGCCTCAGTCTCTCCAAGCGTGGCCCTCCAGCCCAGC
TCAGAGGCCCATGCCATGCCACTAGGCCCGGTTACACCCGCCCTGCCACTCCAGTGTCCCACTGCCAACCTGCAC
AAGCCTGGCGGCAGTCAGCAGTGTACCCCTCCCACACCTGATACTGGGCCTCAGAAATGGACATCCCGAGGGCGTG
CCCCACACCCCTCAACGCAGGTTCCAGCACACTTCAGCTGTCTTACAACCTGCAGCCTGCTTCACCAGTGCCC
CAGCAGTGTGTCCCTGATGACTGGAAAGAAGTGGCACCAGGGGAGAAAAGTGTGCCTGAGACGCGGTCTGGCCCA
TCACCACATCAGCAGGCTATTGTCACTGCCATGCCTGGTGGCCTGCCTGTACCCACGAGCCCTAACATCCAGCCG
TCCCCAGCTCAGGAGACAGGGCAGGGCATTGTTTCATGCACTGACCGACCTCAGCAGCCCCGGCATGACCTCAGGG
AACGGAACTCTGCCTCCAGCATCGCCGGCACTGCCCCCAGAATGGTGAGAATAAACACCACAGGCCATTGTG
AAACCCCAAAATCCTGACGCATGTTATCGAAGGGTTTGTGATCCAGGAGGGGGCGGAGCCTTTCCCGGTGGGACGC
TCGTCCCTGCTGGTGGGGAATCTCAAGAAGAAGTATGCACAGGGGTTCTGCCTGAGAACTTCCACAGCAGGAT
CACACCACCACCACTGACTCGGAGATGGAGGAGCCCTATCTGCAAGAATCCAAAGAGGAGGGTGTCTCCCTCAA
CTCAAGTGTGAGCTCTGTGGCCGGGTGGACTTTGCCTATAAGTTCAAGCGTTCCAAGCGTTCTGTTCCATGGCT
TGTGCAAAGAGGTACAACGTGGGATGCACCAAACGGGTGGGACTTTTCCACTCAGACCGGAGCAAGCTGCAGAAG
GCAGGAGCTGCGACCCACAACCGCCGTCGGGCCAGCAAAGCCAGTCTGCCACCACTTACCAAGGATACCAAGAAG
CAGCCAACAGGCACTGTGCCCCCTTCGGTTACTGCTGCTTTGCAGCTAACACACAGCCAGGAAGACTCCAGCCGT
TGCTCAGATAACTCAAGCTATGAGGAACCCCTGTACCCATCTCAGCCAGCTCATCTACTTCCCGCCGGGACAA
GGCCAGCGGGACCTGGAGCTCCCCGACATGCATATGCGGGACCTGGTGGGCATGGGACACCACTTCTGCCAAGT
GAGCCCACCAAGTGGAAATGTAGAAGACGTCTACGAATTATCCGCTCTCTGCCAGGCTGCCAGGATAGCAGAG
GAATTCGCTGCCCAGGAAATCGACGGGCAAGCCCTGCTGCTGCTCAAGGAGGACCACCTGATGAGCGCCATGAAC
ATCAAGCTGGGGCCCCGCCCTGAAGATCTACGCCCCGATCAGCATGCTCAAGGACTCCTAGGGCTGGTGGCAGCCA
GGATTCTGGCCAGGGCGCCTCCTCCCGACTGAGCAGAGCCAGACAGACATTCTGAGGGGCCAGAAATGGGGC
CGGTTGGAGGGCAGGGGCTCTCCCTAGGGGCATAGCTGGTGAGGAGGTCTGGGCACCTCCTCCATGGCTCTCAGG
CGCCTTTCAATTTCTGTGGGAGGGGCAGAGAGGTAGGTGGCACAGAAGATGGGGCTTTATGCTTGTAATATTGAT
AGCACTGGCTTCTTCCAAAGTCCCAATACTCTAGCCCCGCTCTCTTCCCCTCTTTCTGTCCCCATTTTCCAGGG
GGTATATGGTCAGGGCTCCCCAACCTGAGTTGGGTTACTTCAAGGGCAGCCAGCAGGCCTGGATGGAGGCCTAGA
AAGCCCTTGCCTTCCTTCCCTCCCACTTCTTTCTCCAGGCCTGGTTAACTCTTCCGTTGTGAGCTTCTCCCCCTT
AGCCTGTTTCTGCAGCAGCCAGGGTTCTCCCCCTACACCTCTGCAGGTGGAGAGAGAGAAGCTGGGCCCAGCC
GGGCCGTGCCCTGCTGGCACAGACGCCCTTAACGCTGTGTGTATGACTGTGTGACTGTGTGGGAGCCTGGACTGACA
GATAGGCCAAAGGGCTACTCTCTGGCATCTCCAGGTGTTTTGTAGCAAACAGCCACTTAGTGCTTTGTCTGGACT
CCACTCAGCCTCAGGATGGGGAATAGCCAAGAATGGCAGCCTCAGCGCAGAGGCAAGGTGAGAAAGAGACGGCGC
TTCAGAGTTTCTTTCCAGACACCCCTCCCCGCACTGTGAAGTTCCCCTGACCGCCCTCCTGGTTACAAAGAGC
ATTAAGAAAGCTGCGGTGGTCTGAGCAACATAGCCCAAAGGGCTGAGCCTCCTGGCCTGCCTGCCCCGCCACCT
GGGAGTCCCAGTGGTGGGCTCAGAGAACTGCTAAGGGGAAAGAACAGCTGGAGTTTCTGTTGATGTGAAGAAGG
CAGCTCTTGGCCTCCCACTCCCACTTCTTTGCCTATAAATCTTCTAGCAGCAATTTGAGCTACCTGAGGAGG
AGGCAGGGCAGAAAGGGCGAGGGCCTGCCTCTGACCTGCCGTGTCTTTGCAGGAAGGAGGTAGGCACCTTTCTG
AGCTTATTCTATTCCCCACCCACACCCCCAGGCAGGGTTGGAAATGAAGGACTTTTTTAACCTTTGTTTTGTTTT
TTAAAAATAAATCTGTAAATCTG

WO 2004/030615

PCT/US2003/028547

172/6881
FIGURE 162

MPLGPVTPALPLQCPTANLHKPGGSQQCHPPTPDTGPNQGHPEGVPHTPQRRFQHTSAVILQLQPASPVPQQCVP
DDWKEVAPGEKSVPETRSGPSPHQQAIVTAMPGGLPVPTSPNIQPSPAHETGQGIVHALDLSSPGMTSGNGNSA
SSIAGTAPQNGENKPPQAIVKPQILTHVIEGFVIEGAEPFPVGRSSLLVGNLKKKYAQGFLPEKLPQQDHTTTT
DSEMEEPYLQESKEEGAPLKLKCELCGRVDFAYKFKRSKRFCSMACAKRYNVGCTKRVGLFHSDRSKLQKAGAAT
HNRRRASKASLPPLTKDTKKQPTGTVPLSVTAALQLTHSQEDSSRCSNDSYEEPLSPISASSSTSRRRQGGQDRL
ELPDMHMRDLVGMGHHFLPSEPTKWNVEDVYEFIRSLPGCQEIAEEFRAQEIDGQALLLLKEDHLMSAMNIKLGP
ALKIYARISMLKDS

WO 2004/030615

PCT/US2003/028547

173/6881
FIGURE 163

AGACAAGGCAAATTTAAGTAGGCTCATGGCTTTTCCAGTTGGGTTGGAAAGTTCCTCTCCGATGACTGTTATATT
CTCAAAGAAATATGAGGAGAGGGGCAGGGCATGGTGGCTCACATCCGTAATCCTAGCAAATCATAGTGGCCTACA
GCCAACGCCTTCTTCGCTCACTGGCCAAC TGAAACTTCAGTCCCCCATGCCTCCCGCCTCTCACCCAGGGGCC
AATAGGAATGATCAGAGGTTGCAACTTAGTGTCATCAAGCATAGTAATTGCAATTGGCTATTGGAGCTGTCGAT
CGTGGAGTAGCGGGGCCGTGCCAGCTGGCCTATATAAGACGAGGACAAAGGCGGCGCGCCGCCTGTGTCATCCG
CCATTTTGTGAGAAGCAAGGTGGCCTCCACGTTTCTTGAGCGTCTTCTTCGCTTTTGCCTCGACCGCCCCCTTGAC
CACAGACATGTCTCGGGATCGGTTCCGGAGTCGTGGCGGTGGCGGTGGTGGCTTCCACAGGCGTGGAGGAGGCGG
CGGCCGCGGCGGCCTCCACGACTTCCGTTCTCGCCGCCCGGCATGGGCCTCAATCAGAATCGCGGCCAGGCCCCG
ACTCCGACCCCCGCGCCTGCAGTCACCTCGGCCCTCCCGGGGCGCGCCACCCACCCCGCCAAGCAGCGGGGTC
CCTACCACACCTCCTCAGGCCGAGGCCCGCCGCTCCGCCCGCGGCAGTCCCGGGCCCGGGTCCAGGGCCTAAG
CAGGGCCCAGGTCCGGGTGGTCCCAAAGCGGCAAAATGCCTGGCGGGCCGAAGCCAGGTGGCGGCCCGGGCCTA
AGTACGCC TGGCGGCCACCCCAAGCCGCCGCATCGAGGCGGCGGGGAGCCCCGCGGGGGCCGCCAGCACCCCG
CCCTACCACCAGCAGCATCACCAGGGGCCCCCGCCGGCGGGCCCGCGGCCGCAGCGAGGAGAAGATCTCGGAC
TCGGAG

WO 2004/030615

PCT/US2003/028547

174/6881
FIGURE 164

MAFPVGLESSPMTVIFSKKYEERGRAWWLTSVILANHSGLOTPSSLTGQLETSVPPCLPPLTQGPIMIRGSQ
LSVIKHSNCNWLELSIVE

WO 2004/030615

PCT/US2003/028547

175/6881
FIGURE 165

GGCGAGCAGTCTGCGCGCGGATGGCCGCGAGCGGCGATGGCGGCAGCGGCAGGTGGAGGGGCTGGCGCGGGCCCGCT
CCCTCTCGCGCTTCCGAGGCTGCCTGGCTGGTGCGCTGCTCGGGGACTGCGTGGGCTCCTTCTACGAGGCCCACG
ACACCGTCGACCTGACGTCAGTCCTGCGTCATGTCCAGAGTCTGGAGCCGGACCCCGGCACGCCCGGGAGTGAGC
GGACAGAAGCCTTGTACTACACAGATGACACAGCCATGGCCAGGGCCCTGGTGAGTCCCTGCTAGCCAAGGAGG
CCTTTGACGAGGTGGACATGGCTCACAGATTTGCTCAGGAGTACAAGAAAGACCCTGACAGGGGCTATGGTGCTG
GAGTAGTCACTGTCTTCAAGAAGCTCCTGAACCCCAAATGTCGCGATGTCTTTGAGCCTGCCCGGGGCCAGTTTA
ACGGGAAAGGCTCCTATGGCAATGGAGGTGCCATGCGGGTGGCTGGCATCTCCCTGGCCTATAGCAGTGTCAGG
ATGTGCAGAAGTTTGGCCGGCTCTCGGCCAGCTGACACACGCCTCCTCCCTGGGTTACAATGGCGCCATCCTGC
AGGCCCTGGCTGTGCACCTGGCCTTGACAGGGCGAGTCTTCCAGCGAGCACTTCTCAAGCAACTCCTGGGCCACA
TGGAGGATCTGGAGGGTGATGCCAGTCCGTCTTGGATGCCAGGGAGTTGGGCATGGAGGAGCGTCCATACTCCA
GCCGCCTGAAGAAGATTGGAGAGCTTCTAGACCAGGCATCGGTGACCAGGGAGGAAGTGGTGTCTGAGCTAGGGA
ATGGCATTGCTGCCTTTGAGTCGGTACCCACCGCCATCTACTGCTTCCCTACGCTGCATGGAGCCAGACCCTGAGA
TCCCTTCTGCCTTCAATAGCCTCCAAAGGACTCTCATTTATTCCATCTCACTTGGTGGGGACACAGACACCATTG
CCACCATGGCTGGGGCCATTGCTGGTGCTACTATGGGATGGATCAGGTGCCAGAGAGCTGGCAGCAAAGCTGTG
AAGGCTACGAGGAGACAGACATCCTGGCCCAAAGCCTGCACCGTGTCTTCCAGAAGAGTTGATGAGGGCTACAGC
TGTTGGGGCTCTGCCAGGTCCCTGGGACCAACTACAGCTCCAATCAGAAACCCTGCGCTTCCCTGAGTGTGGCT
TCCCACTTTTCTGCTGCTTGTGGAGCTGACTGAGTACACCGGTGAGGCTGGGGTCTCTGCAGGGGAGGTCACTGGA
ACAGCGAGCAAGGGACTGGTGCTCGCTGGTGCTGGGTCTCTGGTTTGCTGCAGAGCCGTAGGACACTCCTGGCT
CCTCAGTAGGACAGACAGACGCGAGGCGGGTTATTTTGGAGGGGTACTTGTGGCATTTCCTGTATTGTCTTGA
CATGGGATGTGGGGAGGTGGAAATGATGAGCAGTAGCATCATTTCTCCCTGTTGGGTTTTAGCCAGTTTGCCAGC
AAGCGCATCCTAGCAGGGTCCCCGAGCAGCAGGTTGTGTGGATGAAGGGACAGGCACTTGCATCCAGCTGATCTA
GGTCACACCTGGCTCTTGGCTGCCATGTGGCTTATTAACAGCTTCCAGTGGAAGTCGCAATAAACAGTTTTTGGT
AAATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

176/6881
FIGURE 166

MAAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDTVDLT SVLRHVQSLEPDPGTPGSERTEALYY
TDDTAMARALVQSLLAKEAFDEVDMHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCRDVFEPARAQFNGKGSYG
NGGAMRVAGISLAYSSVQDVQKFARLSAQLTHASSLGYNAILQALAVHLALQGESSEHFLKQLLGHMEDLEGD
AQSVLDARELGMEERPYSRLKKIGELLDQASVTREEVVSELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNS
LQRTLIIYISLGGDDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILAQSLHRVFKS

WO 2004/030615

PCT/US2003/028547

177/6881
FIGURE 167

CCGTGGCTAGGCGAGTGGGGCGGGGCGGCCGGCACCATGTCGAGGCAGGCGAACCGTGGCACCGAGAGCAAGAAA
ATGAGCTCTGAGCTCTTACCCTGACCTATGGTGCCCTGGTCACCCAGCTATGTAAGGACTATGAAAATGATGAA
GATGTGAATAAACAGCTGGACAAAATGGGCTTTAACATTGGAGTCCGGCTGATTGAAGATTTCTTGGCTCGGTCA
AATGTTGGGAGGTGCCATGACTTTGGGAAACTGCGGATGTCATTGCCAAGGTGGCGTTCAAGATGTACTTGGGC
ATCACTCCAAGCATTACTAATTGGAGCCCAGCTGGTGATGAATTCTCCCTCATTTTGGAAAATAACCCCTTGGTG
GACTTTGTGGAACCTTCTGATAACCACTCATCCCTTATTTATTCCAATCTCTTGTGTGGGGTGTTCGGGGGAGCT
TTGGAGATGGTCCAGATGGCTGTGGAGGCCAAGTTTGTCCAGGACACCCTGAAAGGAGACGGTGTGACAGAAATC
CGGATGAGATTTCATCAGGCGGATTGAGGACAATCTTCAGCTGGAGAGGATAACCATCCCTACAACCTCGAGGAT
AGCCATCAGGAGCACTGTTGGAATCAGCAGGCCTCTGTGCTCCCTCTGCCCTCCAGAACTCAGTGACTCTTGAAC
ATGGATGTTATATATTCTTATAACCTGTTTCCATTCTCCATTCAAATAAAGAGCAGACTGCGATATAGTCCATTT
ACCCCATGTGTGCACATTGAGGAGCGACAGTCTCTGCCCCATTCCCTTGAGAGGGGCTGGATGTAATCACCTTT
GGTTGGACTAGAAAGAGCTCAAACCATTTTACATTCTGTTTGAATTTTCAAAGCAAACCTCACTTTGACCCCA
TTAAGAGGCAAGCCTGGCACATCTATCCCTGGGCCTTTAGAAAGCCATTTGCCTCAAATGGCTATAGGGTTGTGG
GGTGGAGGGAGGAAGGGCTGGGAGGGAGTGGGAGGAATTGCTAGCTGTAGTGTGACACATTGTAGTGTGTTGCCA
GGAAAGGAGCCAGTCATGCCGAAACACTGACTTCTGGGAAGCCACCCAGGTCTCATTCTCCCTGCTGTTGGAG
GCAACATCTCTCTTTTTTACAGAGGGTACATCCTTTTTTCTTACAAATCTTCAATAAAGACACATTCTTGAGTG
AAATCCCTAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

178/6881
FIGURE 168

MSRQANRGTESKKMSSELFLLTYGALVTQLCKDYENDEDVNKQLDKMGFNIGVRLIEDFLARSNVGRCHDFRETA
DVIKVAFAKMYLGITPSITNWSPAGDEFSLILENNPLVDFVELPDNHSSLIYSNLLCGVLRGALEMVQMAVEAKF
VQDTLKGDGVTEIRMRFIRRIEDNLPAGEE

WO 2004/030615

PCT/US2003/028547

179/6881
FIGURE 169A

ACTTACTATTGGAGGCAGTGGGCAGCGCAGGACAGGCCCCAGGGCCGCCGACCCTGGCAATGACTGTCACCAGCTG
GAGGGAAGAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCAGGGCCAAGGCTCT
AGGAAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTTCATCCTTGGTCCCCGTCTGGGCAACTCACC
GGTGCCAAGCATAGTGCACTGTTTGGCGAGGAAAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCT
GGAGGAGAGGGGGGACCAAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTC
ACTGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACCGCACCTGTGAAAT
CGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGCGCATCTGCCTCGTCTGGACTGCCTCTG
TGCTCATGACTTCAGCGATAAGACCGCTGACCTCATCAACCTGCAGCACTACGTCATCAAGGAGAAGAGGCTCAG
CGAGAGGGGAGACTGTGGTAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCA
CAGAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCACCTTCTGCCTCGG
GAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGAGCCCTGCCTACATCAGTCCCGACGTGCT
CAGCGGCCCGCCGTACCGTGGCAAGCCAGTGACATGTGGGCCCTGGGCGTGGTGTCTTACCATGCTGTATGG
CCAGTTCCCCCTTCTACGACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGA
GGATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGACCCCCAGCAGCGCCTGGC
CGCCGCCGACGTCTGGAGGCCCTCAGTGCCATCATTGCATCATGGCAGTCCCTGTCTCTGAGTGGGCCCTT
GCAAGTGGTTCTGACATTGATGACCAAATGAGCAATGCGGATAGCTCCAGGAGGTGAGTTGGGGAGGGCAGAT
GGGCCATTACCCAGCCCCAAGGGACAGGCTTCTGGGGGCAGGCAGGGCAAGGGCAGAGGTGGCAGCTACCCGCAG
GCCACAGAGTTTCTTGGTCTTCTTCCCCAGCCTTGGGGTGGGAAAGGGAGACTTCAGTCTCAGCCTGAGCTGC
CTGGGGCCTGCCTTGGGCTTGGTGTAGCTGGAGATCTTTGGCCAGAGAGACCTGTGAGACAGCCGAGCTGGAGCC
AGTGCCCAAGTGCGCCAGGCCCTCTCAGCTTCTTCTGCTGCCCAAGTCACATTTCTCTGCCCTGACTC
AGAGTTCTCTCTCACCCTTCTGCTTTTTCATTTTTTCAGATGATTTCATTTCTCCCTATTTCTTTCTCCCATTC
CTGCACTGGAGAAAGTGTTGGGCCTAGGCTGGGGGCAGAGACTTGGGCACCAGGCAGCAGAGGGAGTATCTT
AGGGTGCCCCCTGGAGGGCAGGGCTTGGCCGAGCAACAGCATTGCTGGGCCCTGGATATTGGAAGGACTTCCCT
CCCTGGCCACCTTGGAGCTCCACAGTGAGCAGTGTGCAGGTAGGACCAGGAGGGGCCGTGCCGAGAGCCCTC
CCAGAGCCTCCTGGCCCCGAGGAAAGAGAGTTCCAATCCCTACCCACCTCCAGCTTCCACCCTTAGCTGTTTG
GCTAAATCATCATCACTAGCCCGCAGTGAGTGCTACCCCGAGGGCACCTCATTACGCCCTCACTGCGGGCCTG
CGTGGCCTGTGTTCTTAGCCCCATGTTACAGAAGAGGAAACAGGGTTAGAGAGGACTTTCCCAAAGCCACACAGC
TTAGAAGTAGTGGAGCTAAGCCTTGAACCCAAGTCTCATCCGGAAGCCCTGCTGTCTCCTGTGGTGACTGGCAGC
GGGACACCCTTACGCTTCTGTTACCATCTGCCTAGACCATCCAGGGAGCTCAGCATGGGGCCCTGCGTATGTG
GCTCCTCCAGGTGCTGCGCCCCCAGCCAGGGCTTGTCTGTACCTCTTGACGTGCATTAGCCGCTCAGGGCTCA
GAGAACCTTTGCGAGGGGCCAGACAGCTAAGGCTTCTGAGGTAAAGTGACCTCTCACGCAGCCAGTGAGTTAGGA
AGCATGAGTCTGCGTCAGTCCCGGTCCGAGGGCGGCCCTGCAAGGGGAGTTGAGGTGGCTGGAGGGGGTCAGG
GACCCACCCTCAGCGCCACTCCACCCCCGGCCTTGAAGGCTGAGGGTGTGGTGCCTGGAAGGGTGACTGCAGGA
GCCAGGCTGCCAGCACTCTTGCTGCCCTCCTGTCTGCTGCGTGCCTTCATCTGGGTTTATCTTTGTCTCCTTC
CCACCCTCCCCGCCTCAAAGGCGAAGGTGACGGAGGAGTGCTCCCACTACGAGTTTGAGAACTACATGCGTCAGC
AGTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACGCCCGGAGCTGGGTACCCAAGCGGCAGTTCCGGCAGCG
CACCACCGGTGCGACGGCTGGGCCACGACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCT
ACCTGCGGAAATAACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCGTGG
CTGTACGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGCAGGGACAGGGACAGCCCA
GGTCACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTTTGGGATGATTGCTCGATTGTTTGGTTTTTAAAT
CTGAGAAGCCTAGATAACTAATCTGCTTTTAAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTC
TCTGGACTGAGCAAGAGGGAGGAGGGAGCCTGCTACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTGACC
TGGGGCGCTGCTCCCAACAGTCCAAATAAGCTGAAAGTGACGCTCGCTGCAGGCCCCAGAGCGAGCTTCCCCCTC
TCCCTGCTCTCCAGGCCCTGCCACAGCCTCTTCCGTCCCTCTCTTCTGATCCAGGCCCTCAGTCCAAGCT
TTGGAACCTTACCTCATCTTAAACCGAACTCAAATATATTTATTTTTTACCATAACCACTTCTCTCCCATC
TCTAGGTGGCTCAGTCCATGGCCACTCCCTGCCCCAGCCTGGCTGGACAGCAAGGAATCCACAGCCACACAGTG
AGCTCCCTCTCACCCTCAGGCAGGGAAGCCCTCCTGCCAGTCCCTGTCCCTTTTACGCCACCACTCCCTCTC
TGCTGCCGCTGATGGGAGGCCTTTCTAGACCTGGCTCTTCTCTCCCGTCTCAGTGGCTTCTCTGAGGTGCTGTA

WO 2004/030615

PCT/US2003/028547

180/6881
FIGURE 169B

CACGCGCGTTAACCTGTTCCCTTCTCTATCCTTCCCCGTGGTACTGAGCTCACGTGGACTCCCAGTGCGAAGGGG
CCCATGGGTTGGGCTGCAGGCCTGGCCGTGAGCGGGGGCTGCCTGCACGCTCCCCTAGCCTACTCTTGTGTTTAG
GGGATGGTGGGAACATATCCCAGTGCCCTTGCCTCATAATAGATGTGGTGACTCTCCCGGTAGACCCTAGCAAGG
GTCTCCATGGTGGTGAGGGACTCAGGAGAATTGTAGGGATTGGGGGACCCTGCCTGCCTGGCTTGAGAACAGCC
CTGCTGCCCTTTTGAAGCCGAGATTTTGAAGTGGATGCCCGTCTTGCCAGAAATGCTGTTCTCACCAGAATGCCCC
CTCCCCCTTGCCCTTACTGGACTTGGCCCTGCCTGATGCCAAGCAAAGACCCTTCCCCAGAGGCCTACCCCCATA
TGTCTCAGAGAGGCTGAGTGTCCCTCCAGGCAGTCATGGGCCCTGAGGCCCTCCTGCCTGGCCCTGCTCCCC
AGTGGGGAGGTGACTGTGTTTCCCAGAGTGTGAGCCGCTCTCCTCCCCCTAAAAAGCTGACTCACTGTGAGTGAC
CTTGGGCAAGTTCCCAAACCTCCTTGTGCCTCAGTTTCCCCATCTGGAAAAAATGGGGCCACCTCTTGCCAGCAG
TAGCAGGGCTGCCCCAGCCCCCTTCTCCCCATGCCCCATCCAGCACTTGGGCGACTCATGCCCTCTGCCTCAGTGG
GCCTGTGGGAGCCTACTGGAGCCCAGCACTTACTCCCCCTGAGCAGCGAGCCTGCGTCTGTCTCAGCTGTCCAGC
GCTGAGGGCCAGGGTCTTGTGCTGTGGGGCTGGGGGATGCCCTCTTTTCTATATTTATTTATAGAAAAGTCTCCT
GCGGGAGCGGAAATGCAGTCCGGCCTAGGGCTCCCAGCCCTTGACTGTCCTCCTGTGAGGGCCTGAAGCTGGGCC
AGGGCCCGTCGCAGCGGAGCCCCCTCTCAGCAGCCCACCGGTCCCTCCAGGCTGCTGCCCCGTGCGTGGTCTTTC
TCCTCCTTTTCAAAGCAATAGCCGCCGGGTCTGCAAAGCCCTGTGACACAGACTGGGCCCTTCCAAGGTCAAGCC
ATGTGTCTGATGACATTCTGGTGAAGCAAAGGAGAGGAGGATGGGTGAGCCCTCACTGGGTGTCACACACTGAG
AGAAGTCCTATTGTAAAGAAACGGAAAAAGTCACAAAAAAGTTTGTATAAAGACATATTTTGTACTACATGGGG
ACTCTTCTGCATGTCAGCAATAAACTTCCTGATCTGG

WO 2004/030615

PCT/US2003/028547

181/6881
FIGURE 170

MKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLARKDGTDDFYQLKILTLEERGD
QGIESQEERQKGKMLLHTEYSLLSLLHTQDGVVHHHGLFQDRTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFS
DKTADLINLQHYVIKEKRLSERETVVIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFC LGKHLVS
EGDLLKDQRGSPAYISPDVLSGRPYRGKPSDMWALGVVLF TMLYGQFPFYDSIPQELFRKIKAAEYTIPEDGRVS
ENTVCLIRKLLVLDPPQRLAAADVLEALSAI IASWQSLSSLSGPLQVVPDIDDQMSNADSSQEVSWGGQMGHYPA
PRDRLLGAGRARA EVAATRRPQSFLGLLPQPWGGKGR LQSSA

WO 2004/030615

PCT/US2003/028547

182/6881
FIGURE 171

ATTGGGACGCTGCGGCCTGGCCTTCAGGCCACTGGCTACCGAACCCCGGGGCTCTTCACCAGTCCAGCTCGTTTC
CAGCACCAATGTCGGTGCGGACGCTACCGCTGCTCTTCTTGAACTTGGGCGGGGAGATGCTTTACATCCTCGACCA
ACGGCTGCGGGCCCAAGAACATCCCGGGAGACAAGGCCCGCAAAGTTCTGAATGACATCATCTCCACCATGTTCAA
TAGAAAGTTTATGGAGGAATTATTCAAGCCTCAAGAGCTCTACTCCAAGAAGGCCCTGAGGACTGTCTATGAGCG
CCTGGCTCATGCCTCCATTATGAAACTGAACCAGGCCAGCATGGATAAGCTCTATGACCTGATGACCATGGCTTT
CAAATATCAAGTATTGCTGTGTCCCCGACCCAAGGATGTGCTGCTGGTCACTTTCAATCACTTGGATACCATCAA
GGGATTATCCGAGACTCCCCAACCATCCTGCAGCAAGTGGACGAGACTTTGCGGCAGCTGACAGAAATATATGG
TGGTCTCTCTGCAGGGGAGTTCCAGCTGATCCGGCAGACACTCCTCATCTTCTTCCAAGACCTGCACATCCGAGT
ATCCATGTTTCTAAAGGACAAAGTTCAGAATAATAACGGTCGCTTTGTGTTGCCGGTGTCCGGGCCTGTTCTTG
GGGAAGTGAAGTTCAGGACTCATCAGAATGTTCAACAACAAAGGTGAAGAAGTGAAGAGGATAGAATTCAGCA
TGGTGGAAACTATGTCCCTGCACCCAAAGAAGGTTCTTTTGAACTTTATGGAGACCGAGTCCTGAAACTGGGAAC
TAACATGTACAGCGTGAATCAGCCTGTGGAAACTCATGTGTCTGGATCATCAAAGAACTTAGCCTCATGGACCCA
GGAAAGCATTGCTCCAAACCTCTTGCTAAAGAAGAGCTGAATTTCTTGCCAGGCTGATGGGAGGGATGGAGAT
TAAGAAACCCAGTGGCCCTGAGCCCAGATTCCGGTTGAATCTCTTTACCACCGATGAAGAAGAGGAACAAGCAGC
GCTAACCAAGGCCAGAAGAGTTATCCTATGAAGTTATCAACATACAAGCCACCCAGTCTCTTTTCAGCAATCTGGC
CACCATTACAGGGGGGCCTGACTGGGTGACAGATGAATGGGAAGGTTCTGACCTGTTTTGAGTCCGGCTCCCACCT
TGCTGTACATATCAGAATGTCACTGCTCTGAGTGTGTCCCAGGGCCTTGGAGGTGGGCCGTGAGGTGCCGAGAA
GCAGCCGCAGCCTCCTCCCTCCACCTATCCCAGAGCGATGCTGGTGATTTCAAACGTATCTGTCCTATCAGTAAA
TAAACAAGATGCAGATCTCTGGT

WO 2004/030615

PCT/US2003/028547

183/6881
FIGURE 172

MSVRTLP LLFLNLGGEMLYILDQRLRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALRTVYERLA
HASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVLLVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGL
SAGEFQLIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGTEVPGLIRMFNNKGEEVKRIEFKHGG
NYVPAPKEGSFELYGDRV LKLGTMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNFLARLMGGMEIKK
PSGPEPGFRNLNLTDEEEEAALTRPEELSYEVINIQTQSLFSNLATIQQGLTG

WO 2004/030615

PCT/US2003/028547

184/6881
FIGURE 173

GAAGCTGGACTGCAGCTGGTTTCAGGAACCTTCTCTTGACGAGAAGAGAGACCAAGGAGGCCAAGCAGGGGCTGGG
CCAGAGGTGCCAACATGGGGAACTGAGGCTCGGCTCGGAAAGGTGAAGTAACTTGTCCAAGATCACAAAGCTGG
TGAACATCAAGTTGGTGCTATGGCAAGGCTGGGAACTGCAGCCTGACTTGGGCTGCCCTGATCATCCTGCTGCT
CCCCGGAAGTCTGGAGGAGTGCGGGCACATCAGTGTCTCAGCCCCATCGTCCACCTGGGGGATCCCATCACAGC
CTCCTGCATCATCAAGCAGAACTGCAGCCATCTGGACCCGGAGCCACAGATTCTGTGGAGACTGGGAGCAGAGCT
TCAGCCCCGGGGCAGGCAGCAGCGTCTGTCTGATGGGACCCAGGAATCTATCATCACCTGCCCCACCTCAACCA
CACTCAGGCCTTTCTCTCCTGCTGCCTGAACTGGGGCAACAGCCTGCAGATCCTGGACCAGGTTGAGCTGCGCGC
AGGCTACCTCCAGCCATACCCCAACCTCTCCTGCCTCATGAACCTCACAAACCAGCAGCCTCATCTGCCAGTG
GGAGCCAGGACCTGAGACCCACCTACCCACCAGCTTCACTCTGAAGAGTTTCAAGAGCCGGGGCAACTGTCAGAC
CCAAGGGGACTCCATCCTGGACTGCGTGCCCAAGGACGGGCAGAGCCACTGCTGCATCCACGCAAACACCTGCT
GTTGTACCAAGATATGGGCATCTGGGTGCAGGCAGAGAATGCGCTGGGGACCAGCATGTCCCACAACTGTGTCT
TGATCCCATGGATGTTGTGAACTGGAGCCCCCATGCTGCGGACCATGGACCCAGCCCTGAAGCGGGCCCTCC
CCAGGCAGGCTGCCTACAGCTGTGCTGGGAGCCATGGCAGCCAGGCCTGCACATAAATCAGAAGTGTGAGCTGCG
CCACAAGCCGCAGCGTGGAGAAGCCAGCTGGGCACTGGTGGGCCCCCTCCCCTTGGAGGCCCTTCACTATGAGCT
CTGCGGGCTCCTCCCAGCCACGGCTACACCTGCAGATACGCTGCATCCGCTGGCCCCCTGCCTGGCCACTGGAG
CGACTGGAGCCCCAGCCTGGAGCTGAGAACTACCGAACGGGCCCCCACTGTGAGACTGGACACATGGTGGCGGCA
GAGGCAGCTGGACCCAGGACAGTGCAGCTGTTCTGGAAGCCAGTGCCCTGGAGGAAGACAGCGGACGGATCCA
AGGTTATGTGGTTTCTTGGAGACCTCAGGCCAGGCTGGGGCCATCCTGCCCCCTGTGCAACACACAGAGCTCAG
CTGCACCTTCCACCTGCCTTCAGAAGCCCAGGAGGTGGCCCTTGTGGCCTATAACTCAGCCGGGACCTCTCGCCC
CACCCCGGTGGTCTTCTCAGAAAGCAGAGGCCAGCTCTGACCAGACTCCATGCCATGGCCGAGACCCTCACAG
CCTCTGGGTAGGCTGGGAGCCCCCAATCCATGGCCTCAGGGCTATGTGATTGAGTGGGGCCTGGGCCCCCCCCAG
CGCGAGCAATAGCAACAAGACCTGGAGGATGGAACAGAATGGGAGAGCCACGGGTTTCTGCTGAAGGAGAAT
CAGGCCCTTTCAGCTCTATGAGATCATCGTGACTCCCTTGTACCAAGACACCATGGGACCCTCCCAGCATGTCTA
TGCCTACTCTCAAGAAATGGCTCCCTCCCATGCCCCAGAGCTGCATCTAAAGCACATTGGCAAGACCTGGGCACA
GCTGGAGTGGGTGCTGAGCCCCCTGAGCTGGGGAAAGAGCCCCCTTACCCACTACACCATCTTCTGGACCAACGC
TCAGAACCAGTCCTTCTCCGCCATCCTGAATGCCTCCTCCCGTGGCTTTGTCTCCATGGCCTGGAGCCCGCCAG
TCTGTATCACATCCACCTCATGGCTGCCAGCCAGGCTGGGGCCACCAACAGTACAGTCTCACCCTGATGACCTT
GACCCAGAGGGGTGCGAGCTACACATCATCCTGGGCCTGTTTCGGCCTCCTGCTGTTGCTCACCTGCCTCTGTGG
AACTGCCTGGCTCTGTTGCAGCCCCAACAGGAAGAATCCCTCTGGCCAAGTGTCCCAGACCCAGCTCACAGCAG
CCTGGGCTCCTGGGTGCCACAATCATGGAGGAGGATGCCTTCCAGCTGCCCGGCCTTGGCAGGCCACCCATCAC
CAAGCTCACAGTCTGAGGAGGATGAAAAGAAGCCGGTGGCCTGGGAGTCCCATAACAGCTCAGAGACCTGTGG
CCTCCCCACTCTGGTCCAGACCTATGTGCTCCAGGGGGACCCAAGAGCAGTTTCCACCCAGCCCCAATCCCAGTC
TGGCACCAGCGATCAGGTCTTTATGGGCAGCTGTCTGGGCAGCCCCACAAGCCAGGGCCAGGGCACTATCTCCG
CTGTGACTCCACTCAGCCCCCTTGGCGGGCCTCACCCCCAGCCCCAAGTCTATGAGAACCTCTGGTTCCAGGC
CAGCCCCCTGGGGACCTGGTAACCCAGCCCCAAGCCAGGAGGACGACTGTGTCTTTGGGGCACTGCTCAACTT
CCCCCTCCTGCAGGGGATCCGGGTCCATGGGATGGAGGCGCTGGGGAGCTTCTAGGGCTTCTGGGGTTCCCTTC
TTGGGCCTGCCTCTTAAAGGCCTGAGCTAGCTGGAGAAGAGGGGAGGGTCCATAAGCCCATGACTAAAACTACC
CCAGCCCAGGCTCTCACCATCTCCAGTACCAGCATCTCCCTCTCCTCCCAATCTCCATAGGCTGGGCCTCCCAG
GCGATCTGCATACTTTAAGGACCAGATCATGCTCCATCCAGCCCCACCAATGGCCTTTTGTGCTTGTTCCTAT
AACTTCAGTATTGTAAAC

WO 2004/030615

PCT/US2003/028547

185/6881
FIGURE 174

MARLGNC SLTWAALI I I I I I L L L P G S L E E C G H I S V S A P I V H L G D P I T A S C I I K Q N C S H L D P E P Q I L W R L G A E L Q P G G R Q
Q R L S D G T Q E S I I T L P H L N H T Q A F L S C C L N W G N S L Q I L D Q V E L R A G Y P P A I P H N L S C L M N L T T S S L I C Q W E P G P E T
H L P T S F T L K S F K S R G N C Q T Q G D S I L D C V P K D G Q S H C C I P R K H L L L Y Q N M G I W V Q A E N A L G T S M S P Q L C L D P M D V V
K L E P P M L R T M D P S P E A A P P Q A G C L Q L C W E P W Q P G L H I N Q K C E L R H K P Q R G E A S W A L V G P L P L E A L Q Y E L C G L L P A
T A Y T L Q I R C I R W P L P G H W S D W S P S L E L R T T E R A P T V R L D T W W R Q R Q L D P R T V Q L F W K P V P L E E D S G R I Q G Y V V S W
R P S G Q A G A I L P L C N T T E L S C T F H L P S E A Q E V A L V A Y N S A G T S R P T P V V F S E S R G P A L T R L H A M A R D P H S L W V G W E
P P N P W P Q G Y V I E W G L G P P S A S N S N K T W R M E Q N G R A T G F L L K E N I R P F Q L Y E I I V T P L Y Q D T M G P S Q H V Y A Y S Q E M
A P S H A P E L H L K H I G K T W A Q L E W V P E P P E L G K S P L T H Y T I F W T N A Q N Q S F S A I L N A S S R G F V L H G L E P A S L Y H I H L
M A A S Q A G A T N S T V L T L M T L T P E G S E L H I I L G L F G L L L L L T C L C G T A W L C C S P N R K N P L W P S V P D P A H S S L G S W P
T I M E E D A F Q L P G L G T P P I T K L T V L E E D E K K P V P W E S H N S S E T C G L P T L V Q T Y V L Q G D P R A V S T Q P Q S Q S G T S D Q V
L Y G Q L L G S P T S P G P G H Y L R C D S T Q P L L A G L T P S P K S Y E N L W F Q A S P L G T L V T P A P S Q E D D C V F G P L L N F P L L Q G I
R V H G M E A L G S F

WO 2004/030615

PCT/US2003/028547

186/6881
FIGURE 175

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCTCTCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCCGCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCTTCAAAGCAGGAGCAGCTCCATATGTGCAGGCATTG
ACTCGCTGCTTGCTGGTCCTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTCCGGGAGAAGAACC
GAGGCAGCAAGTTGTTTAATCACCTGTGAGCTGTGAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCTCTCAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCACCGGACTGGCCTGGAGCAAAACGGGGCCTGTGGCAAAAGAACTGAGCGGACTGCCATCTG
GACCTCTGCGGATCATGTCTCTCTCCCTCCACCATGCCCCCTCTCTCCCCAGTCTCTACCATTTTCATGCT
CATATGAGTCTGCTTCCCGCTCATCACTGTTGCGCGAGATTATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAAGAACCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACAGCCCATCCCCAAACGAGCCACAAAGAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAATCAGGAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAAATCAAGGGCAAAATTAACCTCATTACAGTAG
ATAACTGTAAGAACTTGGCCTGGTATTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTACAGTAATGGGTAAAGTGCCAAACCATATCCATCAACAAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCCTGGATTGTGAAATAGTCAGTGCCAAATCTTCCGAGATGAATGTCTCTATTCTACAGAAGGCGGTGACT
TTAATGAATTCAGTTCCTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCAACCACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTTCTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTTCTAGATTTCTCTACCTTTTTGCTCTTAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTGAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAAGTGGCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGTTATTCTACCAACAAACAGTCCATTGGAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTACACTGTTAATCTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAACTAATTTTTCACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAAGGCTGAGGCTTGGCCATC
TAGCATTCCATACAAAATTGTTTCTATAAGCATTCCTTTTATTCTCTATTCTATCCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGGCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCAGCACCTTCCTATAGAGATGACTTTAAAGGAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCCTGAATCCTTCTTCCCTGCCAGGTGCCTGTACCTGTCTTCACTGCC
TCCTTTTCCCTGTGATGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGACAGCACTGCTAATGTAAATTTTCAAGTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTGGTGGGAAGAGAGATTGTCCTGTGATTTCTACCCATT
TCCTGAGGCCTGTGGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAATAGAATAAAGTTAATACCAAACTT
G

WO 2004/030615

PCT/US2003/028547

187/6881
FIGURE 176

CCGGAGTCTCGCGCCCGCGGTTCATGTGACACAGCGAAGATCGCGTCGCCCCGGCTGCCTGTGGCTCTTGGCTGTGG
CTCTCCTGCCATGGACCTGCGCTTCTCGGGCGCTGCAGCATCTGGACCCGCCGGCGCCGCTGCCGTTGGTGATCT
GGCATGGGATGGGAGACAGCTGTTGCAATCCCTTAAGCATGGGTGCTATTAAAAAATGGTGGAGAAGAAAATAC
CTGGAATTTACGTCTTATCTTTAGAGATTGGGAAGACCCTGATGGAGGACGTGGAGAACAGCTTCTTCTGTAATG
TCAATTCCCAAGTAACAACAGTGTGTCAGGCACTTGCTAAGGATCCTAAATTGCAGCAAGGCTACAATGCTATGG
GATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAGAGATGCCCTTCACCTCCCATGATCAATCTGATCT
CGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGATGCCAGGAGAGAGCTCTCACATCTGTGACTTCA
TCCGAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTTTCAGGAACGCCTCGTGCAAGCCGAATACGGCATG
ACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTCTTGGCAGATATAAATCAGGAGCGGGGTATCAATG
AGTCCTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTGATGGTGAATTCCTCAATGATTCCATTGTGGACC
CTGTAGATTTCGGAGTGGTTTTGGATTTTACAGAAGTGGCCAAGCCAAGGAAACCATTCCCTTACAGGAGACCTCCC
TGTACACACAGGACCGCCTGGGGCTAAAGGAAATGGACAATGCAGGACAGCTAGTGTCTTGGCTACAGAAGGGG
ACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCACATCATACCATTCCCTTGGATGAACCCGTATAGTTCAC
AATAGAGCTCAGGGAGCCCCCTAACTCTTCCAAACCACATGGGAGACAGTTTCCTTCATGCCCAAGCCTGAGCTCA
GATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCCTACTTGGAAAGATCTAAGATCTGAATCTTATCCT
TTGCCATCTTCTGTTACCATATGGTGTGGAATGCAAGTTTAATTACCATGGAGATTGTTTTACAACTTTTGATG
TGGTCAAGTTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATCAGTGCCAGAAGTGTGCCAGGCCCAAAGGAGACA
ACTAACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTTTTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTG
CCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGGTGATTTAACCAAGTGCTTGGAAAAATCTTGCTTGG
CTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAGTACGTTGCCCTCTGTGCTATCATCTTATCATCAA
TTATTAGACAAATCCCCTGGCCTACAGTCTTGCTTCTGCAGCACCCACTTTGCTCTCCTCAGGTAGTGATGAATT
AGTTGCTGTACAAAAGGAGGGAAGTAGCACCCAAATTAAGTTGCTTAAGAGAGGAAATGTACATCTTGTATAAC
TTAGGGAGCGAAGAAAATGTAGGCGCGAAAGTGAAAAGTGAGGCAGCTAGTTCTTCTTCTTCCATTCTCGACCAA
CCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAGTCAACTTACTCTGTTGCTGGCTTTAGCAGAGAAT
AGGAGGAACCATATGAAAAAGATCAGGCTTCTGACTTCCATCCCCAAAACACATTTACCAGCATACTCCAACT
GTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAAAAGCTTGGAAAATACTACACACTCCCTTTCTCCT
TCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGAGAATTCCTGTTACAGTAAACAAAACCTAACGTAAT
CTACCATTTCCTACACTATTTGAGCATGGAAATCATAGTCCCCACTCTGTGAAAACCTAACGCTTTTGGGAAGAC
ATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGCCTTGATGAAAGAACCGTGTGGTGCTGCTAAGTT
TAGCCATTATGGTTTTCTCTCTCTCTTAAGCCTTATTCTTCAACTAAAAGATGAGGATTAAGAGCAAGAAG
TTGGGGGGGATGTGAAAATAATTTTATGAGGTTGTCTAAAT

WO 2004/030615

PCT/US2003/028547

188/6881
FIGURE 177

MASPGCLWLLAVALLPWTCASRALQHLDPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIYVLSLEIGKT
LMEDVENSFFLNVSQVTTVCQALAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMINLISVGGQHQG VFGLP
RCPGESSHICDFIRKTLNAGAYSKVVQERLVQAEYWHDP IKEDVYRNHSIFLADINQERGINESYKKNLMALKKF
VMVKFLNDSIVDPVDSEWFGFYRSGQAKETIPLQETSLYTQDRLGLKEMDNAGQLVFLATEGDHLQLSEEWFYAH
IIPFLG

WO 2004/030615

PCT/US2003/028547

189/6881
FIGURE 178

CCTTACGGCCAGAAACGCCACCTTCCAGTAATTCGCCAAAATGACAAACACAAAGGGAAAGAGGAGAGGCACCCG
ATACATGTTCTCTAGGCCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCATGTATATGCGAATCTATAAGAAAGG
TGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGGAATGTCCACAAAGTGTTACCATGGCAAAACTGG
AAGAGTCTACAATGTTCCCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAA
GAGAATTAATGTGTGTATTGAGCACATTAAGCACTCTAAAAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAA
TGATCCTCCACCCAGAGAAGCACAGTGTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAAACTATTCCCTA
TGAATTCATGGCA~~TAA~~TAGGTGTT

WO 2004/030615

PCT/US2003/028547

190/6881
FIGURE 179

MTNTKGKRRGTRYMF SRPFRKHGVVPLAMYMRIYKKGDIVDIKGMGTVQKGMSHKCYHGKTGRVYNVPQHAVGIV
V NKQVKGKILAKRINVCIEHIKHSKSRDSFLKRVKENDPPPREAQCVRTNGKEPELLETIPYEFMA

WO 2004/030615

PCT/US2003/028547

191/6881
FIGURE 180A

CGGACGCGTGGGCTGCTGCGGAGCCGGCAGCGCAGGCGGGCGGAGCGGAGCTGCCCCGTGGTGGCGGGCGATGC
CCCCGTGAGCCTCCCTCGCCGCCCTCCCCGCCCGCGTGCTATCCACTCGGAGTCCGCGCCAGCCTGGGGCCG
GGCCGCGCCTACTGCCGGGTTCGCGGGGCGGGGTCCCGGGGCGACCTGCCCGCCTTGCAGGAGCCGCTCGGC
CTGTGGAGGCCCCCTCCCTGTCTGGACCCGGCCCCACCTCCGACCCCTTTTATCACATCGCCTCCTCTGGGAGC
CTGCCCTGATTGCCTTACCTCATTTCTTGAAAATTGGTGTGTTTGGCAGAAGTCAATTGAAGCCTTGTGCAAATG
CCCTAGGGGTGTGCTGTTGGGAGGCAGCCCCCTGTGATGCGGAACACCAGGCTCAGATTTCATCAGTTCGAGCTGC
CTGAGGCCCTGCCACCCCGGGGACCATGTTTAACGGGGAGCCAGGTCTGCCTCATCTGGGGCCTCCAGGAATGT
GGTGGCGAGCTCCAGCATTGGCGGTGAAATCTGCGGATCCCAGCAAGCCGGGGGCGGGGCTGGGACCACCACCGC
CAAGAAGCGGCGGAGCAGCCTGGGTGCCAAGATGGTGGCCATCGTGGGCCTGACTCAGTGGAGCAAGAGCACACT
CCAGCTTCCGCGAGCCTGAAGGGGCCACCAAGAAGCTGCGCAGCAACATCCGCCGGAGCACGGAGACAGGCATCGC
GGTGGAGATGCGGAGCCGGGTACACGCCAGGGCAGCCGGGAGTCCACCGATGGGAGCACCAACAGCAACAGCTC
CGACGGCAGGTTTCATCTTCCCCACTACCCGGCTAGGGGCTGAAAGCCAGTTCAGCGATTTCTGGATGGGCTGGG
ACCAGCTCAGATTGTGGGGCGACAGACACTGGCAACACCACCCATGGGAGATGTGCACATTGCCATCATGGACCG
GAGTGGCCAGCTGGAGGTGGAAGTGATTGAAGCTCGGGGCCTGACCCCCAAACCAGGCTCCAAATCCCTCCCAGC
CACCTATATCAAGGTTTACCTGTGAGAATGGGGCCTGCTTGGCCAAGAAGAAGACAAAGATGACCAAGAAGAC
CTGTGATCCCTGTACCAGCAGGCTCTGCTCTTTGACGAGGGACCCCAGGGCAAGGTGCTGCAGGTGATCGTCTG
GGGAGACTATGGCCGCATGGACCACAAGTGCTTCATGGGCATGGCCCAGATCATGCTGGACGAGCTGGACCTCAG
CGCCGCGGTACCGGCTGGTACAAACTCTTCCCCACCTCCTCAGTGGCAGACTCCACACTCGGATCCCTCACCAG
GCGCCTGTCCCAGTCTTCCCTGGAGAGTGCCACCAGCCCCCTCATGCTCTTAAGGATGTGAGGAAGAGGCCAGGAT
GGTGGTGTGGGGAGGGGTGCTGCTGGCCCCATGTCTCCCTGTACATAGTCTTCGTGTCTTTCTGGACCCCTT
GTCTGTGCTGATGCCTGTGGCTACTGGGCTCATCCCAGCTGGCAGTGGAGACTGTAGTGTGTGCGTGTGTGCGT
GCGTGTGTGTGTGTGTGTACGTGACCACGTTCTATCTGTTTCATTGTCTGGGTATAGTCACTCCTGGTGATGATA
TGGGCTGAAATGTCTCCACGTCTCTTTGTGTCTTGTGAAAAGAAACCCAAAGGAGTGTGTGTGGACATGACTC
ACCCTGAGGAGTCTCCAGGGATGGAGGTGGGGCATGCGGCCACTGGTCGGTGTGCTGGTGGTCTGGCCGGCA
GAGCCTGTGTGTTCTTACCTGTGCTGCTCCTGGTGGTCTCTGCTTTGTTTCTGTCTTTTGTCTTCTTGTCCACT
CTTGACTCTCCCGGCTCTGCCACTGTTTTCTGAGAAATGTAGCATCCGCTGCAGCTGGCCACACTGAGGGCCCTC
TGGGAACCCACCCCACTGGAGCCGCTCCGGCAGCTCTTCTGCCACTGAATGCGTTCTGCAGCATGTAGCATGC
CCACCTAGCTCCCTGGCCAGGGCCCTGGGGAGGCAGAGGGTACCCAGGGGACTGAGGGCTTAGAAATGACTTTCT
CTATGAGGCTGGAACCTCCTCCTTCTTCCAGTGAAGCACGAGGTCTTGGTTCCAGGGTTCTTGCCAGGTGCCCC
CTTAGCATTTGTTCTTTCATCTCCTGTCTCTTCAAGCCTCCCCACTCCACCGTGCCGAAGGAGCTCTGCCAGTGGG
CCTGGGCAGGCAGCCACAGAGGGCATGTTATCTGCTAAAGCAAACAGTCTCCTGAGGCCCTGAGGGTGGCCCTG
ACCCCTCAGGGCTCATTCTGGTGGGCATGACTCGGTAAGGAGTTCTGTGGGTAGGGCTGTTGTGCTGGAATAA
GGAGGGCTGAGGCTGAGTTGTTCCCGCCACTGTTGAGGATCCCATCTGACATTGGGGATTCACTGCATGAAGT
TGTTTCATTGGGGCTCCAGTTTTTGTGCATTTCCAGACCAGGTCCCTGTCTGGGAGCTCAGACTTAGCTGGGCT
CCAGCAGCCTGGCTCCGGACTCTGCTGCTGCCACCATCACCAGCTCTGTCTAAGCAATACTTACCCCTCCGGGCTT
CCCTGCTTTCTGTGCCCCACTGCTGCCCTCTGCAGAGCCATCTGCTCCAGGCACCCACCTGCCTCTGCTTGCTT
TCTACCCATGTCTGGTTGGAGCTTCTCACAGCCACTCAAACCTGACTTGATTGACAACCTGGGCCCTGTGGT
GGAGACCAGTGCCTGAACCTGGACCCTGTGAAATCTGTCCCGTGGGAATCCTGAAGTCTGACTCAGGAATGCCAG
ACCTGTCCCTGTCCCTCCTCAGCTCTAGGGTGAAAGGCAGAGGTTGCACAGGACATGGACAGAGCAGCCCTTGG
GTTGTATCTGGTAGGGGAGAAAGCAGCAGGACATGGAGGTGTGTGGAAGGCACCTTTCCACCTCTCTCCAGG
CATTATCCCCAGGTGCTGAAATGGCTGTGGCCCCAGCACTGAGGCAGGGGTACGCTACCTGGGGTAGCAGTAGA
AAGGTCTTGGGGTCTGAATGACTTGGGGCTCCATTCTATAACCAAAGTTGTAGGGGCATGGAGGCAGTGGCGCCT
TATGGATAGGTCTCTCAGCCCAAAGGGCTCCTTGGCTGGCATGGTTCTGTGTTACGTTGAAGCCAGAGTCTTA
TAACACCTCCCAAGAAAGATAGGGGAAGAAGCCAGAACCCACCTGGCCTGCCACAGGACAAGAAGTGGGTAAG
GGCAGGAAGGAAATGAACGGAGTTAGCTCCAGGCTCCTATCTCTGCTGAGCCTCTATTCTTATATTATCAGAG
AAAGGGACCATTGGGTGCATAGAGATGGGGAGGAGGCCACTGGGCTGAATTTCTCTTTAGGCGGAAATGCTCTC
CCAGGCCCCATTGCGTTCTGCAAGTTCTTGAAATGGACAAAGGGCTCTGTCTCCTCGACCCCTAGTGGGGGATC
AAGAAGGAAACTCCGTTGCAAAAGGGTATTTTAATCTCCTGTTTATGATATATTACCTCTAGAGCAGTCACTGT

WO 2004/030615

PCT/US2003/028547

192/6881
FIGURE 180B

CAGGGTGTTCGAAAATACTCTACACCTTTGGGATGATAGGGTTGTTAGTGACCCACAGGACAGTATAGATGTTT
GTGGATGTAGCACTGAGTGGTGATACCCAGACCAGCAGTCACCCAGGAAGTGGGGGCTACCCATACCCCTCATT
CTCTGGTGGGGAGCTGCCTGCAGAGAGGCTGCCACTGGGGGTTCAGGCCGTGGTGACCCCTGCCTCTGGGGAA
GGGTTAGCACAGGGGAGGTTCTAGCTGGAGGAGGGGTCTGATGTGCTGGTAACTTGGGCTGACCTACCTACAGTC
CCTGGCTGCCAAAACCTGCTCAGCAGTTGGGCCACTCCACTATTCCACCTCTCTAAAAGAAGGTAATTTCCCTCCCC
AAATTGACCTTGGGGAATTATTCTTTAACCCTTTGCACCAAATAAGTTACTCATCCCCACCTGGATTTTACCCC
ATGAGGGTAAAGTTGTGTGAGGCTGACACGTCTGTGTGATGCAGTGTGGCTGCACTTAAGGGTCTGTTTCTCAGC
ATCATGGATGCAGGGGCTTGTCTGAAAAGCCACTCTGGACCTAGCCTGTCCAGAAAGAGGAGAATGCACAAGTGT
AACTCCTGGTTGTTTGTCTGGGGTGGGGGAGCATCTGCTGTTTGGAGACGGGGGTGGGGAAGGAAGGAACATGAT
CCCTCCAGAAGTCTCCACCCCTGGGGCCAACCTCACTGCCATGTTTCACTGTCCCGGCTCCAAATGCCCCCTTGCCC
AGATGAAACCCTGCAGTGGTTACAGGAATGGAGCTCTTTGTCTTCCACCTCCTCTGGTCAGGCGAGGTTCACTG
TGCATATGGCAGAGACAGGAGTGGCCCTGCAGTGTGTTGGGTTGTGGGCAGGACAGTGTGATGACTCAGAG
CGTCTGTCTTTGTATTTCTGCTCTGTTTCTGCTCCACTTTCTTCATAGACTCCTTTTCCCTGCAATGGGTTT
TTGGTATGAAAAGGCTCCAGTAAATGGAGCCAAGTCTTGGTTTGACAAGGGGAACCTGATCCTTCAGGGAAGAA
TCATCTCCAAAATGACTCCCCATCTGGTTTCTTCTACCACCAATTTCTACTAGGAAAGGAGCACTTAGGAGGCTC
TTGGGATGCAGCAAGTCCCAGGCAATGCCAGCATTTCATGGGGGTGAGGCAGAACCCAGGAGCTCCAAGAAAGG
CCACCCATAGAGCTCATCCTCTGTGGAATCACTGCCGGTTAGAACACTGAGGTCAAGCCAGTCTCTCCATGGTCA
TGCCACCCACCAGGGAAGCATGCCTGATCTCTTTTACTGCCAGCCTTGAGGAGAGCAGAAGCCTCCATTTTAA
AAGACAATAAAGACCTCCAAGGGTACTTCTTTGGAATGAAATGTAGCAATCTTAGCCTACGTTACAGGAGC
CCTGACATGCAACCAGGGTCCCTCTTCCATGCCCTGCTGCCAGGAGTTGCTGAGCTCCTCTTCCCCTGGGGTTC
CAGCCCTCCTAATACCTCATATTCCCCATCTTCTCAGCCAGAAAGCAATGGGGCTTTAGTGATGCTCCTCTTT
TGTGTCTCTCTGGTTGCCTCTAGCACTGTGCAAACTCTGCAAGAAATGCTGCCTTTGCTTGATGTTGTAGATGA
GTTGCCCTCCACCTGGCTGGAGAGATGGCACATCATTAGGGCCAGAAAGGTTGTCCAGCAGTGTCTCTGCACTGG
CTGCAGGGAGATGGAAGAAGAGCCCTGCTTCCCTGCCTCCTCTTCTCTTCCACTCCTCAGAGTTTTTC
TTCTCCAGTATCCTGACATGTAAAGAGATTCTTTAAATGCTGCTTCTTCTACTGGACTGTCTTTCACTGAGTAG
TCAGGGAGGAGATGAAATGTGGACACATCCCCCGCCTTCTCCCTCAACCTTTTCACTCACGTCAGAAAGAGGTT
GGGGCAAAACAAACAAGCATGATTGAAGAGCAGGGGAAGCCACACAATCAGGTGAGCCCTGATGGGGGCTGGA
CTGGCCTGGTCTGGCTGGGAAAGGATTCTTTTAAAGCGTGCTGAGCATCTCAGAGCAATGTGATGATGCCAA
AGAGAGCAACTTGGCCTCCTTGGGCACCAACTCTGATGGCTGAGTTGCACAAAAGTGGCTCAGATGTTGGCATGC
CCGATGGTGGGACCTTGTCTCTGATAAAGGGCTTAATCTTTCCATGTAGCAAAGCAACTTTCCCTCCCTCCCCT
CCCCCGAACCTGAGCTTGGGCTTGTGTGGGCCAGCATGGCTGTGCTGTGAGGGAAGCCACATCAGTGAGAG
AAAGTTGCATTCTCTCAGGGGCTTAGATTGGCTTGGGCAGGTGCTTGTGAAAAGCATGAGTGTCTGCTTTG
GGAAACCCTTCCAGGGCTCTGGTTGGAACCTTGGCCAGTAAGGACAGGGCCTTGGGCCTCCCAAGGAGTTCACAA
TGATGCCAGGAAGGGTCCCTGAGCCTGGGTCCAGTCAGCTTGGCTAACAGAATGGGGCTTGGGAATTCCAGGGG
CAACTGAGCATCCACCCATTAGCCAGTGATCTGGACAGGGACAGCTGGCTACAGGGAATCAAAGGCTGTTCTGT
ACAGTTTTTACCAGAACTGTGACCTTGGGTAAAGGCTCCTCACTTTTCTGGGCCTCAACTTCTCATCTGCAAAAT
CAGAGCATTAGCTGCTCTCCCCATGATTCCCTCCCAGTTTAAATTAAGAGTCTCTGATCTGGAGCACATGAGGGT
TGCGAGCCTGGTGCACCTGGTCTGCTCCGTGGGCTGGTTTCTTCCAGCCCTGATGCCCAGGCTGGGTGCAG
GCTCTCATCTGGTCCATGCCAGATGCTGCCCTCAGACAAGAACTCTGGGAATCCTAACAGACTCTGCTTTCTCT
CTTCGTGGTTTGTCTCCTCTTTTATTCTTGTGTAATGATGAGACATAATTAAGGGTCATCTACAATGGACAAT
TTTCAAGGTGCTGATGTGATGTACAACTCCGCTACATCTGAGTAAGTCAGTGTCCCCAACAGCAGATGAGGC
TGGGTCTTTCTCATTTCTGCTTCTGGGATGACATCAGTGGGAGAGTTGAAGATCTGAGAATTCTAAAGGAAATG
TTCTCTGATGGGAGGAGAGAGGGAACCTATTTCCTTCAAAGTAGTTTGCTTCTTAAGACCACTCCTCCCTCCAG
AATGTCTTTAACCAGACATCATTTCAGAAGGTGGGGCAGCTGCTTCTTAGGAAGAGTGGGCCTGATAGCTCAAC
CAACTCCTTTAGCATGTAACTCACAGAAGGCAAGAACCCCTTTTTTGTAGCTTTCCAAATGCATCCTGCAAGA
GAGAGATAGCTGATAGGGACTGACAAGCACACTGTTTAGATAAGAAGCAATTACCCCTTTTATATCTGTGCTCTAT
ACATTTTCTATGTGCAGCATCTTCTTAACCTTGTGTGGTTCCCGGGTGGCAGGTGCACAGCTGGGAGGGACTGC
CGGCTGTTTCGTACAACATTCTTGCCAATTCCCTTGAGGAGAAAATCTTTCACATGGCTTCTGCATGTACAGTAT

WO 2004/030615

PCT/US2003/028547

193/6881
FIGURE 180C

TTGGGCAGCAAAACATGATTAAAGTCAGTTTGAAAATGG

WO 2004/030615

PCT/US2003/028547

194/6881
FIGURE 181

MFNGEPGPASSGASRNVVRSSSIGGEICGSQQAGGGAGTTTAKKRSSLGAKMVAIVGLTQWSKSTLQLPQPEGA
TKKLRNIRRTETGIAVEMRSRVTRQGSRESTDGSTNSNSSDGTFFPTTRLGAESQFSDFLDGLGPAQIVGRQ
TLATPPMGDVHIAIMDRSGQLEVEVIEARGLTPKPGSKSLPATYIKVYLLENGACLAKKKTMTKKTCDPLYQQA
LLFDEGPQGKVLQVIVWGDYGRMDHKCFMGMAQIMLDELDSLAAVTGWYKLFPTSSVADSTLGSLTRRLSQSSLE
SATSPSCS

WO 2004/030615

PCT/US2003/028547

195/6881
FIGURE 182

AAGCTGCTGACATCCTGGATCTAGGGTTGTAAAGAAGATTACATGAGCTAATGGATGTGAAAACATCTTAAAAAC
TCTCAAATACTTTTCAACTTTGGAGGATTATTATGATTTTCATTCTGTTTCAGCGGCTATACTCAGACTTTACTCT
AAAAGTCAAATCTTCTGACATTCTTTGAAGTGAAGCATTCTATGAATGTGAGCTGAAGAAATGAATGAAATGAAA
TAATGCAGCATCTAGTGCTTTTTGCATGGCCCAAAGGGGCTCTGTGCTGCTCCACTACAGAGGAACTTCAAGAA
ATGCTGGTTTGTACAGTGTTTTAGCTTGTGAGATTCTCTGGGACCTTCCCTGCTCCATCATGGGGTCACCTCTA
GGTCATTTTACCTGGGACAAATACCTAAAAGAAACATGTTTCAGTCCCAGCGCTGTCCATTGCTTCAAGCAGTCC
TACACACCTCCAAGCAACGAGTTCAGATCAGTATGAAATTGGAAGCACAGGACCCCAGGAACACCACATCCACC
TGTATTGCCACAGTAGTTGGACTGACAGGTGCCCGCTTCGCCTGCGCCTTGATGGGAGCGACAACAAAAATGAC
TTCTGGCGGCTGGTTGACTCAGCTGAAATCCAGCCTATTGGGAACTGTGAAAAGAATGGGGGTATGCTACAGCCA
CCTCTTGGATTTTCGGCTGAATGCGTCTTCTTGGCCCATGTTCCTTTTGAAGACGCTAAATGGAGCAGAGATGGCT
CCCATCAGGATTTTCCACAAGGAGCCACCATCGCCTTCCCACAACCTTCTTCAAATGGGAATGAAGCTAGAAGCT
GTGGACAGGAAGAACCCTCATTTTCATTTGCCAGCCACTATTGGGGAGGTTTCGGGGCTCAGAGGTGCTTGTCACT
TTTGATGGGTGGCGAGGGGCCCTTGACTACTGGTGCCGCTTCGACTCCCAGACATCTTCCCTGTGGGCTGGTGT
TCCTTGACTGGAGACAACCTGCAGCCTCCTGGCACCAAAAGTTGTGATTCCAAAGAATCCCTATCCTGCCTCCGAT
GTGAATACTGAGAAGCCCAGCATCCACAGCAGCACCAAAACCTGTCTTGGAAATCAACCAGGGCAGAGGGGGCGT
AAACCAGGAAAGAAGCGGGGGCCGGACACCCAAGACCCTAATTTCCCATCCCATCTCTGCCCCATCCAAGACAGCT
GAACCTTTGAAATTTCCCAAAGAAGAGAGGTCCCAAACCTGGCAGCAAGAGGAAACCTCGGACTTTGCTGAACCCA
CCACCTGCCTCACCAACAACCAGCACTCCTGAACCGGATACCAGCACTGTACCCCAGGATGCTGCCACCATCCCC
AGCTCAGCCATGCAGGCCCAACAGTTTGTATCTACTTGAACAAGAATGGCAGCACAGGCCCCCACTTAGATAAG
AAGAAGGTCCAGCAACTCCCTGACCATTTTGGACCAGCCCGTGCTCTGTGGTGTGACAGAGGCTGTCCAGGCC
TGTATCGACTGTGCTTATCACCAGAAAACCGTCTTCAGCTTCCCTCAAGCAAGGCCATGGTGGTGAGGTTATCTCA
GCCGTGTTTGACCGGGAACAGCATACCCTCAACCTCCCAGCAGTCAACAGCATCACCTACGTCTCCGCTTCCCTG
GAGAACTCTGCCACAACCTTCGTAGTGACAATCTGTTTGGCAACCAGCCCTTTACACAGACTCACTTGTCACTC
ACTGCCATAGAGTACAGCCACAGCCACGACAGGTACCTACCAGGTGAAACCTTTGTCTTGGGGAATAGTCTGGCC
CGCTCCTTGAACCACACTCAGACTCAATGGACTCTGCCTCAAATCCCACCAACCTTGTGACGACCTCCCAAAGG
CACCGGCCCTTGCTTTCATCCTGTGGCCTCCCACCAAGCACTGCCTCAGCTGTGCGCAGGCTATGCTCCAGGGGA
GTGTTAAAAGGATCAAATGAAAGAAGGGATATGGAATCATTTTGGAACTAAATCGTTCCCCAGGGTTCGGACCGA
TACCTGGAGAGCCGCGATGCCTCTCGACTGAGTGGCCGGGACCCCTCCTCATGGACAGTCGAGGATGTGATGCAG
TTTGTCCGGGAAGCTGATCCTCAGCTTGGACCCACGCTGACCTGTTTCGCAAACACGAGATCGATGGCAAGGCC
CTGCTGCTGCTGCGCAGTGACATGATGATGAAGTACATGGGCCTGAAGCTGGGGCCTGCACTCAAGCTCTCCTAC
CACATTGACCGGCTGAAGCAGGGCAAGTTCTGAACCAGGAGAGGCAGCCTAGACAACCAAGTGGCAGCAGGTGGG
GGCATTCTTCTAGGAATGAGGGGCATCAGCCCACCCAGGCACCTCAGTGGGGTTCCGGGCCACCTCAGGACTCC
AAGAGGCTGTGTGGAGCCACCCTCCTAGCCACAGCTGCCATGATAAGTCCCTTCCATGAAGGACTGAGGAGGGAG
AGTGGGGGTCCAGGGCTGGTGTCTCTTCCCTCAGCTCTGCCGGGGCTCTAAGGTCCCTCTATTTATTTCTCAA
CCCTGGCTGGCCTCTCACCAGGAGTTTAGGCTGAATGCCTTCCACGTGATGGAGGAAAAGGCCAACTCTGTCTG
GTCTTGCTGTGGCACCCCATCGCCCCACAGCTCGTACCTTCTCACCAGATTCCCTGAATCCAAACTCGTGGTGC
AAACCTCTACCTTTTTTACAAAAAGATCTTATTGTTAATTTATTGTTTCTGGCACTTGGGCAAACCTGTAGTTA
ATACTCCTCCACACTAGACACTGGGTTTTCAGGAGGAGGGAGACTGCCCTGCTTTGGTCCCAGAGAGGCCCTCTG
CAGATAGGCGTGGCCCTCTTTCAGAGGACACTACCCTAGGGCACTTTCTCTTTGAGGTGGAGAGACCCATAAAGC
CTTGACCACATCACTCCATATGGGGAGGAGAAGGATCCCTGTCACCTTCTCCTCTCTTACGGGGCCCTTTTGCA
GCCCTAGGCCTCATCTGTGGGAAGGGAGTCCCTGGCTTATACTGCCCCACCACAGCTCCTTGCCCTGGCCAGAA
CTGCTGTGCAAGAAAATCAGGCCGGAAGGCCAAGAAGGCGCTAAGGGGGATGGGAGGGCAGGTTTTCCAGGCTGG
AGTCGGTTCCACCCACTCGCCTGTCCACAGGCTTCTTGTAAAGCAAGTCAGCAGCACAGCTACTCACGCTGCCAT
CTGGACTTATTTTATGTCAATCTGTTTATAAATAAAAACCAATATAGAT

WO 2004/030615

PCT/US2003/028547

196/6881
FIGURE 183

GCTGCAGATGGCGGAAATGGATCCGGTAGCCGAGTTCCCCAGCCTCCCGGTGCTGCGCGCTGGGCTGAGGTTAT
GGCTCGCTTCGCGGCCAGGCTGGGCGCGCAGGGCCGGCGGGTGGTGTGGTTACGTCAGGCGGCACCAAGGTCCC
ACTGGAAGCGCGGCCGGTGCCTTCTGGACAACCTCAGCAGCGGGCGGCGCGGTGCAACCTCGGCCGAGGCCTT
CCTAGCCGCCGGCTACGGGGTCTGTCTTGTATCGCGCTCGCTCTGCCTTCCCTATGCCCCACGCTTCCCACC
CCAGACTTGGCTGTCCGCTCTGCGGCCTTCGGGCCAGCCCTTTCGGGCTTGCTGAGCCTGGAGGCCGAGGAGAA
TGCACTTCCGGGTTTTGCTGAGGCTCTGAGGAGCTACCAGGAGGCTGCGGCTGCAGGCACCTTCTGGCAGTAGA
GTTCAACCACTTTGGCGGACTATTTGCATCTGTTGCAGGCTGCGGCCAGGCACTCAATCCGCTAGGCCCTTCTGC
GATGTTTTACCTGGCTGCGGCTGTGTGAGATTTCTATGTTTCTGTCTCTGAAATGCCTGAACACAAGATCCAGTC
ATCTGGGGGGCCCACTGCAGATAACAATGAAGATGGTGCCAAACTGCTTTCTCCTTTGGTTAAAGATTGGGCTCC
CAAAGCAATTTATAATTTCCCTTTAAGTTGGAGACTGACCCCGCCATTGTAATTAATCGAGCTCGGAAGGCTTTGGA
AATTTATCAGCATCAAGTGGTGGTGGCTAATATCCTTGAGTCACGACAGTCCTTTGTGTTTATTGTAACCAAAGA
CTCGGAACCAAGTTATTGCTATCAAGGAAGAAATAGAAAAAGGCGTAGAGATAGAAGAGAAGATAGTGGATAAT
CTTCAGTCTCGACACACAGCTTTTATAGGTGACAGAACTGAAGTAAAAAGCCCTTATAGGATTAAAAATTGTT
AGGGCTCTTAGAGATGGTGAAACTACAAAAAAACCATGGCTTTCATATGGACAGAGAAATGAAAGAAAGGGA
AAAGGCAGTGGTGTGTAGGCAAATATGGTTTGGCATTCTGCTTTTAAATGACACCTGATATGATGTCATTTTGATT
TTGAAATTGAACACTAGAACTGTTAATCACCTTTAAAAAGAAGAGCTTATTGGGAATTATATATCCTTAAATA
TACATGGGGGCCTGAATGTCAGCCATCTTTATACTATAGAAAAAGGATTATGGATGCATGAATGGTCATGCTTTG
GAGATCAAAATATTGGTTGAATGCCTATGTATGTCAGGCCCTGTGCTGAGCCATGAGGATTAAAAAGATGAATAAA
CATATCTTGTTTAGGAAATGGATGTATAAAAAAATCAAGTGCAATAAAGTGTGTGTCCAAAAGCTGACACAATGG
AAAGG

WO 2004/030615

PCT/US2003/028547

197/6881
FIGURE 184

MAEMDPVAEFPQPPGAARWAEVMARFAARLGAQGRRVVLVTSGGTKVPLEARPVRFLDNFSSGRRGATSAEAFLA
AGYGVLFLYRARSAPFPYHRFPQTWLSALRPSGPALSGLLSLEAEENALPGFAEALRSYQEAAAAGTFLAVEFT
TLADYLHLLQAAAQALNPLGPSAMFYLA AAVSDFYVPVSEMPEHKIQSSGGPLQITMKMVPKLLSPLVKDWAPKA
FIISFKLETDP AIVINRARKALEIYQHQQVVANILESRSQSFVFIIVTKDSETKLLLSRKK

WO 2004/030615

PCT/US2003/028547

198/6881
FIGURE 185

CGGGAGCGGAGAGCGGACCCAGAGAGCCCTGAGCAGCCCCACCGCCGCCGCCGGCCTAGTTACCATCACACCCC
GGGAGGAGCCGCAGCTGCCGCAGCCGGCCCCAGTCACCATCACCGCAACCATCGAGCAGCGAGGCCGAGACCCAGC
AGCCGCCCCGCCGCCCCCCCCCGCCGCCCCCGCCCTCAGCGCCGCCGACACCAAGCCCGGCACTACGGGCAGCGGGC
CAGGGAGCGGTGGCCCCGGGCGGCCTCACATCGGCGGCGCCTGCCGGCGGGGACAAGAAGGTCATCGCAACGAAGG
TTTTGGGAACAGTAAATGGTTCAATGTAAGGAACGGATATGGTTTCATCAACAGGAATGACACCAAGGAAGATG
TATTTGTACACCAGACTGCCATAAAGAAGAATAACCCAGGAAGTACCTTCGCAGTGTAGGAGATGGAGAGACTG
TGGAGTTTGATGTTGTTGAAGGAGAAAAGGTGCGGAGGCAGCAAATGTTACAGGTCCTGGTGGTGTTCAGTTC
AAGGCAGTAAATATGCAGCAGACCGTAACCATTATAGACGCTATCCACGTCGTAGGGGTCCTCCACGCAATTACC
AGCAAAATTACCAGAATAGTGAGAGTGGGGAAAAGAACGAGGGATCGGAGAGTGCTCCCGAAGGCCAGGCCAAC
AACGCCGGCCCTACCGCAGGCGAAGGTTCCACCTTACTACATGCGGAGACCCTATGGGCGTCGACCACAGTATT
CCAACCTCCTGTGCAGGGAGAAGTGATGGAGGGTGCTGACAACCAGGGTGCAAGGAGAACAAGGTAGACCAAGTGA
GGCAGAATATGTATCGGGGATATAGACCACGATTCCGCAGGGGCCCTCCTCGCCAAAGACAGCCTAGAGAGGACG
GCAATGAAGAAGATAAAGAAAATCAAGGAGATGAGACCAAGGTCAGCAGCCACCTCAACGTCGGTACCGCCGCA
ACTTCAATTACCGACGCAGACGCCCAGAAAACCCTAAACCACAAGATGGCAAAGAGACAAAAGCAGCCGATCCAC
CAGCTGAGAATTTCGTCCGCTCCCGAGGCTGAGCAGGGCGGGGCTGAGTAAATGCCGGCTTACCATCTCTACCATC
ATCCGGTTTAGTCATCCAACAAGAAGAAATATGAAATTCCAGCAATAAGAAATGAACAAAAGATTGGAGCTGAAG
ACCTAAAGTGCTTGCTTTTTGCCCCGTTGACCAGATAAATAGAACTATCTGCATTATCTATGCAGCATGGGGTTTT
TATTATTTTTACCTAAAGACGTCTCTTTTTGGTAATAACAAACGTGTTTTTTAAAAAAGCCTGGTTTTTCTCAAT
ACGCCTTTAAAGG

WO 2004/030615

PCT/US2003/028547

199/6881
FIGURE 186

MSSEAETQQPPAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVLGTVKWFNVRNGYGF I
NRNDTKEDVFVHQTAIKKNNPRKYLRVGDGETVEFDVVEGEKGAEAAANVTGPGGVPVQGSKYAADRNHYRRYP R
RRGPPRNYQQNYQNSESGEKNESGESAPEGQAQORRPYRRRRFPYIMRRPYGRRPQYSNPPVQGEVMEGADNQG
AGEQGRPVQRNMYRGYRPRFRRGPPRQRQPRREDGNEEDKENQGDDETQGGQPPQRRYRRNFNYRRRRPENPKPDG
KETKAADPPAENS SAPEAEQGGAE

WO 2004/030615

PCT/US2003/028547

200/6881
FIGURE 187

GGCGGGTGGCTGGCGGTTCCGTTAGGTCTGAGGGAGCGATGGCGGTACGCGCGTTGAAGCTGCTGACCACACTGC
TGGCTGTCTGTTGGCCGCTGCCTCCCAAGCCGAGGTTCGAGTCCGAGGCAGGATGGGGCATGGTGACGCCCTGATCTGC
TCTTCGCGCGAGGGGACCGCAGCCTACGCGCGCGGGGACTGGCCCCGGGGTGGTCCTGAGCATGGAACGGGCGCTGC
GCTCCCCGGGCAGCCCTCCGCGCCCTTCGCTGCGCTGCCGCACCCAGTGTGCCGCCGACTTCCCGTGGGAGCTGG
ACCCCGACTGGTCCCCAGCCCCGGCCAGGCCTCGGGCGCCGCCGCCCTGCCGACCTGAGCTTCTTCGGGGGCC
TTCTGCGTTCGCGCTGCCTGCCTGCCCGCTGCCTCGGGCGCCGCCGCCCTCGCTCAGCGAAGAGATGGAGC
TGGAGTTCCGCAAGCGGAGCCCCCTACAACCTACCTGCAGGTTCGCTACTTCAAGATCAACAAGTTGGAGAAAAGCTG
TTGCTGCAGCACACACCTTCTTCGTGGGCAATCCTGAGCACATGGAAATGCAGCAGAACCCTAGACTATTACCAAA
CCATGTCTGGAGTGAAGGAGGCCGACTTCAAGGATCTTGAGACTCAACCCCATATGCAAGAATTCGACTGGGAG
TGCAGCTCTACTCAGAGGAACAGCCACAGGAAGCTGTGCCCCACCTAGAGGCGGCGCTGCAAGAATACTTTGTGG
CCTATGAGGAGTGCCGTGCCCTCTGCGAAGGGCCCTATGACTACGATGGCTACAACCTACCTTGAGTACAACGCTG
ACCTCTTCCAGGCCATCAGATCATTACATCCAGGTCTCAACTGTAAGCAGAACTGTGTACGGGAGCTTGCTT
CCCACCCAAGTCGAGAGAAGCCCTTTGAAGACTTCTCCCATCGCATTATAATTATCTGCAGTTTGCCCTACTATA
ACATTGGGAATTATACACAGGCTGTTGAATGTGCCAAGACCTATCTTCTTCTTCCCCAATGACGAGGTGATGA
ACCAAAATTTGGCCTATTATGCAGCTATGCTTGGAGAAGAACACACCAGATCCATCGGCCCCCGTGAGAGTGCCA
AGGAGTACCGACAGCGAAGCCTACTGGAAAAAGAACTGCTTTTCTTCGCTTATGATGTTTTTGGAAATTCCTTTG
TGGATCCGGATTTCATGGACTCCAGAAGAAGTGATTCCCAAGAGATTGCAAGAGAAAACAGAAGTCAGAACGGGAAA
CAGCCGTACGCATCTCCCAGGAGATTGGGAACCTTATGAAGGAAATCGAGACCCCTTGTTGAAGAGAAGACCAAGG
AGTCACTGGATGTGAGCAGACTGACCCGGGAAGGTGGCCCCCTGCTGTATGAAGGCATCAGTCTCACCATGAACT
CCAACTCCTGAATGGTTCAGCGGGTGGTGATGGACGGCGTAATCTCTGACCACGAGTGTGAGGAGCTGCAGA
GACTGACCAATGTGGCAGCAACCTCAGGAGATGGCTACCGGGGTCAGACCTCCCCACATACTCCCAATGAAAAGT
TCTATGGTGTCACTGTCTTCAAAGCCCTCAAGCTGGGGCAAGAAAGTTCCTCTGCAGAGTGCCACCTGT
ACTACAACGTGACGGAGAAGGTGCGGCGCATCATGGAGTCTACTTCCGCTGGATACGCCCCCTCTACTTTTCT
ACTCTCATCTGGTGTGCCGCACTGCCATCGAAGAGGTCCAGGCAGAGAGGAAGGATGATAGTCATCCAGTCCACG
TGGACAACTGCATCCTGAATGCCGAGACCCCTCGTGTGTGTCAAAGAGCCCCCAGCCTACACCTTCCGCGACTACA
GCGCCATCCTTTACCTAAATGGGGACTTCGATGGCGGAACTTTTATTTCACTGAACTGGATGCCAAGACCGTGA
CGGCAGAGGTGCAGCCTCAGTGTGGAAGAGCCGTGGGATTCTCTTCAGGCACTGAAAACCCACATGGAGTGAAGG
CTGTCACCAGGGGGCAGCGCTGTGCCATCGCCCTGTGGTTCACCCTGGACCCCTCGACACAGCGAGCGGGTGAGAG
CAGCTCGAGCGGGTGAGAGCAGCTGGTGTGTGGTGACCCGTTCCAGAGCGCCCTTGCTTTGCCCTTTCTCTTCC
CCAAATCCCATTGCCAGTGGCTGAGACACGAAAGGAGCACTTGGGACACCAGCTCCAACGCCCTGTCAATTATGGT
CACATTGCCCTTGTCTCCCTGGGCCTGCTGTGAACGGGATCCAGGTGGGGAAGAGGTCAAGACAGGGAGCGATG
CTGAGTTCTTGGTTCCCTCCTTGGGCCCCACTTCAGCTGTCTTTTCCAGAGAGTAGGACCTGCTGGGAAGGAGA
TGAGCCTGGGGCCATTAAAGGAACCTTCCTTGTCCCTGGGAAGTAGCAGCTGAGAGATAGCGAGTGTCTGGAGCG
GAGGCCTCTCTGAATGGGCAGGGGTTTGTCTTGCAGGACAGGGTGACGGCAGATGACCTGGTGAAGATGCTCTT
CAGCCCAGAAGAGATGGACCTCTCCAGGAGCAGCCCTGGATGCCAGCAGGGTCCCCCGAACCTGCACAAGA
GTCTCTCTCAGGCAGTGAATCGAAGCCCAAGGATGAGCTATGACAGCGTCCAGGTGAGACGGATGGGTGACTAGA
CCCATGGAGAGGAACCTTCTGCACTCTGAGCTGGCCAGCCCTCGGGGCTGCAGAGCAGTGAGCCTACATCTGC
CACTCAGCCGAGGGGACCCCTGCTCACAGCCTTCTACATGGTGTCTACTGCTCTTGGAGTGGACATGACCAGACACC
GCACCCCTGGATCTGGCTGAGGGCTCAGGACACAGGCCAGCCACCCCGAGGGGCTCCACAGGCCGCTGCATG
ACAGCGATACAGTACTTAAGTGTCTGTGTAGACAACCAAGAATAAATGATTTCATGGTTTTTTTTT

WO 2004/030615

PCT/US2003/028547

201/6881
FIGURE 188

TAGTCGCGGGTCCCCGAGTGAGCACGCCAGGGAGCAGGAGACCAACGACGGGGGTGCGAGTCAGAGTCGCAGTG
GGAGTCCCCGGACCGGAGCACGAGCCTGAGCGGGAGAGCGCCGCTCGCACGCCCGTCGCCACCCGCTACCCGGC
GCAGCCAGAGCCACCAGCGCAGCGCTGCCATGGAGCCAGCAGCAAGAAGCTGACGGGTGCGCTCATGCTGGCTG
TGGGAGGAGCAGTGCTTGGCTCCCTGCAGTTTGGCTACAACACTGGAGTCATCAATGCCCCCAGAAGGTGATCG
AGGAGTTCTACAACCAGACATGGGTCCACCGCTATGGGGAGAGCATCCTGCCACCACGCTCACCACGCTCTGGT
CCCTCTCAGTGGCCATCTTTTCTGTTGGGGCATGATTGGCTCCTTCTCTGTGGGCCCTTTTCGTTAACCGCTTTG
GCCGGCGGAATTCAATGCTGATGATGAACCTGCTGGCCTTCGTGTCCGCCGTGCTCATGGGCTTCTCGAAACTGG
GCAAGTCCTTTGAGATGCTGATCCTGGGCCGCTTCATCATCGGTGTGTACTGCGGCCGTGACCACAGGCTTCGTGC
CCATGTATGTGGGTGAAGTGTACCCACAGCCTTTTCGTGGGGCCCTGGGCACCCTGCACCAGCTGGGCATCGTCG
TCGGCATCCTCATCGCCAGGTGTTGGCCCTGGACTCCATCATGGGCAACAAGGACCTGTGGCCCCCTGCTGCTGA
GCATCATCTTCATCCCGGCCCTGCTGCAGTGATCGTGTGCCCTTCTGCCCGAGAGTCCCCGCTTCTCTGCTCA
TCAACCGCAACGAGGAGAACC GGCCAAAGAGTGTCTAAAGAAGCTGCGCGGGACAGCTGACGTGACCCATGACC
TGCAGAGATGAAGGAAGAGATCGGCAGATGATGCGGGAGAAGAAGGTCACCATCCTGGAGCTGTTCCGCTCCC
CCGCCTACCGCCAGCCCATCCTCATCGCTGTGGTGTGTCAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCT
TCTATTACTCCACAGCATCTTCGAGAAGCGGGGGTGTCAGCAGCCTGTGTATGCCACCATTTGGCTCCGGTATCG
TCAACACGGCCTTCACTGTCTGTCTGCTGTTTGTGGTGGAGCGAGCAGGCCGGCGGACCCCTGCACCTCATAGGCC
TCGCTGGCATGGCGGGTGTGCCATACTCATGACCATCGCGCTAGCACTGCTGGAGCAGCTACCCCTGGATGTCTCT
ATCTGAGCATCGTGGCCATCTTTGGCTTTTGTGGCCTTCTTTGAAGTGGGTCTCTGGCCCCATCCCATTGGTTTCATCG
TGGCTGAACTCTTCAGCCAGGGTCCACGTCCAGCTGCCATTTGCCGTTGCAGGCTTCTCCAAGCTGGACCTCAAAAT
TCATTGTGGGCATGTGCTTCCAGTATGTGGAGCAACTGTGTGGTCCCTACGTCTTCATCATCTTCACTGTGCTCC
TGTTTCIGTTCTTCATCTTCACCTACTTCAAAGTTCCTGAGACTAAAGGCCGACCTTCGATGAGATCGCTTCCG
GCTTCCGGCAGGGGGGAGCCAGCCAAAGTGATAAGACACCCGAGGAGCTGTTCCATCCCCTGGGGGCTGATTCCC
AAGTGTGAGTCGCCCCAGATCACCAGCCCGCCTGCTCCAGCAGCCCTAAGGATCTCTCAGGAGCACAGGCAGC
TGGATGAGACTTCCAAACCTGACAGATGTCAGCCGAGCCGGGCTGGGGCTCCTTTCTCCAGCCAGCAATGATGT
CCAGAAGAATATTCAGGACTTAACGGCTCCAGGATTTTAACAAAAGCAAGACTGTTGCTCAAATCTATTTCAGACA
AGCAACAGGTTTTATAAATTTTTTTATTACTGATTTTGTATTTTTATATCAGCCTGAGTCTCCTGTGCCACATC
CCAGGCTTCACCCTGAATGGTTCCATGCCTGAGGGTGGAGACTAAGCCCTGTGAGACACTTGCCCTTCTTCACCC
AGCTAATCTGTAGGGCTGGACCTATGTCTAAGGACACACTAATCGAACTATGAACACAAAGCTTCTATCCCAG
GAGGTGGCTATGGCCACCCGTTCTGCTGGCCTGATCTCCCCACTCTAGGGGTGAGGCTCCATTAGGATTTGCCC
CTTCCCATCTCTTCTACCCAACCACTCAAATTAATCTTTCTTTACCTGAGACCAGTTGGGAGCACTGGAGTGCA
GGGAGGAGAGGGGAAGGGCCAGTCTGGGCTGCCGGGTTCTAGTCTCCTTTGCACTGAGGGCCACACTATTACCAT
GAGAAGAGGGCCTGTGGGAGCCTGCAAACTCACTGCTCAAGAAGACATGGAGACTCCTGCCCTGTTGTGTATAGA
TGCAAGATATTTATATATATTTTTGGTTGTCAATATTAAATACAGACACTAAGTTATAGTATATCTGGACAAGCC
AACTTGTAATAACACCACCTCACTCCTGTTACTTACCTAAACAGATATAAATGGCTGGTTTTTAGAAACATGGTT
TTGAAATGCTTGTGGATTGAGGGTAGGAGGTTTGGATGGGAGTGAGACAGAAGTAAGTGGGGTTGCAACCACTGC
AACGGCTTAGACTTCGACTCAGGATCCAGTCCCTTACACGTACCTCTCATCAGTGTCTCTTGCTCAAAAATCTG
TTTGATCCCTGTTACCCAGAGAATATATACATTCTTTATCTTGACATTCAAGGCATTTCTATCACATATTTGATA
GTTGGTGTTCAAAAAACACTAGTTTTGTGCCAGCCGTGATGCTCAGGCTTGAAATCGCATTATTTTGAATGTGA
AGGGAA

WO 2004/030615

PCT/US2003/028547

202/6881
FIGURE 189

MEPSSKKLTGRLMLAVGGAVLGSLQFGYNTGVINAPQKVIEEFYNQTWVHRYGESILPTTLTTLWSLSVAIFSVG
GMIGSFVGLFVNRFGRNSMLMMNLLAFVSAVLMGF SKLGKSFEMLIIGRFIIGVYCGLTTGFVPMYVGEVSPT
AFRGALGTLHQLGIVVGILIAQVFGLD SIMGNKDLWPLLSIIFIPALLQCIVLPFCPESPRFLLINRNEENRAK
SVLKKLRGTADVTHDLQEMKEESRQMMREKKVTILELFRSPAYRQPILIAVVLQLSQQLSGINAVFYSTSI FEK
AGVQQPVYATIGSGIVNTAFTVVS L FVVERAGRRTLHLIGLAGMAGCAILMTIALALLEQLPWMSYLSIVAIFGF
VAFFEVGPGPIPWFI VAELFSQGPRPAALAVAGFSNWT SNFIVGMCFQYVEQLCGPYVFIIFTVLLVLFFIFTYF
KVPETKGRTFDEIASGFRQGGASQSDKTPEELFHPLGADSQV

WO 2004/030615

PCT/US2003/028547

203/6881
FIGURE 190

CACGTCGTTTCACGGCCTTCTTCGGCCCCCTCTAGCACGACATTGAGGCCTGGCTTCAGAAGCCCTCGGGAAAACGC
ATCCTGCAACTCTCTGTCTGTGACAAGGGATTTCATCGGATTCCGACTCCGAATCCGAGAGCGGGGAGTGTCCAT
CTCGCCGCACGCACGTCCACACAGCTACTGCTCAACTTTTGATTGGGACTTCCGCTTCCGGCGGCAAAACCATAC
TTCCGGTTTGTCTGTTGCTATAGGAACCGCTACGGCGTTTGAAAGTGTCGGGTGCTTAGGATCCCTACAGGTAG
CGCCTCTGGATACATGCGTGGTCTGCTGACCCAGAGAGAAAACGAAAGCAGAAGTGTTCGGCGGAGATCATGTCA
GCCGTGGTAGCTCAGACGCTGCATGTTTTTGGTCTTCGATCCACGTGGCCAACAATATCTTCTACTTCGATGAA
CAGATCATTATATTTTCTTCAGGAAATCACTGTGTGAAGTACAATGTGGATCAGAAATGGCAAAAATTCATTCCA
GGCTCAGAGAAGAGTCAGGGCATGTTGGCCTTGTCCATCAGTCCCAATCGGCGGTACCTCGCTATCTCTGAGACT
GTGCAAGAAAAACCTGCCATCACCATTTATGAATTGTCTATCCATCCCTTGCCGGAAGCGCAAGTTCTTAATAAT
TTTGACTTCCAAGTTCAGAAATTTATTAGCATGGCTTTTTCTCCAGACTCCAAATACCTATTGGCTCAGACGTCA
CCTCCAGAGTCAAATCTTGTCTACTGGCTGTGGGAAAAACAGAAAGTAATGGCCATTGTTAGAATCGACACTCAG
AACAACCTGTCTACCAGGTGAGCTTCAGTCCACAGGATAACACTCAGGTGTGTGTCTACTGGAATGGGATGTTT
AAGCTTCTCCGTTTTGCTGAGGGAACCCCTGAAGCAAACCAGCTTTCAGAGGGGAGAACCCCAAACTATCTAGCC
CACACCTGGGTGGCTGATGACAAGATTGTCGTTGGCACTGACACAGGCAAACCTTCTCTTTGAATCTGGAGAT
CAGCGTTGGGAGACCAGCATAATGGTCAAGGAACCTACCGATGGCTCAAAGAGCCTGGATGTCATTACAGGAATCA
GAGAGCCTGATTGAATTTCCACCAGTCAGTTCTCCACTCCCTTCCATGAACAGATGGTGGCGGCCAGTAGCCAT
AGCCAGATGTCCATGCCCCAGGTGTTTGCCATTGCAGCCTATTCAAAGGGATTGCGCTGTTCTGCTGGGCCAGGG
AGAGTTCTGCTGTTTGAGAAGATGGAAGAAAAGGATTTTACCCTGAGAGCAGAGAAATCAGGATTCTGTGGAC
CCGCAGAGCAATGATCCAAGTCAGTCTGACAAACAGGACGTTCTCTGCGCTGTGCTTCAGCCCCCTCAGAGGAAACT
CTGGTTGCCAGCACCAGTAAGAACCAACTCTACAGCATCACCATGTCCCTGACAGAGATCAGCAAGGGAGCCTGC
TCACTTTGAGTATTTGATGTATCCATTGCACTCAGCACCCATCACCAGGTCTAGCTACCTGCATCCGCAAAACCCCT
TATAGCCACCTGTTCTCTGGATCGATCCATCCGCTTTTGAATTTATGAAACAAACACCCCTGGAACTATTTAAGGA
ATACCAAGAAGAGGCATATTCCATCAGCCTTCATCCATCTGGACACTTCATTGTAGTAGGGTTTGCTGACAACT
ACGCCTCATGAATCTACTCATTGATGATATACGTTCTTTCAAAGAATACTCTGTTAGAGGATGCGGAGAGTGTTT
CTTTAGCAATGGAGGTCACCTGTTTGCTGCAGTCAATGGAATGTGATTACGTTTACACCACCACGAGCCTAGA
GAACATCTCAAGCCTGAAAGGACACACAGGGAAGATTGCTCAATTGTGTGGAATGCAGATGATAGCAAACTGAT
TTCTGGTGGCACAGATGGTGTGTGTATGAATGGAATCTGTCCACAGGAAAGAGAGAGACAGAATGCGTGCTCAA
GTCTTGACGCTACAACTGTGTTACTGTCTCCCCGATGCCAAAATATCTTTGCTGTTGGATCAGACCACACCCT
CAAGGAGATTGCAGATTCTTGCCTTCGAGAGATATCGGCGTTTGATGTCACCTACACCGCCATTGTCATCTCGC
ATTCTGGACGCATGATGTTTGTGGGCACCTCGGTGGGAACCATTCGTGCCATGAAGTACCCTCTGCCTCTGCAGA
AGGAATTCAATGAGTACCAGGCCCATGCCGGTCTATCACCAAGGTGAGCAGGGCCCTCTCCCCAGGAACCCAGT
CCCACACCTGCCTGCTACGTGCCCTTGTTTCATCCCTTCAACCTCCCAATGTCTTTTCTCTCTCTCTCTCTCTT
ATTTATTCATCCATCATTGATTGAATCACCATCTATTGACTATGAATATACTCTTTGTTTAACTACTTCCAGGA
ATTTAGCCTAGGAAATCATCAGAGATACACCTAAAAATGTATGTACAACGTTTTTACCATAATATTATGCATAAT
AAGGGGCCGTTTGGTGGATGCCGTAGCTGCCGTGAGTGTGGGCTGCACCTGACCACAGCTGCCTCCTCCTCCAGA
GAATGCCCCAGACTGAAAGGAGCCATAGCCCTGAAGATTGGCCCCCTACCTCTCCCTGAGGGTACAAAAGGCCACC
CCAGGGGCAATACCATGAGTACACATTTGTAATTTGTCTTCCATTACCCCTTCTCATAAAGTAGTATCTATGTT
CAACAGTCAAAATGTGGAAGCAACCAAGCATCCATCGACAGACGAATGCATAAGCAAAAGATGGTATATCTATAC
AATGGAACAATACCCTGCCTAAAAAGGAAGGGAATTCTGCAATGTGCTACACATGGATGAACCTTGAGGATGTT
ATGCTAAATTAATAAGGCCAACCAAAAAAGATAAGTACAGTGTGATTCCACTTTTAGGAGATACTTGGAGCAG
TCAGAATCACAAGACAGAGTGGTGGTTGGCAGGGGCTGCAGGAAGGGGGAATGAGGAATGATTGTTTCATAGGT
ATAGAGTTTTGTTTTACAAGACAAAAGGATTATGGGGGTAGTTGGTGGCAATGGCTGCACAACATTACAAATGT
ATTTAATAACATGAACCTGTACACTTGAAAAATGGTTAAGATAGCAAATTTTACAGAATATGTATTTTACGACAATT
TAAAAATGAAATAAAAAAGAATTATCTTGC

WO 2004/030615

PCT/US2003/028547

204/6881
FIGURE 191

MSAVVAQTLHVFLRSHVANNIFYFDEQIIIFPSGNHCVKYNVDQKWQKFIPGSEKSQGMLALSISPNNRYLAIS
ETVQEKPAITIIYELSSIPCRKRKVLNNFDFQVQKFISMAFSPDSKYLLAQTSPPESNLVYWLWEKQKVMAIVRID
TQNNFVYQVSFSPQDNTQVCVTGNGMFKLLRFAEGTLKQTSFQRGEPQNYLAHTWVADDKIVVGTDGTGKFLFES
GDQRWETSIMVKEPTNGSKSLDVIQESSESLIEFPPVSSPLPSYEQMVAASSHSQMSMPQVFAIAAYS KGFAC SAG
PGRVLLFEKMEEKDFYRESREIRIPVDPQSNDPSQSDKQDVLCLCFSPSEETLVASTSKNQLYSITMSLTEISKG
EPAHFEYLMYPLHSAPITGLATCIRKPLIATCSLDRSIRLWNYETNTLELFKEYQEEAYSSISLHPSGHFIVVGFA
DKLRLMNLIDDIRSFKEYSVRGCGECSFSNGGHLFAAVNGNVIHVYTTTSLENISSLKGHTGKSLNCVECR

WO 2004/030615

PCT/US2003/028547

205/6881
FIGURE 192

GCGATTTCGGTGGCACGTGGAGCCACGGCGTGGGAGTAGGGGGCTGAAGGCAGGCAGCAGCGGCCAGGGCCGCCCT
CTGCTAGCCGCTTGGGTCTCGGGATACCCGTTTCTTCCCTGTAGGTGTGGGACGTGCGTGCGGCAGATGGACAC
-TCCCCCGCTCTCGGATTTCGGAGTCGGAATCCGATGAATCCCTTGTACAGACAGAGAGTTGCAGGATGCGTTTTTC
CCGAGGGCTTCTGAAGCCAGGCCTCAATGTCGTGCTAGAGGGGCCGAAGAAGGCCGTGAACGACGTGAATGGCCT
GAAGCAATGTTTGGCAGAATTCAAGCGGGATCTGGAATGGGTTGAAAGGCTCGATGTGACACTGGGTCCGGTACC
GGAGATCGGTGGATCTGAGGCGCCAGCACCTCAGAACAAGGACCAGAAAGCTGTTGATCCAGAAGACGACTTCCA
GCGAGAGATGAGTTTTCTATCGCCAAGCCCAGGCCGCGAGTGCTTGCACTTACCCCGCCTCCATCAGCTCAAAGT
CCCTACGAAGCGACCCACTGATTATTTTGCAGAAATGGCCAAATCTGATCTGCAGGTGCAGAAGATTCGACAGAA
GCTGCAGACTAAACAGGCTGCCATGGAGAGGTCTGAAAAAGCTAAGCAACTGCGAGCACTTAGGAAATACGGGAA
GAAGGTGCAAACGGAGGTTCTTCAGAAGAGGCAGCAGGAGAAAGCCCATATGATGAATGCTATTAAGAAATATCA
GAAAGGCTTCTCTGATAAACTGGATTTCTTGAGGGAGATCAGAAACCTCTGGCACAGCGCAAGAAGGCAGGAGC
CAAAGGCCAGCAGATGAGGAAGGGGCCAGTGCTAAACGACGGTATAAAAAACCAGAAGTTTGGTTTTGGTGGAAA
GAAGAAAGGCTCAAAGTGGAACACTCGGGAGAGCTATGATGATGTATCTAGCTTCCGGGCCAAGACAGCTCATGG
CAGAGGCCTCAAGAGGCCTGGCAAGAAAGGGTCAAATAAGAGACCTGGAAAACGAACAAGAGAGAAGATGAAGAA
CAGAACACACTAAATAGCATCTTTGAATACAAAGAACCAAGAAAAAGGAATGAAGACTCGCAATTTACGACACA
CTTTGATCCCTTCTGTTGGTGTGATGTTGTAAACATTTCTTTCAATAAACTAAAGAAAAATTATTAAAGGAACAC
ATACCTTTGGTTAAATAGTCTAGACTAAAAGATTGAGAAGTTACTTTCCATTGCTATCTATTGATAATTTAGACA
TTGAGTTCAAATTGCCTTCATTTTATGATAAATAATGATTTAACTGAAAA

WO 2004/030615

PCT/US2003/028547

206/6881
FIGURE 193

MDTPPLSDSESESDSLVTDRELQDAFSRGLLKPGLNVVLEGPKKAVNDVNGLKQCLAEFKRDLEWVERLDVTLG
PVPEIGGSEAPAPQNKDQKAVDPEDDFQREMSFYRQAQAAVLAVLPRLHQLKVPTKRPTDYFAEMAKSDLQVQKI
RQKLQTKQAAMERSEKAKQLRALRKYGKKVQTEVLQKRQKEAHMMNAIKKYQKGFSDKLDLFLEGDQKPLAQRKK
AGAKGQQMRKGPSAKRRYKNQKFGFGGKKKGSKWNTRESYDDVSSFRAKTAHGRGLKRPGKKGSNKRPGKRTREK
MKNRTH

WO 2004/030615

PCT/US2003/028547

207/6881
FIGURE 194

CCACGCGTCCGGGCGTAAGCCAGGCGTGTTAAAGCCGGTCGGAAGTCTCCGGAGGGCACGGGGCTCCGTAGGCAC
CAACTGCAAGGACCCCTCCCCCTGCGGGCGCTCCCATGGCACAGTTTCGCGTTTCGAGAGTGACCTGCACTCGCTGC
TTCAGCTGGATGCACCCATCCCCAATGCACCCCTGCGCGCTGGCAGCGCAAAGCCAAGGAAGCCGAGGCCCGG
CCCCCTCACCCATGCGGGCCGCCAACCGATCCCACAGCGCCGGCAGGACTCCGGGCCGAACCTCTGGCAAATCCA
GTTCCAAGGTTTACAGACCACTCCTAGCAAACCTGGCGGTGACCGCTATATCCCCCATCGCAGTGCTGCCCAGATGG
AGGTGGCCAGCTTCTCTCTGAGCAAGGAGAACCAGTCTGAAAAACAGCCAGACGCCCCACCAAGAAGGAACATCAGA
AAGCCTGGGCTTTGAACCTGAACGGTTTTTGATGTAGAGGAAGCCAAGATCCTTCGGCTCAGTGGAACCAACAAA
ATGCGCCAGAGGGTTATCAGAACAGACTGAAAGTACTCTACAGCCAAAAGGCCACTCCTGGCTCCAGCCGGAAGA
CCTGCCGTTACATTCTTCCCTGCCAGACCGTATCCTGGATGCGCCTGAAATCCGAAATGACTATTACCTGAACC
TTGTGGATTGGAGTTCTGGGAATGTACTGGCCGTGGCACTGGACAACAGTGTGTACCTGTGGAGTGCAAGCTCTG
GTGACATCCTGCAGCTTTTGCAAATGGAGCAGCCTGGGGAATATATATCCTCTGTGGCCTGGATCAAAGAGGGCA
ACTACTTGGCTGTGGGCACCAGCAGTGCTGAGGTGCAGCTATGGGATGTGCAGCAGCAGAAACGGCTTCGAAATA
TGACCAGTCACTCTGCCCCAGTGGGCTCCCTAAGCTGGAACAGCTATATCCTGTCCAGTGGTTACGTTCTGGCC
ACATCCACCACCATGATGTTTCGGGTAGCAGAACACCATGTGGCCACACTGAGTGGCCACAGCCAGGAAGTGTGTG
GGCTGCGCTGGGCCCCAGATGGACGACATTTGGCCAGTGGTGGTAATGATAACTTGGTCAATGTGTGGCCTAGTG
CTCCTGGAGAGGGTGGCTGGGTTCTCTGCAGACATTCACCCAGCATCAAGGGGCTGTCAAGGCCGTAGCATGGT
GTCCCTGGCAGTCCAATGTCTGGCAACAGGAGGGGGCACCAGTGATCGACACATTTCGCATCTGGAATGTGTGCT
CTGGGGCCTGTCTGAGTGCCGTGGATGCCCATTCCCAGGTGTGCTCCATCCTCTGGTCTCCCCATTACAAGGAGC
TCATCTCAGGCCATGGCTTTGCACAGAACCAGCTAGTTATTTGGAAGTACCCAACCATGGCCAAGGTGGCTGAAC
TCAAAGGTCACACATCCCGGGTCTGAGTCTGACCATGAGCCCAGATGGGGCCACAGTGGCATCCGCAGCAGCAG
ATGAGACCCTGAGGCTATGGCGCTGTTTTGAGTTGGACCCTGCGCGGCGGGGAGCGGGAGAAGGCCAGTGCAG
CCAAAAGCAGCCTCATCCACCAAGGCATCCGCTGAAGACCAACCCATCACCTCAGTTGTTTTTTATTTTTCTAAT
AAAGTCATGTCTCCCTTCATGTTTTTTTTTTTTAAAA

WO 2004/030615

PCT/US2003/028547

208/6881
FIGURE 195

MAQFAFESDLHSLQLDAPIPNAPPARWQRKAKEAAGPAPSPMRAANRSHSAGRTPGRTPGKSSSKVQTTPSKPG
GDRYIPHRSAQMEVASFLLSKENQSENSQTPTKKEHQKAWALNLNGFDVEEAKILRLSGKPQNAPEGYQNRLKV
LYSQKATPGSSRKTCRYIPSLPDRILDAPDIRNDYYLNLVDWSSGNVLAVALDNSVYLWSASSGDILQLLQMEQP
GEYISSVAWIKEGNYLAVGTSSAEVQLWDVQQKRLRNMTSHSARVGSLWNSYILSSGSRSGHIHHHDVRVAEH
HVATLSGHSQEVCGLRWAPDGRHLASGGNDNLVNVWPSAPGEGGWVPLQFTQHQGAVKAVAWCPWQSNVLTGG
GTSDRHIRIWNVCSGACLSAVDAHSQVCSILWSPHYKELISGHGFAQNQLVIWKYPTMAKVAELKGHTSRVLSLT
MSPDGATVASAAADETLRLWRCFELDPARRREREKASAAKSSLIHQIR

WO 2004/030615

PCT/US2003/028547

209/6881
FIGURE 196

GGCACGAGGGGAACCGTCCGCAGCCGCCGGAGCCGGGAGCCCTGCCCAAGTCGGAGCGGCGTCCCCTGCTGAGCCC
CGAGCGCCGGGCCAGCAGCCGGATGCCCCGGGCCACTGGGCGGGCCAGTGGCCGCCTGCGGGATGAGCAGACTGC
TGGGGGGGACGCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCCTCGTGGCCGTCATCC
TCTACTTTGACGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGGCCGAGGCCCCTGCCATGCCCTCC
ACCCAGCTGCTAGCAGCAGCAGCAGCAGCAACTGCTCCCGGCCAACGCCACCGCCTCTAGCTCCGGGCTCC
CTGAGGTCCCCAGTGGCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCTGACTCGCCACCTGGTCTTG
CGGGTGCACAGGGAGAACCCAGGCGTGCTCATGGGCGGCCGATACACACCGCCCGACTGCACCCCAGCCCAGACG
GTGGCGGTTCATCATCCCCCTTTAGACACCGGGAACACCACCTGCGCTACTGGCTCCACTATCTACACCCCATCTTG
AGGCGGCAGCGGCTGCGCTACGGCGTCTATGTATCAACCAGCATGGTGAGGACACCTTCAACCGGGCCAAGCTG
CTTAACGTGGGCTTCCCTAGAGGCGCTGAAGGAGGATGCCGCCTATGACTGCTTCATCTTCAGCGATGTGGACCTG
GTCCCCATGGATGACCGCAACCTATACCGCTGCGGCGACCAACCCCGCCACTTTGCCATTGCCATGGACAAGTTT
GGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTACGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAAT
GGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGATGACATCTTCAACCGGATCTCCCTGACTGGGATG
AAGATCTCACGCCCAGACATCCGAATTGGCCGCTACCGCATGATCAAGCACGACCGCGACAAGCATAACGAACCT
AACCCCTCAGAGGTTTACCAAGATTCAAAACACGAAGCTGACCATGAAGCGGGACGGCATTGGGTGAGTGCAGGTAC
CAGGTCTTGGAGGTGTCTCGGCAACCACTCTTACCAATATCACAGTGGACATTGGGCGGCCTCCGTCTGAGGCCC
CCTCGGGGCTGACACTAATGGACAGAGGCTCTCGGTGCCGAAGATTGCCTGCCAGAGGACTGACCACAGCCTGGC
TGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGGCTCTGTTTTCCAAGGCTCTTCACTAGGCCCCCTA
GCTACACCTGGAAGTTTTCAGAACCACTTTGGGGGGCCTCCTGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTT
GGAGTCAACCCCTCCTTCCCCGACCCCTCCCCCTAGCCAGCCCCAGTCACTGTCAGGGTCGGGCCAGCCCTGCA
CTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTCTGTGCCTCAGTTTCCCCCCTTGAGTCCCCTAGG
GCCTGGAAGGGTGGGAGGTATGTCTAGGGGGCAGTGTCTCTTCCAGGGGGAATTCTCAGCTCTTGGGAACCCCT
TGCTCCCAGGGGAGGGGAAACCTTTTTTCAATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCTGCTGAGGAG
CAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTGCTGCCTGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCA
GGTGGGGCTTGGATCAGTAAGTCTGGTTCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTT
GTGTTTGTACATTGCACAGAACTTGTGTGGGTGCTTTAGTAAAAAACGTGAATGGAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

210/6881
FIGURE 197

MSRLGGTTLERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHFAASSSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPDPPGLAGAQGEPRRAHGRPIHTARLHPSPDGGGHHPL

WO 2004/030615

PCT/US2003/028547

211/6881
FIGURE 198

CCCAGTGCCCTGCCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCCTGACTCGCCACCTGGTCTTGTGGGCAGA
CTGCTGATCGAGTTCACCTCACCCATGCCCCCTGGAGCGGGTGTCAGAGGGCCTGGAAGGGTGGGAGGTATGTCTAG
GGGGCAGTGTCTCTTCCAGGGGGAATTCTCAGCTCTTGGGAACCCCTTGCTCCCAGGGGAGGGGAAACCTTTTT
CATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGAT
GCTGTGTCGCTGCCCTGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGGATCAGTAAGTCTGGT
TCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTTGTACATTGCACAGAACTTGT
GTGGGTGCTTTAGTAAAAAACGTGAATGG

WO 2004/030615

PCT/US2003/028547

212/6881
FIGURE 199

GCCAGCAGCCGGATGCCCCGGGCCCCACTGGGCGGGCCAGTGGCCGCCTGCGGGATGAGCAGACTGCTGGGGGGGAC
GCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCTCGTGGCCGTCATCCTCTACTTTGA
CGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGGCCGAGGCCCTGCCCATGCCCTCCACCCAGCTGC
TAGCAGCAGCAGCAGCAGCAGCAACTGCTCCCGGGCCCAACGCCACCGCCTCTAGCTCCGGGCTCCCTGAGGTCCC
CAGTGGCCTGCCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCTGACTCGCCACCTGGTCTTGTGGGCAGACT
GCTGATCGAGTTACCTCACCCATGCCCTGGAGCGGGTGAGAGGGAGAACCAGGCGTGCTCATGGCGGCCG
ATACACACCGCCCGACTGCACCCAGCCAGACGGTGGCGGTTCATCATCCCTTTAGACACCGGGAACACCACCT
GCGCTACTGGCTCCACTATCTACACCCATCTTGAGGCGGCAGCGGCTGCGCTACGGCGTCTATGTCATCAACCA
GCATGGTGAGGACACCTTCAACCGGGCCAAGCTGCTTAACGTGGGCTTCCTAGAGGCGCTGAAGGAGGATGCCGC
CTATGACTGCTTCATCTTCAGCGATGTGGACCTGGTCCCCATGGATGACCGCAACCTATACCGCTGCGGCGACCA
ACCCCGCCACTTTGCCATTGCCATGGACAAGTTTGGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTC
AGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAATGGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGA
TGACATCTTCAACCGGATCTCCCTGACTGGGATGAAGATCTCACGCCAGACATCCGAATCGGGCCGCTACCGCAT
GATCAAGCAGCAGCCGCGACAAGCATAACGAACCTAACCTCAGAGGTTTACCAAGATTCAAAAACAGGAAGCTGAC
CATGAAGCGGGACGGCATTGGGTGAGTGCAGGTACCAGGTCTTGAGAGGTGTCTCGGCAACCACTCTTACCAATAT
CACAGTGGACATTGGGCGGCCTCCGTCTGCGCCCCCTCGGGGCTGACACTAATGGACAGAGGCTCTCGGTGCCGA
AGATTGCCTGCCAGAGGACTGACCACAGCCTGGCTGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGG
CTCTGTTTTTCAAGGGTCTTCACTAGGCCCCCTAGCTACACCTGGAAGTTTCAAGACCCACTTTGGGGGGCCTCC
TGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTTGGAGTCAACCTCCTTCCCGACCCCCCTCCCCCTAGCCCAGC
CCCAGTCACTGTGAGGGTCGGGCGCAGCCCCCTGCACTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTC
TGTGCCTCAGTTTCCCCCCTTGAGTCCCTAGGGCCTGGAAGGGTGGGAGGTATGTCTAGGGGGCAGTGTCTCT
TCCAGGGGGAATTCTCAGCTCTTGGAACCCCTTGCTCCAGGGGAGGGGAAACCTTTTTTCATTCAACATTGTA
GGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTGCTGCC
TGGGAICTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGATCAGTAAGTCTGGTTCCCGCCTCCCTGT
CTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTGTACATTGCACAGAACTTGTGTGGGTGCTTTAGT
AAAAACGTGAATGG

WO 2004/030615

PCT/US2003/028547

213/6881
FIGURE 200

MSRLLGGTLERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHPAASSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPCCPDSPPGLVGRLLIEFTSPMPLERVQRENPGVLMGGRYTPPDCTPAQTVAVIIP
FRHREHHLRYWLHYLHPILRRQRLRYGVYVINQHGEDTFNRAKLLNVGFLEALKEDAAYDCFIFSDVDLVPMDDR
NLYRCGDQPRHFAIAMDKFGFRLPYAGYFGGVSGLSKAQFLRINGFPNEYWGWGGEDDDIFNRISLTGMKISRPD
IRIGRYRMIKHDRDKHNEPNPQRFTKIQNTKLTMKRDGIGSVRYQVLEVSRQPLFTNITVDIGRPPSWPPRG

WO 2004/030615

PCT/US2003/028547

214/6881
FIGURE 201

GCGGAGAAACAGTAGTTAGGATGGCTGAAGGGGATACTCACCGGCTGAAGGCCGACTGTGATTCCCCCTACCCCC
ACAAGGCGATTTTACCCCCCTGAGGGGCTGCTCTAGAGGACTCAGGCCCCGAAGCTGTCCAGGGAGGTCCCCGCT
GCATCCCACCACCCAAGCTGTGCCTCATGGAGTCGATGTTTAGCAGCCCTGCCGAGCGGGCGCTGCAGCGAGAGA
CCGGGGTGCCAGGACTGCTTACTCCTCTTCCGGACCTGGACGGAGTGTACGAGCTGGAGCGAGTCGCTGGATTG
TCCGCGACCTGGGGTGTGAACGAGTTGCCTTGCACTTCCCTGACCAGCTATTGGGAGATGCTGTGGCTGTGGCTG
CACGACTGGAGGAGACGACAGGGTCAAAGATGTTTCATTCTGGGTGACACAGCCTACGGCAGCTGCTGCGTGGATG
TGCTGGGTGCTGAGCAAGCTGGAGCTCAGGCTCTCATACATTTTGGCCCTGCCTGCTTAAGCCCTCCAGCCCGCC
CACTGCCCGTTGCCTTCGTGCTTCGTCAACGTTCTGTGGCCTTGAGGCTCTGTGTCAAGGCCTTTGAGGCCCA
ACCCAGACCCCAAAGCGCCTGTGGTGTGCTGAGTGAGCCGGCCTGTGCCCATGCCCTGGAGGCTTTGGCTACTC
TCCTGCGCCCCACGGTACCTGGACCTGCTAGTCTCCAGCCAGCTTTTCCCCAACCAAGTGGGTTCCCTGAGTCCAG
AGCCTATGCCCTTAGAGCGTTTGGGGCGCCGCTTCCCCCTTGCCCCAGGGAGGCGTCTAGAAGAGTATGGTGCCT
TCTATGTAGGGGGCTCTAAGGCCAGCCCTGACCCAGACCTTGACCCAGACCTGAGTCGGCTGCTCTTGGGGTGGG
CACCAGGTCAACCCTTCTCCTCCTGCTGTCCAGATACAGGGAAGACTCAGGATGAGGGTGCCCGGGCTGGACGGC
TAAGGGCACGAAGACGATATCTGGTAGAGAGGGCCAGAGATGCCCGCGTGGTAGGGCTGCTGGCAGGCACACTGG
GTGTAGCCCAACACCGTGAGGCACTGGCCCACTTGCGGAACCTGACTCAGGCTGCTGGCAAGCGTAGCTATGTGT
TGGCCCTGGGGCGGGCCACCCCTGCCAAGCTTGCCAACCTTCCCTGAGGTGGATGTCTTTGTGCTATTAGCCTGTC
CTCTGGGTGCTCTAGCCCCCAGCTTCTGGTAGCTTCTTCCAGCCTATACTGGCACCATGTGAGCTGGAAGCTG
CCTGCAACCCTGCCTGGCCACCTCCAGGCCTGGCTCCCCACCTCACACATTATGCGGACTTATTGCCTGGCTCTC
CCTTCCACGTGGCTCTCCCACCACCTGAGTCAGAGCTGTGGGAAACCCAGACGTGTCACTCATTACTGGAGATC
TCCGACCCCACTGCCTGGAAGTCATCAATGATCATGGAAGCTTGGCTCTGACCCACGGCCCCAGCTGGAGC
TGGCTGAGAGCAGTCCTGCAGCCTCATTCCTTAGTTCCCGGAGCTGGCAAGGGCTGGAGCCCCGCCTGGGTGAGA
CGCCAGTGACAGAAGCTGTGAGTGGAAGACGAGGGATTGCCATCGCCTATGAGGATGAGGGAAGCGGCTGATACC
ATGTGGGGCTGGAGACATAGATGGACTTATGAATGGCTGCTAGGACCTTTAGTGCTCCCTGCACCAACCTCCCAT
CCCCCTGCCAAGATCCTTGAAGGACCCTGGAAGGAGGGAGAGCAGGCAGCCCTTCACAGGATAGGATCCGTCTCT
GTCTGTCTCTGGCACTGGCACAAGCTCAGCCCATGCCAGTAATGCGTGTGTTTGGCTGATGGAATAAAGGGCT
TAGGGACTTCCCTGAGGGCTCTGGACCCATCTGTCTTCTGAGGGCAGCCCAGGACCTTTGGCCAATCCAGTTC
CCAGGCTGCAGTTGAGGGTCTGTCTTGTCAAAAGGCAGGTGCTAGACAGTCTAGACCAGGGTTTCTCAAACCTG
TACTTGACATTTGGGGCCAGATAATTCTTTGTTGTGGGGCTGTCTGGTGTATGGTAGGGTGCTCAGCAGCATCCC
TGGCCTCTGCCCCACTAGACATCAGAAGCACTCCCCAGTTGTGACAACCAAAAATATCTCCAGACCTTGCAAAAT
GTTATCTGTGGGGGAAAATTGCCCTCAATTGAGAACCAGTGGTCTAGCTAGACCTGCACTGTCCAGTACAGTAGC
CACTAAATACATGTGGCTAAACTTAAATTTAAGTTAATTAAGATTAAGCTCAGTTTCTCAGTCACATTAGTCA
TTCAAGTGTTTACAGACCCACATGAGGGGACAGTGCAGCTACAGGATATGCCATCATGGCAGAAAGTTCTGTTGG
TTGGACAGCGTTGGTCTATACTGACTCTTATTTCTCAGGGAGATCACAGCAACCTAAATAAACCAGATACCTTTT
C

WO 2004/030615

PCT/US2003/028547

215/6881
FIGURE 202A

GCCTTCGCCTGCTGAAAAAGCAGTAGGATCGGCCAGTGGCGACAGCAGGAGCTGAGCCTAAGCCCTGGCGGGGCT
TTGGGCTGTAGATTCTGTCTGACTAAAGGGACCTCAAAAAGGAGGGAAAATGCTTCTGTAGTCTGAAACTCTGA
ATCCAGTGTAGGATAATGACCTTTTATCCAACATATGGAAGAGTTCGAAACTTCAGTAGATACATTGCCTACA
TTGAATCCCAAGGAGCTCATCGGGCAGGGCTAGCCAAGTTGTTCCCTCCAAAAGAGTGGAAGCCACGAGCATCCT
ATGATGACATTGATGATTTGGTCATTCTGCCCCCATTCACAGCTGGTGACGGGGCAGTCTGGCCTCTTTACTC
AGTACAACATACAGAAGAAAGCCATGACTGTTTCGAGAGTTCGCGCAAGATAGCCAATAGCGATAAGTACTGTACCC
CACGCTATAGTGAGTTTGAAGAGCTCGAGCGGAAATACTGGAAAAATCTTACATTCAATCCTCCAATCTATGGTG
CAGATGTGAATGGTACCCTCTATGAAAAGCATGTTGATGAGTGGAATATTGGCCGGCTGAGAACAATCCTGGACT
TGGTGGAAGAGGAGTGGGATCACCATTGAGGGTGTGAACACCCCATACCTGTACTTTGGCATGTGGAAGACAT
CCTTTGCTTGGCACACTGAAGACATGGACCTCTACAGCATCAACTACCTGCACCTTTGGGAGAACCAGGCTCTGGT
ACTCTGTTCCACCTGAGCATGGAAGCGGTTGGAACGCCCTCGCCAAAGGCTTTTTCCAGGAAGTGCTCAAAGCT
GTGAGGCATTTCTCCGCCACAAGATGACCCTGATTTCCCGTTAATGCTGAAGAAATATGGAATTCCTTTTGACA
AGGTGACTCAAGAGGCTGGAGAGTTTATGATCACTTTCCCTTATGGTTACCATGCCGGCTTTAACCATGGTTTTA
ACTGTGCGGAGTCTACCAATTTTGCTACCCGTCGGTGGATTGAGTACGGCAAGCAAGCTGTGCTGTGCTCCTGTA
GAAAGGACATGGTGAAGATCTCCATGGATGTGTTTGTGAGAAAGTTCCAGCCAGAAAGGTACAAACTTTGGAAAG
CTGGGAAGGACAACACAGTTATTGACCATACTCTGCCACGCCAGAAGCAGCTGAGTTTCTTAAGGAGAGTGAAC
TGCCCTCAAAGAGCTGGCAACGAGGAGGAGTGCCAGAGGAGGACATGGAAGGGGTGGAGGATGGAGAGGAAGGAG
ACCTGAAGACAAGCCTGGCCAAGCACCGAATAGGGACAAAGAGGCACCGAGTTTGCTTGAAATACCACAGGAGG
TGAGTCAGAGTGAGCTCTTCCCAAGGAGGATCTGAGTTCTGAGCAGTATGAGATGACGGAGTGCCCGGCAGCCC
TCGCCCTGTGAGGCCACCCATAGCTCTGTGCGGCAAGTTGAGGATGGTCTTACCTTCCAGATTATTCTGACT
CCACTGAAGTCAAATTTGAAGAGCTTAAAAATGTCAAAC TAGAAGAGGAGGATGAGGAGGAAGAACAAGAAGCAG
CTGCCTTGATCTTTCTGTGAATCCTGCGTCTGTAGGGGGACGCTTGTCTTCTCAGGCTCCAAAAGAAATCAT
CTTCTAGCCTGGGCTCTGGCTCTTCACGGGATTCTATCTCTTCTGATTGAGAACTAGTGAGCCTCTCTCCTGCC
GAGCCCAAGGGCAAACGGGAGTTCTCACTGTGCACAGTTATGCCAAAGGGGATGGCAGGGTCACTGTGGGAGAGC
CATGCACGAGGAAGAAAGGAAGCGCCGCTAGAAGTTTCAGTGAGCGGGAGCTGGCAGAGGTTGCAGATGAATACA
TGTTTTCCCTAGAAGAGAATAAGAAGTCCAAGGGACGCCGTCAGCCTTTAAGCAAGCTCCCCGCCATCACCCAC
TTGTGCTGCAGGAGTGTGTGAGTGATGATGAGACATCTGAACAGCTGACCCCTGAGGAAGAGGCTGAGGAGACAG
AGGCCCTGGGCCAAGCCTCTGAGCCAACCTGTGGCAGAACCGACCTCCAACTTTGAGGCTGAGAAGGAATTCAATG
AGACCATGGCCCAACAGGCCCTCACTGCGCTGTCTGTATGATCTTCCAGACTTATCATCAGGTTGAATTTGGAG
GCTTTAATCAGAACTGTGGAAATGCTTCAGATTTAGCCCCCAGAAGCAGAGGACCAAGCCATTGATTCCAGAAA
TGTGCTTCACTTCGACTGGCTGCAGCACGGACATCAACCTTTCTACTCCTTATCTTGAGGAGGATGGCACCAGCA
TACTCGTTTCTGCAAGAAGTGACGCTCCGGGTCCATGCCAGTTGCTATGGGGTCCCCCTGCAAAGGCTTCTG
AAGACTGGATGTGTTCTCGGTGTTGAGCCAATGCCCTAGAGGAGGACTGCTGTTTATGCTCATTACGAGGAGGGG
CCCTGCAGAGAGCAAATGATGACAGGTGGGTCCACGTTTCATGTGCTGTGGCAATTCTGGAAGCAAGGTTTGTC
ACATTGCAGAAAGAGTCCGGTGATGTGAGCAAAATCCCCCTGCCCCGCTTCAAAC TGAATGTATCTTCTGTA
AGAAGCGGAGGAAAAGAACTGCTGGCTGCTGTGTGCAGTGTTCTCACGGCCGCTGCCCAACTGCCTTCCATGTGA
GCTGCGCCAGGCTGCCGTTGTGATGATGCAGCCTGACGACTGGCCTTTTGTTGGTCTTCATTACCTGCTTTTCGGC
ACAAGATTCCTAATTTGGAGCGTGCCAAGGGGGCCTTGCAAAGCATCACTGCAGGCCAGAAAGTCATTAGCAAGC
ATAAGAACGGGCGCTTCTACCAAGTGTGAAGTGGTCAGGCTCACCACCGAGACCTTCTATGAAGTCAACTTTGATG
ATGGCTCCTTCAGCGACAATCTTTATCCTGAGGACATAGTGAGCCAGGACTGTCTCCAGTTTGGTCTCCTGCTG
AAGGGGAAGTGGTCCAAGTGAGATGGACAGCGCCAAGTCTATGGAGCCAAGTTTGTGGCCTCCACCCATATCC
AAATGTACCAGGTGGAGTTTGAGGATGGCTCACAACCTGTGGTTAAGAGAGATGATGTATACACACTGGATGAAG
AGCTTCCCAAGAGAGTCAAATCTAGACTGTGAGTAGCCTCAGACATGCGCTTCAATGAGATTTTACAGAGAAAG
AGGTTAAGCAAGAAAAAGAAACGGCAACGAGTTATCAACTCAAGATACCGGAAGATTATATTGAGCCTGCACAT
ACCGGGCCATCATGGAGTAGGTGCTTCCAGGGTCCAAGGGATTCTCAGCCATCCAGGCAAGAGCACTCTGGGTTT
CACAGCACAGCAGACATGGAACGCTGAAGTCTCTGAAAGTGAAGTTGTAAAAAGAAAAGGAATGAAATAACCGAC
CCATCATCTTCTCACCCACCCCTCATTGCATTCCGCTGTAGTGAAAGGACGAGCCATTTCTGGGCACGTGGCAGCA
GTCGCTGATCTCCAGCTGAGGGGCTGAGCACTGGAATGCTGTGGCTGCACTGGCCCCAGTCCATAGAGGGGTCA

WO 2004/030615

PCT/US2003/028547

216/6881
FIGURE 202B

ACTATGCTGGCTGGACTGGCTGCCTTGTTTCCTGGCCTAGGACTTAGCTTCATAACTATCACCTGCACCGACTAGG
CTGAGGTGCTGGTACTTGCCCCAACCCCTACTTTTGTATTTATATGTGTGTGTGTGTGTGCGTGCGTGCGTGCGT
GCGTGTATGTTTGGTCTGGACCAGCTTCTGCCAGCCCCTGGCCTTTACTTTCTTCCTTGCCCTATGCAGGGCAAAC
AAAATGTGAAATTCTGCCCTCAGCTGAGCTGAGTAAGGGCTCCTGGGGGTGGCTGGAGATGGGTGTGGCATCTG
TCCAGGCCTGGAACCGTCTCAAGACAGTGCTGGCAAAGCTGCAGTATTGAGATGCTAAGGAGCTGATGCCACCTC
TTTGTCTTCCCCTAAAGGAGAACATGGGGATAACATGGGTGTGTGCCCAACAACACTCTAGGTGCAGAGCCCCCTGT
GGCAAAGTATTACAGGGTGTGGGTGGGGATTACCCTGAATCGGGGATTTTAATGATGGAAGCAGGCAGAGCCTGG
TGGGTGATTCTGTCAACAGAAAATTGCAATCATGCAGGGGCTGGGAGGGTTAGGATGAAAAAACTGGGGCCATTG
GAGGCCCACTGTAGGTGGGAGGGAGCTGATTTTGGGGTGGGGGTGGGACTAGAGGGCAATACTGAAGGGGTAA
ACAGGTTTTTGCTCCTCAAGAATTTGTTTGCCTGGGCCAGGATTGGAGGGCTTCACACCAATACCCTGTGTATA
CAAGAATCAGATTTATAATACTTCCCCTTTTTTGTACGTATGAACACTATAAACCAAAATTATTTTG

WO 2004/030615

PCT/US2003/028547

217/6881
FIGURE 203

MASESETLNPSARIMTFYPTMEEFRNFSRYIAYIESQGAHRAGLAKVVPPKEWKPRASYDDIDDLVIPAPIQQLV
TGQSGLFTQYNIQKKAMTVREFRKIANSDKYCTPRYSEFEELERKYWKNLTFNPPYIYGADVNGTLYEKHVDEWNI
GRLRTILDLVEKESGITIEGVNTPYLYFGMWKTSFAWHTEDMDLYSINYLHFGEPSWYSVPPEHGKRLERLAKG
FFPGSAQSCEAFLRHKMTLISPLMLKKYGIPFDKVTQEAGEFMITFPYGYHAGFNHGFNCAESTNFATRRWIEYG
KQAVLCSCRKDMVKISMDVVRKFQPERYKLWKAGKDNTVIDHTLPTPEAAEFLKESELPPRAGNEEECPEDME
GVEDGEEDLKTSLAKHRIGTKRHRVCLEIPQEVVSQSELPKEDLSSEQYEMTECPAALAPVRPTHSSVRQVEDG
LTFFPDYSDSTEVKFEELKNVKLEEEDEEEEQEAAALDLSVNPASVGGRLVFGSGKKKSSSSSLGSGSSRDSISSDS
ETSEPLSCRAQQGTGVLTVHSYAKGDGRVTVGEPCTRKKGSAARSF SERELAEVADEYMF SLEENKKSKGRRQPL
SKLPRHHPLVLQECVSDDDETSEQLTPEEEAEETEAWAKPLSQLWQNRPPNFEEAEKEFNETMAQQAPHCAVCMIFQ
TYHQVEFGGFNQNCGNASDLAPQKQRTKPLIPEMCFTSTGCSTDINLSTPYLEEDGTSILVSCKKCSVRVHASCY
GVPPAKASEDWMCSRCSANALEEDCCCLCSLRGGALQRANDDRWVHVSCAVAILEARFVNIAERSPDVSKIPLPR
FKLKCIFCKRRRKRTAGCCVQC SHGRCPTAFHVSCAQAAGVMMQPDWPFVVFITCFRHKIPNLERAKGALQSIT
AGQKVISKHKNRFRFYQCEVVRLTTETFYEVNFDDGSFSDNLYPEDIVSQDCLQFGPPAEGEVVQVRWTDGQVYGA
KFWASHPIQMYQVEFEDGSQLVVKRDDVYTLDEELPKRVKSRLSVASDMRFNEIFTEKEVKQEKRRQRVINSRYR
EDYIEPALYRAIME

WO 2004/030615

PCT/US2003/028547

218/6881
FIGURE 204

AGTTACAGACAGCTGACCAATGGAAGCGAATGGGTGGGACCTCAGGGTTTTCCGGAGCTGAAGAATGACACATT
CTGCGAGCAGCCTGGGGAGAGGAAACAGACTACACTCCCCTTTGGTGATGCGCCAGGCAGGCCGTTACTTACCA
GAGTTTAGGGAAACCCGGGCTGCCCAGGACTTTTTTCAGCACGTGTCGCTCTCCTGAGGCCTGCTGTGAAGTACT
CTGCAGCCACTGCGTCGCTTCCCTCTGGATGCTGCCATCATTTTTCTCCGACATCCTTGTGTACCCAGGCACTG
GGCATGGAGGTGACCATGGTACCTGGCAAAGGACCCAGCTTCCCAGAGCCATTAAAGAGAAGAGCAGGACCTAGAA
CGCCTACGGGATCCAGAAGTGGTAGCCTCTGAGCTAGGCTATGTGTTCCAAGCCATCACCCCTTACCCGACAACGA
CTGGCTGGACGTGTGCCGCTGATTGGCTTTGCTGGTGCCCCATGGACCCTGATGACATACATGGTTGAGGGTGGT
GGCTCAAGCACCATGGCTCAGGCCAAGCGCTGGCTCTATCAGAGACCTCAGGCTAGTCACCAGCTGCTTCGCATC
CTCACTGATGCTCTGGTCCCATATCTGGTAGGACAAGTGGTGGCTGGTGCCAGGCATTGCAGCTGTTTGAGTCC
CATGCAGGGCATCTTGGCCACAGCTCTTCAACAAGTTTGCACTGCCTTACATCCGTGATGTGGCCAAGCAAGTG
AAGGCCAGGTTGCGGGAGGCAGGCCTGGCACCAGTGCCCATGATCATCTTTGCTAAGGATGGGCATTTTGCCCTG
GAGGAGCTGGCCCAAGCTGGCTATGAGGTGGTTGGGCTTGACTGGACAGTGGCCCCAAAGAAAGCCCGGGAGTGT
GTGGGGAAGACGGTGACATTGCAGGGCAACCTGGACCCCTGTGCCTTGTATGCATCTGAGGAGGAGATCGGGCAG
TTGGTGAAGCAGATGCTGGATGACTTTGGACCACATCGCTACATTGCCAACCTGGGCCATGGGCTTTATCCTGAC
ATGGACCCAGAACATGTGGGCGCCTTTGTGGATGCTGTGCATAAACACTCACGTCTGCTTCGACAGAACTGAGTG
TATACCTTTACCCCTCAAGTACCACTAACACAGATGATTGATCGTTTCCAGGACAATAAAAGTTTCGGAGTTGAAC
TATTGTGTAGTTTTGTTTGTGAAAGATTGTGCCCATATCCTCAGTTCTTCTTAGCCTCTGCTCCTTCCCTGGGAA
CCCTCTCTATATCCTCTT

WO 2004/030615

PCT/US2003/028547

219/6881
FIGURE 205

MEANGLGPQGFPPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAQQDFFSTCRSPEACCELTLQPLRR
FPLDAAIIFSDILVVPQALGMEVTMVPGKGPSFPEPLREEQDLERLRDPEVVASELG YVFQAITLTRQLAGRVP
LIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQLLRILTALVPYLVGQVVAGAQAALQLFESHAGHLG
PQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAGYEVVGLDWTVAPKKARECVGKTVT
LQGNLDPCALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPDMDPEHVGA FVDAVHKHSRLLRQN

WO 2004/030615

PCT/US2003/028547

220/6881
FIGURE 206

AGCTTTGCGCAGTGGCAGTATCGTAGCCAATGAGGTTTATCCGAGGCGCGATTATTGCTAATTGAAAACTTTTCC
CAATACCCCGCCATGACGACTTGAAATATAGTCGGCATTGGCAATTTTGGACAGTCTCTACGGAGACTGCATGTG
CTGGTGAAGCTCCTGGAAGTGAATGGAAGGAATGGACAAGGAGACGTTTGAGTTCAAGTTTGGGAAGGAACATAACA
TTCACCACTGTACTGAGTGACCAACAGGTGGTGGAGCTGATCCCTGGGGGTGCAGGCATCGTCGTGGGATATGGG
GACCGTTCTCGTTTCATCCAACCTGGTCCAGAAGGCACGGCTAGAGGAGAGCAAGGAGCAGGTGGCAGCTATGCAG
GCAGGTCTGCTGAAGGTGGTACCACAGGCTGTGCTGGACTTGCTGACCTGGCAAGAGTTGGAGAAGAAAGTGTGT
GGGGATCCAGAGGTCACTGTGGATGCTCTGCGCAAGCTCACCCGTTTGGAGACTTCGAGCCATCTGACTCGCGG
GTGCAGTATTTCTGGGAGGCACTGAACAACCTTACCAACGAGGACCGGAGCCGCTTCCTGCGCTTTGTACGGGGC
CGCAGTCGCTGCCAGCACGGATCTACATCTACCCAGACAAGCTGGGCTACGAGACCACAGACGCGCTGCCCGAG
TCTTCCACTTGCTCCAGCACCCCTCTTCTGCCACACTATGCCAGTGCCAAGGTATGCGAGGAGAAGCTCCGCTAT
GCGGCCTACAACCTGCGTGGCCATCGACACTGACATGAGCCCTTGGGAGGAGTGAGGCGTGCCGCCGGCTGTGGGA
CCAGCAAGACTGCACGTGTCCCTCTTGGCCCTTGGCCAGGGCGAAGACACCTTCCCTGCCCTGGTTTGGCTGACGT
GCTCAGCAAAACCCCATGTGCCCTGCTCCTGTGTGCAGTTGGGGTAGGGGCAGCTGGCATGGTCAGGTAACACTA
GTGGCCAGCCCCGAGACCCACAAGCCCTACCCGTGCTGGGGCTTGCTTCCCAGGATATTTACCTCTTAAGAG
GGAATCTTCCACAAGCCCAGCACAAAGCTGCCAGGCCTGAGCTACTTGAAGGGGGCCATCTAGGTCCCCAACCCAT
GGACTTTGCCTCCATTTTCAGCTCCGCTTTTTTCTCCTATTTTCTCTCTGGCTTTCTTCAGCCATGACTCACAA
CTAAAAACATAAAACACTGGAGGTTAGTGGAGGCCCTCCCCAAGCAGGGAGCCTGGGATGGGCAGGGAGTGATA
GCCAACTCCTTGGTCACCTGCTCCAAGAAGGAAGCAGTAGCTGAGCACCTGCCCTCACATACTGCTCTTTTCCC
CTCTCCCTCCACACCAGAGATGTGGTGAGCTCTGTTCTTCTACCAACCCAGTCTCAACACACAAAGTGCCACCAC
CTTCCCTGACTCAGAACCCACATCCACTCAATGTGAACCTCTACTACCACGACCTCCCCATATTCTCACTTCTCC
ATCACCTCCAGCCTGACTCCCTGTCTGCCCTTTCACCCCCAAGATTTTGACAGGTAAAGGCCAGTTATGGCCTT
TTTGAATCTGTAATAGCTCCCCCTTCCCCAACTCTAAAGCCTAGACCTTAAACCTGTTCTAGAGCTATGCACA
CCCTGCCCCAGTTTACCGTTCCTCCCTCAGGGCCTCCGTGACACTCCATGAAAAGAAGTTCTTGATACCGGAA
AGTTGAATAAATGGATGAATTCAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

221/6881
FIGURE 207

MEGMDKETFEFKFGKELTFTTVLSDQQVVELIPGGAGIVVGYGDRSRFIQLVQKARLEESKEQVAAMQAGLLKVV
PQAVLDLLTWQELEKKVCGDPEVTVDALRKLTRFEDFEPDSRVQYFWEALNNFTNEDRSRFLRFVTGRSRLPAR
IYIYPDKLGYETTDALPESSTCSSTLFLPHYASAKVCEEKLRYYAAYNCVAIDTDMSPWEE

WO 2004/030615

PCT/US2003/028547

222/6881
FIGURE 208

CACAATGGTGCGCATGAATGCCCTGGCAGATGCTCTCAAGAGCATCAACAATGCCGAAAAGAGAGGCAAACGCCA
GGTGCTTCTTAGGCCATGCTCCAAAGTCATCGTCCAGTTTCTCACTGTGATGATGAAGCATGGTTACATTGGCGA
ATTTGAAATCACTGATGATCACAGAGCTGGGAAAATTGTTGTGAACCTCACAGGCAGGCTAAACAAGTGTGGAGC
GATCAGCCCCAGATTTGATGTGCAACTCAAAGATCTGGAAAAATGGCAGAATAATCTGCTTCCATCCCGCCAGTT
TGATTTTCATTGTACTGACAACCTCAGCTGGCATCATGGACCATGAAGCAAGACGAAAACACACAGGAGGGAAAAT
CCAGGGATTCTTTTTCTAGGGATGTAATACATATATTTACAAATAAAATGCCTCAAGGAC

WO 2004/030615

PCT/US2003/028547

223/6881
FIGURE 209

MVRMNALADALKSINNAEKRGRQVLLRPCSKVIVQFLTVMMKHGYIGEFEITDDHRAGKIVVNLTGRLNKC
SPRFDVQLKDLEKWQNNLLPSRQFDFIVLTTSAGIMDHEARRKHTGGKIQGFFF

WO 2004/030615

PCT/US2003/028547

224/6881
FIGURE 210

CTCTTTCCAGCCAGCGCCGAGCGATGGGCATCTCTCGGGACAACCTGGCACAAGCGCCGCAAAACCGGGGGCAAGA
GAAAGCCCTACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCAGCTGCCAACACCAAGATTGGCCCCGCGCA
TCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGGAATTTCTCCTGGG
GCTCAGAGTGTTGTACTCGTAAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTA
CCAAGACCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATG
CGCTGCCCCCTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTAAACAAAAACGATCTA
AAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAATCAGCAGTCTCCTGGAGGAGCAGTTCCAGC
AGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGACAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCA
AAGAGTTGGAGTTCTATCTTAGGAAAATCAAGGCCCGCAAAGGCCAAATAAATCCTTGTTTTGTCTTACCCATGT
AATAAAGGTGTTTATTGTTTTGTTCCACA

WO 2004/030615

PCT/US2003/028547

225/6881
FIGURE 211

MGISRDNWHKRRKTGGKRKPYHKKRKYELGRPAANTKIGPRRIHTVRVRGGNKKYRALRLDVGNE¹SWGSECCTRK
TRI IDVVYNASNNELVRTKTLVKNCIVLIDSTPYRQWYESHYALPLGRKKGAKLTPEEEEEILNKKRSKKIQKKYD
ERKKNAKISSLLEEQQQGKLLACIASRPGQCGRADGYVLEGKELEFYLRKIKARKGK

WO 2004/030615

PCT/US2003/028547

226/6881
FIGURE 212

ACGCTTGCGCGCGGGATTAACTGCGGCGGTTTACGCGGCGTTAAGACTTCGTAGGGTTAGCGAAATTGAGGTT
TCTTGGTATTGCGCGTTTTCTCTTCCTTGCTGACTCTCCGAATGGCCATGGACTCGTCGCTTCAGGCCCGCTGTT
TCCCGGTCTCGCTATCAAGATCCAACGCAGTAATGGTTTAATTACAGTGCCAATGTAAGGACTGTGAACTTGGA
GAAATCCTGTGTTTTAGTGGAATGGGCAGAAGGAGGTGCCACAAAGGGCAAAGAGATTGATTTTGATGATGTGGC
TGCAATAAACCCAGAACTCTTACAGCTTCTTCCCTTACATCCGAAGGACAATCTGCCCTTGCAAGAAAATGTAAC
AATCCAGAAACAAAACGGAGATCCGTCAACTCCAAAATTCCTGCTCCAAAAGAAAAGTCTTCGAAGCCGCTCCAC
TCGCATGTCCACTGTCTCAGAGCTTCGCATCACGGCTCAGGAGAATGACATGGAGGTGGAGCTGCCTGCAGCTGC
AACTCCCCGAAGCAGTTTTTCAGTTCCTCCTGCCCCACTAGGCCTTCCTGCCCTGCAGTGGCTGAAATACCATT
GAGGATGGTCAGCGAGGAGATGGAAGAGCAAGTCCATTCCATCCGAGGCAGCTCTTCTGCAACCCCTGTGAACTC
AGTTCGGAGGAAATCATGTCTTGTGAAGGAAGTGGAAGAAATGAAGAACAAGCGAGAAGAGAAGAAGGCCAGAA
CTCTGAAATGAGAATGAAGAGAGCTCAGGAGTATGACAGTAGTTTTCCAACTGGGAATTTGCCCGAATGATTAA
AGAATTTGGGGTACTTTTGGAAATGTATCCACTTACTATGACTGATCCTATCGAAGAGCACAGAATATGTGTCTG
TGTTAGGAAACGCCCACTGAATAAGCAAGAAATGGCCAAGAAAGAAATGATGTGATTTCCATTCTAGCAAGTG
TCTCCTCTTGGTACATGAACCAAGTTGAAAGTGGAAGTAAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACAATCTT
TGAAGGTGGAAGCAACTTGTGTTTGCATATGGCCAGACAGGAAGTGGAAGACACATACTATGGGCGGAGACCT
CTCTGGGAAAGCCCAGAAATGCATCCAAAGGGATCTATGCCATGGCCTCCCGGGACGTCTTCTCCTGAAGAATCA
ACCCTGCTACCGGAAGTTGGGCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGACCT
GCTCAACAAGAAGGCCAAGCTGCGCGTGCTGGAGGACGGCAAGCAACAGGTGCAAGTGGTGGGGCTGCAGGAGCA
TCTGGTTAACTCTGCTGATGATGTCATCAAGATGATCGACATGGGCAGCGCCTGCAGAACCTCTGGGCAGACATT
TGCCAACCTCAATTCCTCCCGCTCCACGCGTGCTTCCAAATTATTCTTCGAGCTAAAGGGAGAATGCATGGCAA
GTTCTCTTTGGTAGATCTGGCAGGGAATGAGCGAGGCGCGGACACTTCCAGTGCTGACCGGCAGACCCGCATGGA
GGGCGCAGAAATCAACAAGAGTCTCTTAGCCCTGAAGGAGTGACATCAGGGCCCTGGGACAGAACAAGGCTCACAC
CCCGTTCCGTGAGAGCAAGCTGACACAGGTGCTGAGGGACTCCTTCATTGGGGAGAATCTAGGACTTGCAGATT
GCCACGATCTCACCAGGCATAAGCTCCTGTGAATATACTTTAAACACCCTGAGATATGCAGACAGGGTCAAGGAG
CTGAGCCCCACAGTGGGCCCAGTGGAGAGCAGTTGATTCAAATGGAAACAGAAGAGATGGAAGCCTGCTCTAAC
GGGCGCTGATTCCAGGCAATTTATCCAAGGAAGAGGAGGAAGTGTCTTCCAGATGTCCAGCTTTAACGAAGCC
ATGACTCAGATCAGGGAGCTGGAGGAGAAGGCTATGGAAGAGCTCAAGGAGATCATACAGCAAGGACCAGACTGG
CTTGAGCTCTCTGAGATGACCGAGCAGCCAGACTATGACCTGGAGACCTTTGTGAACAAAGCGGAATCTGCTCTG
GCCCAGCAAGCCAAGCATTCTCAGCCCTGCGAGATGTATCAAGGCCTTGCGCCTGGCCATGCAGCTGGAAGAG
CAGGCTAGCAGACAAATAAGCAGCAAGAAACGGCCCCAGTGACGACTGCAATAAAAATCTGTTTGGTTTGACAC
CCAGCCTCTTCCCTGGCCCTCCCCAGAGAATTTGGGTACCTGGTGGGTCTAGGCAGGGTCTGAGCTGGGACAGG
TTCTGGTAATGCCAAGTATGGGGGCATCTGGGCCCAGGGCAGCTGGGGAGGGGGTCAAGTGTGACATGGGACACT
CCTTTTCTGTTCTCAGTTGTGCGCCCTCACGAGAGGAAGGAGCTCTTAGTTACCCTTTTGTGTTGCCCTTCTTTC
CATCAAGGGGAATGTTCTCAGCATAGAGCTTTCTCCGCAGCATCCTGCCTGCGTGGACTGGCTGCTAATGGAGAG
CTCCCTGGGGTTGTCTGGCTCTGGGGAGAGAGACGGAGCCTTTAGTACAGCTATCTGCTGGCTCTAAACCTTCT
ACGCCTTTGGGCGGAGCACTGAATGTCTTGTACTTTAAAAAATGTTTCTGAGACCTCTTCTACTTTACTGTCT
CCCTAGAGATCCTAGAGGATCCCTACTGTTTTCTGTTTTATGTGTTTATACATTGTATGTAACAATAAGAGAAA
AAATAAA

WO 2004/030615

PCT/US2003/028547

227/6881.
FIGURE 213A

TAGGCAGGCGGCTGAGCCGGCGGGTGGCCTGCCAACGTGTGCTGGGTGGGAGAAGGCGAGGCGTCAGCGAT
GCTGTCTCTTCCGTGAGGAGCGCAGAGGAGGTCGCGGCGCCGGAGGCCCCAGAAGGCTCGAAGGCGCCGCGGGCT
GGGGTGGGTGGCTTAGGGAGCCCGTCCGGCCATGGTGGCCGCGGGTGGTGGTTGGCGCGCTGCGCTGCGGCCCCG
GGGCAGTGC GGAGCCGGGACAGTCGCGGCGCTGACGCCCGCGGGCCCCAGCTGCAGATATGAAGCGGAGCCGCTG
CCGCGACCGACCGCAGCCGCCGCCGCCGACCGCCGGGAGGATGGAGTTCAGCGGGCAGCGGAGCTGTCTCAGTC
TTTGCCGCGCGCCGGCGAGCGCCGCCGGGAGGCAGCGGCTGGAGGAGCGGACGGGCCCCGCGGGCCCCGAGGG
CAAGGAGCAGGATGTAGTAAGTGGAGTTAGTCCCTGCTCTTCAGGAACTCAGTAATCCTGACATATTTTCATC
CACTGGAAGGTTAACTTCAGCGACAAGTGGAGTCAGGATGATTGTAAGTTATGGAGAGGAAACCTGGCCAGCTC
TCTATCGGGTAAGCAGCTGCTCCCTTTGTCCAGCAGTGTACATAGCAGTGTGGGACAGGTGACTTGGCAGTCGTC
AGGAGAAGCATCAAACCTGGTTCGAATGAGAAACAGTCCCTTGGACAGTCTGCACCTTCTCTTACTGCTGGCCT
GAAGGAGTTGAGCCTTCCAAGAAGAGGCAGCTTTTGTGGACAAGTAACCGCAAGAGCTTGATTGTGACCTCTAG
CACATCACCTACACTACCACGGCCACACTCACCCTCCATGCCACACAGGTAACAGTCCCTTGGACAGCCCCCG
GAATTTCTCTCAAATGCACCTGCTCACTTTTCTTTTGTCTGCCCCGTTAGGACTGATGGGCGGCGCTGGTCTTT
GGCCTCTTTGCCCTCTTCAGGATATGGAACCTAACCTCCTAGCTCCACTGTCTCATCATCATGCTCCTCACAGGA
AAAGCTGCATCAGTTGCCCTTCCAGCCTACAGCTGATGAGCTGCACCTTTTGGACGAAGCATTTCAGCACAGAGAG
CGTACCAGATGAGGAAGGACGGCAGTCCCAGCCATGCGGCCTCGCTCCCGGAGCCTCAGTCCCGGACGATCCCC
AGTATCCTTTGACAGTGAAATAATAATGATGAATCATGTTTACAAAGAAAGATTCCCAAAGGCCACCGCACAAAT
GGAAGAGCGACTAGCAGAGTTTATTTCTCCAACACTCCAGACAGCGTGCTGCCCTTGGCAGATGGAGCCCTGAG
CTTTATTCATCATCAGGTGATTGAGATGGCCCGAGACTGCCTGGATAAAATCTCGGAGTGGCCTCATTACATCACA
ATACTTCTACGAACCTCAAGATAATTGGAGAACTTTTACAAGATGCTCATGAGCGCTCAGAGAGCTCAGAAGT
GGCTTTTGTGATGCAGCTGGTGAAGAGCTGATGATTATCATTGCCCGCCAGCACGTCTCCTGGAATGCCTGGA
GTTTGACCCCTGAAGAGTTCTACCACCTTTTGAAGCAGCTGAGGGCCACGCCAAAGAGGGACAAGGGATTAAATG
TGACATTCCCCGCTACATCGTTAGCCAGCTGGGCCTCACCCGGGATCCCCTAGAAGAAATGGCCAGTTGAGCAG
CTGTGACAGTCTGACACTCCAGAGACAGATGATTCTATTGAGGGCCATGGGGCATCTCTGCCATCTAAAAAGAC
ACCTCTGAAGAGGACTTCGAGACCATTAGCTCATCAGCAATGGCGCCTATGGGGCTGTATTTCTGGTGGCGCA
CAAGTCCACCCGGCAGCGCTTTGCCATGAAGAAGATCAACAAGCAGAACCTGATCCTACGGAACCAGATCCAGCA
GGCCTTCGTGGAGCGTGACATACTGACTTTGCTGAGAACCCCTTTGTGGTCAGCATGTTCTGCTCCTTTGATAC
CAAGCGCCACTTTGTGATGGTGTGAGTACGTTGAAGGGGGAGACTGTGCCACTCTGCTGAAGAATATTGGGGC
CCTGCTGTGGACATGGTGGCTCTATACTTTGCGGAACTGTGCTGGCCCTGGAGTACTTACACAACCTATGGCAT
CGTGACCCGTGACCTCAAGCCTGACAACCTCCTAATTACATCCATGGGGCACATCAAGCTCACGGACTTTGGACT
GTCCAAAATTGGCCTCATGAGTCTGACAACGAACCTGTATGAGGGTCATATTGAAAAGGATGCCCGGGAATTCTT
GGACAAGCAGGTATGCGGGACCCAGAATACATTGCGCCTGAGGTGATCCTGCGCCAGGGCTATGGGAAGCCAGT
GGACTGGTGGGCCATGGGCATTATCCTGTATGAGTTCTGCTGGGCTGCGTCCCTTTTTTTGGAGATACTCCGGA
GGAGCTCTTTGGGCGAGTGATCAGTGATGAGATTGTGTGGCCTGAGGGTGATGAGGCAGTGCCTATGAGGTGAAGCA
GCACCCATTCTTTACTGGTCTGGACTGGACAGGACTTCTCCGCCAGAAGGCTGAATTTATCTCAGTTGGAGTC
AGAGGATGATACTAGCTATTTTGACACCCGCTCAGAGCGATACCACCACATGGACTCGGAGGATGAGGAAGAAGT
GAGTGAGGATGGCTGCCCTGAGATCCGCCAGTTCTCTTCTGCTCTCCAAGGTTCAACAAGGTGTACAGCAGCAT
GGAGCGGCTCTCACTGCTCGAGGAGCGCCGGACACCACCCCGACCAAGCGCAGCCTGAGTGAGGAGAAGGAGGA
CCATTGAGATGGCCTGGCAGGGCTCAAAGGCCGAGACCGGAGCTGGGTGATTGGCTCCCCTGAGATATTACGGAA
GCGGCTGTGGTGTCTGAGTCATCCACACAGAGAGTGACTCAAGCCCTCCAATGACAGTGCGACGCCGCTGCTC
AGGCCTCCTGGATGCGCCTCGGTTCCCGGAGGGCCCTGAGGAGGCCAGCAGCACCCCTCAGGAGGCAACCACAGGA
GGGTATATGGGTCTTGACACCCCATCTGGAGAGGGGGTATCTGGGCCTGTCACTGAACACTCAGGGGAGCAGCG
GCCAAAGCTGGATGAGGAAGCTGTTGGCCGGAGCAGTGGTTCCAGTCCAGCTATGGAGACCCGAGGCCGTGGGAC
CTCACAGCTGGCTGAGGGAGCCACAGCCAAGGCCATCAGTGACCTGGCTGTGCGTAGGGCCCGCCACCGGCTGCT
CTCTGGGGACTCAACAGAGAAGCGCACTGCTCGCCCTGTCAACAAAGTGATCAAGTCCGCTCAGCCACAGCCCT
CTCACTCCTCATTCTTCGGAACACCACACCTGCTCCCGGTTGGCCAGCCCCATGTCCCCACATTCTCAGTCGTC
CAACCCATCATCCCGGACTCTTCTCCAAGCAGGGACTTCTTGCCAGCCCTTGGCAGCATGAGGCCTCCCATCAT

WO 2004/030615

PCT/US2003/028547

228/6881
FIGURE 213B

CATCCACCGAGCTGGCAAGAAGTATGGCTTCACCCTGCGGGCCATTGCGGTCTACATGGGTGACTCCGATGTCTA
CACCGTGCACCATATGGTGTGGCACGTGGAGGATGGAGGTCCGGCCAGTGAGGCAGGGCTTCGTCAAGGTGACCT
CATCACCCATGTCAATGGGGAACCTGTGCATGGCCTGGTGACACGAGGTGGTAGAGCTGATCCTGAAGAGTGG
AAACAAGGTGGCCATTTCAACAAC TCCCCTGGAGAACACATCCATTAAAGTGGGGCCAGCTCGGAAGGGCAGCTA
CAAGGCCAAGATGGCCC GAAGGAGCAAGAGGAGCCGCGGCAAGGATGGGCAAGAAAGCAGAAAAAGGAGCTCCCT
GTTCCGCAAGATCACCAAGCAAGCATCCCTGCTCCACACCAGCCGAGCCTTTCTTCCCTTAACCGCTCCTTGTC
ATCAGGGGAGAGTGGGCCAGGCTCTCCACACACAGCCACAGCCTTTCCCCCGATCTCCCACTCAAGGCTACCG
GGTGACCCCGATGCTGTGCATTGAGTGGGAGGGAATTCATCACAGAGCAGCTCCCCAGCTCCAGCGTGCCCCAG
TTCCCCAGCCGGCTCTGGGCACACAGGCCAGCTCCCTCCACGGTCTGGCACCCAAGCTCCAACGCCAGTACCG
CTCTCCACGGCGAAGTCAGCAGGCAGCATCCCACTGTGACCACTGGCCACACCCCTTCTCCCCACCCCCAAC
AGCTTCACCTCAGCGGTCCCCATCGCCCTGTCTGGCCATGTAGCCAGGCCTTTCCCAAAAGCTTCACCTTGTC
ACCTCCCCTGGGCAGGCAACTCTCACGGCCCCAAGAGTGGGAGCCACCCCGTTCACTACTCAAGAGGGTGCA
GTCGGCTGAGAACTGGCAGCAGCACTTGCCGCTCTGAGAAGAAGCTAGCCACTTCTCGCAAGCACAGCCTTGA
CCTGCCCCACTCTGAACTAAAGAAGGAACTGCCGCCAGGGAAGTGAGCCCTCTGGAGGTAGTTGGAGCCAGGAG
TGTGCTGTCTGGCAAGGGGGCCCTGCCAGGGAAGGGGGTGTGTCAGCCTGCTCCCTCACGGGCCCTAGGCACCT
CCGGCAGGACCGAGCCGAACGACGGGAGTCGCTGCAGAAGCAAGAAGCCATTGCTGAGGTGGACTCCTCAGAGGA
CGACACCGAGGAAGGGCCTGAGAACAGCCAGGGTGACAGGAGCTGAGCTTGGCACCTCACCCAGAAGTGAGCCA
GAGTGTGGCCCTTAAAGGAGCAGGAGAGAGTGGGGAAGAGGATCCTTTCCCGTCCAGAGACCTAGGAGCCTGGG
CCCAATGGTCCCAAGCCTATTGACAGGGATCACACTGGGGCCTCCCAGAATGGAAGTCCCAGTGGTCCCCACAG
GAGGCTCGGGAGCCACAAGCCATTGAGGAGGCTGCCAGCTCCTCCTCAGCAGGCCCAACCTAGGTCAGTCTGG
AGCCACAGACCCCATCCCTCCTGAAGGTTGCTGGAAGGCCAGCACCTCCACACCCAGGCACCTAACAGCACTTTC
TCCCAGCACTTCGGGACTCACCCCAACAGCAGTTGCTCTCCTCCAGCTCCACCTCTGGGAAGCTGAGCATGTG
GTCCTGGAAATCCCTTATTGAGGGCCAGACAGGGCATCCCCAAGCAGAAAGGCAACCATGGCAGGTGGGCTAGC
CAACCTCCAGGATTTGGAAAACACAACCTCCAGCCCAGCCTAAGAACCTGTCTCCAGGGAGCAGGGGAAGACACA
GCCACCTAGTGCCCCCAGACTGGCCCATCCATCTTATGAGGATCCAGCCAGGGCTGGCTATGGGAGTCTGAGTG
TGCACAAGCAGTGAAAGAGGATCCAGCCCTGAGCATCACCCAAGTGCCCTGATGCCTCAGGTGACAGAAGGCAGGA
CGTTCCATGCCGAGGCTGCCCCCTCACCCAGAAGTCTGAGCCAGCCTCAGGAGGGGGCAAGAACCAGGGGGCCA
TCAAAAGCATCGGGATTGGCATTGGTTCCAGATGAGCTTTTAAAGCAAACATAGCAGTTGTTTGCCATTTCTTG
CACTCAGACCTGTGTAATATATGCTCCTGGAAACC

WO 2004/030615

PCT/US2003/028547

229/6881
FIGURE 214

GCAAGATGGTGGGTGAAAAAGTTGAGAAGCCAGATGCTAAAGAGAAGAAACCCAAAGCCAAGAAGGCTGATGTTG
GTGGCAAGGTGAAAAAGGGTAACCTCAAGGCTAAAAAGCCCAAGAAGGGAAAGCCCCATTGCAGCCGCAACCCCTG
TCCTTGTGAGAGGAATTGGCAGGTATTGCCGATCTGCCATGTATTCCAGAAAGGCCATGTACAAGAGGAAGTACT
CAGCCGCTAAATCTAAGGTTGAAAAGAAAAAGAAGGAGAAGGTTCTTGCAACTGTTACAAAACCAGTTGGTTGTG
ACAAGAATGGCGGTGCCCGGGTGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAA
AGCTGTTGAGCCATGGCAAAAAATCCTTCAGTCAGCACGTGAGGCCATTAGGGGCAAGAAGGTGGTTTTCTGAAG
CAGCTGGCTAGTGGTTTGTACTTGTGACTGGACCTCTGGTCCTCAATCGAATTCCTCTACGAAGAACATACCAG
AAATTTGTCATTGCCAC

WO 2004/030615

PCT/US2003/028547

230/6881
FIGURE 215

MVGEKVEKPDAKEKKPKAKKADVGGKVKKGNLKAKKPKKGKPHCSRNPVLVRGIGRYCRSAMYSRKAMYKRKYS
AKSKVEKKKKEKVLATVTKPVGCDKNGGARVVKLRLKMPRYPTEDVPRKLLSHGKKSFSQHVRP

WO 2004/030615

PCT/US2003/028547

231/6881
FIGURE 216

AATCTGCCATTTTCTGTCCCTGAGTGAGTCTCTGGCGTCCCAAATTGCCTGTTTTTCTCGCAGGCTCTATTCCGT
TCGCTGGTTCGCCACCTCAGGGGAACGATGGCCATGGAGTCCACAGCCACTGCCGCCGTGCGCCGCGGAGCTGGTT
TCTGCCGACAAAATTGAAGATGTTCTGCTCCTTCTACATCTGCAGATAAAGTGGAGAGTCTGGATGTGGATAGT
GAAGCTAAGAACTATTGGGTTTAGGACAGAAACATCTGGTGATGGGGGATATTCCAGCAGCTGTCAATGCATTC
CAGGAAGCAGCTAGTCTTTTAGGTAAGAAGTATGGAGAGACAGCTAATGAGTGTGGAGAAGCCTTCTTTTCTAT
GGGAAATCACTTCTGGAGTTGGCAAGAATGGAGAATGGTGTGTTGGGAAACGCCTTGAAGGTGTGCATGTGGAA
GAGGAAGAAGGAGAAAAACAGAAGATGAATCTCTGGTAGAAAAATAATGATAACATAGATGAGGAAGCAAGGGAA
GAGTTGAGAGAACAGGTTTATGACGCCATGGGAGAAAAAGAAGAAGCCAAAAAACAGAAGACAAGTCTTTGGCA
AAGCCTGAACTGATAAAGAACAGGACAGTGAAATGGAGAAGGGTGAAGAGAAGATATGGATATAAGTAAATCT
GCAGAGGAGCCACAGGAAAAAGTTGACTTGACTCTAGATTGGTTAACTGAAACCTCTGAAGAGGCAAAAGGAGGA
GCAGCACCAGAAGGACCGAATGAAGCTGAGGTCACTTCTGGGAAGCCAGAACAGGAAGTACCAGATGCTGAGGAA
GAAAAATCAGTTTCTGGAAGTGTATGTTCAAGAAGAGTGCAGAGAAAAAGGAGGTGAGGAGAAGCAGGGAGAGGTA
ATTGTGAGCATAGAGGAGAAGCCAAAAGAAGTTTCAAGAAGAGCAGCCTGTGGTGACTCTAGAAAAGCAGGGCACT
GCAGTGAGGTAGAAGCAGAGTCTTTAGACCCGACAGTCAAGCCAGTGGATGTGGGTGGGGACGAGCCAGAGGAG
AAGGTAGTTACCTCTGAAAACGAGGCAGGAAAGCGGTTCTTGAACAAGTGGTAGGTCAAGAAGTACCACCTGCT
GAAGAGTCACCAGAGGTGACAACAGAGGCTGCAGAGGCCTCAGCTGTAGAGGCTGGATCAGAAGTCTCTGAAAAG
CCTGGGCAGGAGGCTCCAGTTCTCCCTAAGGATGGTGCAGTCAATGGACCGTCAGTTGTAGGAGATCAGACTCCT
ATTGAACCACAGACTTCTATAGAAAAGACTGACAGAAACAAAAGATGGCTCAGGACTAGAGGAGAAGGTGAGGGCA
AAGCTGGTTCTAGTCAGGAGGAGACTAAGCTGTCTGTAGAAGAGTCTGAGGCAGCTGGAGATGGGGTTGATACC
AAGGTAGCCAGGGAGCTACTGAGAAATCACCTGAAGACAAAGTTCAAGATAGCTGCTAATGAAGAGACACAAGAG
AGAGAAGAACAGATGAAAGAGGGTGAAGAACTGAAGGCTCAGAAGAGGATGATAAAGAAAATGATAAGACCGAA
GAAATGCCAAATGATTAGTCTCTGAAAACAAGTCTCTTCAAGAAAATGAGGAGGAGGAGATTGGGAACCTAGAG
CTTGCTGGGATATGCTGGATTAGCAAAGTCACTTTTAAAGGCAAGAAACAAAAGAAGCACAGCTTTATGCT
GCCAGGCACATCTTAAACTCGGAGAAGTTAGTGTGAATCTGAAAACATATGTGCAAGCTGTGGAGGAGTTCCAG
TCCTGCCTTAACCTGCAGGAACAGTACCTGGAAGCCCACGACCGTCTCCTTGCAGAGACCCACTACCAGCTGGGC
TTGGCTTATGGGTACAACCTCTCAGTATGATGAGGCAGTGGCACAGTTCAGCAAATCTATTGAAGTCATTGAGAAC
AGAATGGCTGTACTAAACGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGCTGAATACAAGAAAGAAATTGAGGAA
CTAAAGGAAGTCTACCCGAAATTAGAGAGAAGATAGAAGATGCAAAGGAGTCTCAGCGTAGTGGGAATGTAGCT
GAACTGGCTCTGAAAGCTACTCTGGTGAGAGTTCTACTTCAGGTTTTCACTCCTGGTGGAGGAGGCTCTTCAGTC
TCCATGATTGCCAGTAGAAAGCCAACAGACGGTGCTTCTCATCAAATTGTGTGACTGATATTTCCACCTTGTC
AGAAAAGAAGAGGAAACCAGAGGAAGAGAGTCCCCGAAAGATGATGCAAAGAAAGCCAAACAAGAGCCGGAGGTG
AACGGAGGCAGTGGGGATGCTGTCCCCAGTGGAAATGAAGTTTTCGGAAAACATGGAGGAGGAGGCTGAGAATCAG
GCTGAAAGCCGGGCAGCAGTGGAGGGGACAGTGGAGGCTGGAGCTACAGTTGAAAGCACTGCATGTTAAGAGGGG
GCACAGCCCTCCTCCCAAGGGAAAGTGTTTTTGTATATAATGTATTTTTTCACTTTTGGAGGATTCTTTTTGTAT
AACTTCAATAAAGATTGTAAGCAAAGGTTGAGGCTTTGATGGTTTTTTTCTTAATTATTGGCTGAATCTGCCTTG
GAGCACTGCTGGTTTTATATATTAGCCAAAGGTTTTGTTCTGGCCTTCTGTACTGATCTGTGTTTCTGATCCTAA
TTCTATCTGTCTAACGTGGAGGTGATCAAGTGTGGCTGTAGGCCTTTGTTTTCCAATGGTGCTATATTCTGTTT
TCAAACACTTCACTGAACCCAGCTGTCTTGCAAACCTTTCAGTGGTGCTGTCCCTGGATGGGGGCTACAAAAACA
GAATTGGTGAAGATCTTGCTCTTCAGTGCTGAAAATGGATGATGGACTTTGGCTGTGAGCCAGGCCTAGGATGGT
TCTTGCTATATCCACCTAGTCTTCACCTGGGGCTATAATTCTGTCTGGAAAAAGAACTCTGAAAACCTGGGT
CAGGGGAATGATTCTAAGGAAAACGGTCTGCATTTGAGCTCTGGTTTGAAAGTAGCCAAGGGGACTGATGGTGG
ACACTCCAGATGTGGTTGGAAGCATATGTGGGGAGGCTGGCTGGTTGAGTTTTGTTATTTTCTGTATAGAAAGGT
TGAGATATATCAACACTTGAATTTGTTACCCATCTGCAGAATTGACTTCTCAAATAAAGATGCTAAAAATCT

WO 2004/030615

PCT/US2003/028547

232/6881
FIGURE 217

MAMESTATAA VAAELVSADKIEDVPAPSTSADKVESLDVDSEAKLLGLGQKHLVMDIPAAVNAFQEAASLLGK
KYGETANECGEAFFFYGKSLLLELARMENGVLGNALEGVHVEEEEKEKTEDESLENNDNIDEEAREELREQVYDA
MGEKEEAKKTEDKSLAKPETDKEQDSEMEKGGREDMDISKSAEEPQEKVDLTLDWLTETSEEAKGGAAPEGPNEA
EVTSGKPEQEVPADEEEKSVSGTDVQEECREKGGQEKQGEVIVSIEEKPKEVSEEQPVVTTLEKQGTAVEVEAESL
DPTVKPVDVGGDEPEEKVVTSENEAGKAVLEQLVGQEVPPAEESPEVTTEAAEASAVEAGSEVSEKPGQEAPVLP
KDGAVNGPSVVG DQTP IEPQTSIERLTETKDGSGLEEKVRACLVP SQEETKLSVEESEAGDGVDTKVAQGATEK
SPEDKVQIAANEETQEREEQMKEGEETEGSEEDDKENDKTEEMPND SVLENKSLQENEEEEIGNLELAWDMLDLA
KIIFKRQETKEAQLYAAQAHKLGLGEVSVESENYVQAVEEFQSCNLQEQYLEAHRLLAETHYQLGLAYGYNSQY
DEAVAQFSKSI EVIENRMAVLNEQVKEAGSSAEYKKEIEELKELLPEIREKIEDAKESQRSGNVAELALKATLV
ESSTSGFTPGGGGSSVSMIASRKPTDGASSSNCVTDISHLVRKKRKPEEESPRKDDAKKAKQEPEVNGGSGDAVP
SGNEVSENMEEEAENQAESRAAVEGTVEAGATVESTAC

WO 2004/030615

PCT/US2003/028547

233/6881
FIGURE 218

AGCCAGAAATGTGAAGTGCTAGCTGAAGGATGAGCAGCAGCTAGCCAGGCAAAGGGGGCAATGGCGGCTTCCTGT
GTTCTACTGCACACTGGGCAGAAGATGCCTCTGATTGGTCTGGGTACCTGGAAGAGTGAGCCTGGTCAGGTAAAA
GCAGCTGTTAAGTATGCCCTTAGCGTAGGCTACCGCCACATTGATTGTGCTGCTATCTACGGCAATGAGCCTGAG
ATTGGGGAGGCCCTGAAGGAGGACGTGGGACCAGGCAAGGCGGTGCCTCGGGAGGAGCTGTTTGTGACATCCAAG
CTGTGGAACACCAAGCACCACCCCGAGGATGTGGAGCCTGCCCTCCGGAAGACTCTGGCTGACCTCCAGCTGGAG
TATCTGGACCTGTACCTGATGCACTGGCCTTATGCCTTTGAGCGGGGAGACAACCCCTTCCCAAGAATGCTGAT
GGGACTATATGCTACGACTCCACCCACTACAAGGAGACTTGGAAGGCTCTGGAGGCACTGGTGGCTAAGGGGCTG
GTGCAGGCGCTGGGCCTGTCCAACCTTCAACAGTCGGCAGATTGATGACATACTCAGTGTGGCCTCCGTGCGTCCA
GCTGTCTTGCAGGTGGAATGCCACCCATACTTGGCTCAAAATGAGCTAATTGCCCACTGCCAAGCACGTGGCTTG
GAGGTAACCTGCTTATAGCCCTTTGGGCTCCTCTGATCGTGCATGGCGTGATCCTGATGAGCCTGTCTTGCTGGAG
GAACCAGTAGTCCTGGCATTGGCTGAAAAGTATGGCCGATCTCCAGCTCAGATCTTGCTCAGGTGGCAGGTCCAG
CGGAAAGTGATCTGCATCCCCAAAAGTATCACTCCTTCTCGAATCCTTCAGAACATCAAGGTGTTTGACTTCACC
TTTAGCCCAGAAGAGATGAAGCAGCTAAATGCCCTGAACAAAAATTGGAGATATATTGTGCCTATGCTTACGGTG
GATGGGAAGAGAGTCCCAAGGGATGCAGGGCATCCTCTGTACCCCTTTAATGACCCGTACTGAGACCACAGCTTC
TTGGCCTCCCTTCCAGCTCTGCAGCTAATGAGGTCTGCCACAACGGAAAGAGGGAGTTAATAAAGCCATTGGAG
CATCCAT

WO 2004/030615

PCT/US2003/028547

234/6881
FIGURE 219

MAASCVLLHTGQKMPLIGLGTWKSEPGQVKA AVKYALSVGYRHIDCAA IYGNEPEIGEALKEDVGPGKAVPREEL
FVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYA FERGDNPF PKNADGTICYDSTHYKETWKALEAL
VAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNELIAHCQARGLEVTAYSPLGSSDRAW RDPDE
PVLLEEPVVLALAEKYGRSPAQIILLRWQVQRKVICIPKSITPSRILQNIKVDFTF SPEEMKQLNALNKNWRYIV
PMLTVDGKRVPRDAGHPLYPFNDPY

WO 2004/030615

PCT/US2003/028547

235/6881
FIGURE 220

GTTCTTGCCTGGTGTCTGGTGGTTAGTTTCTGCGACTTGTGTTGGGACTGCTGATAGGAAGATGCTCTTCAGGAAAT
GCTAAAATTGGGCACCCCTGCCCCCAACTTCAAAGCCACAGCTGTTATGCCAGATGGTCAGTTTAAAGATATCAGC
CTGTCTGACTACAAAGGAAAATATGTTGTGTTCTTCTTTTACCCTCTTGACTTCACCTTTGTGTGCCCCACGGAG
ATCATTGCTTTTCAGTGATAGGGCAGAAGAATTTAAGAACTCAACTGCCAAGTGATTGGTGCTTCTGTGGATTCT
CACTTCTGTCACTAGCATGGGTCAATACACCTAAGAAACAAGGAGGACTGGGACCCATGAACATTCCTTTGGTA
TCAGACCCGAAGCGCACCATTTGCTCAGGATTATGGGGTCTTAAAGGCTGATGAAGGCATCTCGTTCAGGGGCCTT
TTTATCATTGATGATAAGGGTATTCTTCGGCAGATCACTGTAAATGACCTCCCTGTTGGCCGCTCTGTGGATGAG
ACTTTGAGACTAGTTCAGGCCTTCCAGTTCCTGACAAACATGGGGGAAGTGTGCCAGCTGGCTGGAAACCTGGC
AGTGATACCATCAAGCCTGATGTCCAAAAGAGCAAAAGAATATTTCTCCAAGCAGAAGTGAGCGCTGGGCTGTTTT
AGTGCCAGGCTGCGGTGGGCAGCCATGAGAACAAAACCTCTTCTGTATTTTTTTTTTCCATTAGTAAACACAAG
ACTTCAGATTGAGCCGAATTGTGGTGTCTTACAAGGCAGGCCTTTTCTACAGGGGGTGGAGAGACCAGCCTTTCT
TCCTTTGGTAGGAATGGCCTGAGTTGGCGTTGTGGGCAGGCTACTGGTTTGTATGATGTATTAGTAGAGCAACCC
ATTAATCTTTTGTAGTTTGTATTAAACTTGAACCTGAG

WO 2004/030615

PCT/US2003/028547

236/6881
FIGURE 221

MSSGNAKIGH PAPNFKATAVMPDGQFKDISLSDYKGKYVVFYPLDFTFVCPTEIIAFSDRAEEFKKLNCQVIG
ASVDSHFCHLAWVNTPKKQGGGLGPMNIPLVSDPKRTIAQDYGVKADEGISFRGLFIIDDKGILRQITVNDLPVG
RSVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQKSKEYFSKQK

WO 2004/030615

PCT/US2003/028547

237/6881
FIGURE 222

GCTCGGCTCACTGAGACCCGGTGGTCCAGACGCTGCTCCTGGCTGGGGTGGCGCTGCAGGGAGAACC GCGAGCTC
TCAGGGGTTCGGCGGTGACTTCTTTCCGGAAGAAAGCGAGGAACGCGCTCTGCGGGGTGAGCCGGACTCCCCAAC
TCCGGACGATCAGCCCAGGACTGAGAGCCCCGAAGTCCCCAACCACAAGTAAGCGGCCCCAGAAGGACAAGTCTA
GGTCGCCGTCCAGAGCGCCATGCGCGCGCCCGCCCTTCGTTTGTGCCACATCGCCTTCCACGTGCCCGCCGGGCA
GCCCCTAGCCCCGAACCTGCAGCGCCTCTTCGGCTTCCAGCCCCTGGCTTCGCGGGAGGTGGACGGCTGGCGGCA
GCTAGCCCTGCGCAGCGGCGACGCGGTCTTTTTGGTGAACGAGGGCGCAGGGTCTGGAGAGCCGCTGTACGGCCT
GGATCCGCGTCACGCCGTGCCAGCGCCACAAACCTGTGCTTCGACGTGGCGGACGCCGGCGCTGCAACCCGGGA
GCTGGCAGCGCTGGGCTGCAGCGTGCCTGTCCCTCCCGTTTCGCGTGCGGGACGCGCAGGGTGCCGCCACTTACGC
CGTGGTCAGCTCGCCTGCCGGCATCCTCAGCCTGACCTTGCTGGAGCGCGCTGGCTACCGCGGACCCTTCTTACC
CGGCTTCAGGCCCGTGTCTCTGCGCCTGGCCCCGGGTGGGTGAGCCGCGTGGACCACCTGACCTTGGCCTGCAC
CCCCGGCAGCTCCCCACACTTTTTCGCTGGTTCCACGACTGCCTGGGCTTTTGCCACTTGCCGCTGAGCCCAGG
TGAGGATCCCGAGCTGGGCCTCGAAATGACAGCAGGGTTTGGGCTTGGGGGACTGAGGCTTACAGCCCTGCAGGC
CCAGCCGGGCAGCATTGTCCCCACTCTTGTTCTGGCTGAGTCCCTTCCGGGGGCGACGACACGACAGGACCAGGT
GGAGCAGTTCCTGGCCCCGACACAAGGGGCCAGGCCTGCAGCACGTGGGGCTGTATACGCCTAACATTGTGGAGGC
CACTGAGGGGGTGGCAACTGCTGGAGGCCAGTTCTGGCTCCCCCTGGGGCATACTACCAGCAGCCAGGAAAGGA
GAGGCAGATCCGAGCTGCAGGGCACGAGCCTCATCTGCTTGCTCGACAGGGGATCCTGCTAGATGGTGATAAAGG
CAAGTTTCTGCTTCAGGTCTTCACCAAGTCCCTTTTTACTGAGGACACTTTCTTCCTGGAGCTGATTCAGAGGCA
GGGGGCCACTGGCTTTGGTCAGGGCAACATCAGAGCTCTGTGGCAGTCCGTACAGGAGCAATCTGCCAGGAGCCA
GGAAGCCCTAAGGATGCCCCAGGGCTGGGTGCAGCCAGCTGTCTGCAGCTCTGGGGAGACCAGCACAGAAGTGAAG
AACATCTGCAGGAGGCCCAACTAGTGAAAGGCTTTGCCTCCGGGGGGCAGGTGTGACTTCCATTTTCATCAGTGCC
TGCCAGAAGCTGTGTCTCTCATTGGGCTCCAAAGAGGTGGGATTTTTTAAACTAAAACATTTCTTATATACAGT
CTATAATAAATATGTAAGATACAAAGAACAATAAAAGAATTACACACTAGGAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

238/6881
FIGURE 223

MAAPALRLCHIAFHVPAGQPLARNLQRLFGFQPLASREVDGWRQLALRSGDAVFLVNEGAGSGEPLYGLDPRHAV
PSATNLCFDVADAGAATRELAALGCSVPVPPVRVRDAQGAATYAVVSSPAGILSLTLLERAGYRGPFLPGFRPVS
SAPGPGWVSRVDHLTLACTPGSSPTLLRWFHDCLGFCHLPLSPGEDPELGLEMTAGFGLGGLRLTALQAQPGSIV
PTLVLAESLPGATTRQDQVEQFLARHKGPGLQHVGLYTPNIVEATEGVATAGGQFLAPPGAYYQQPGKERQIRAA
GHEPHLLARQGILLDGDGKGKFLQVFTKSLFTEDTFFLELIQRQGATGFGQGNIRALWQSVQEQSARSQEA

WO 2004/030615

PCT/US2003/028547

239/6881
FIGURE 224

GACCACGATGAGTGTGCCGCACTTCCGGCCAGATCGCCGGATTTCCGCTGAGTGACCCTTACAAGTCCTTCTTGA
TCCTGAACTGGGTTAGGTGCCGCTGTTGCTGCTCGTGTTGAATCTAGAACCGTAGCCAGACATGGGACTGGAGGA
CGAGCAAAAGATGCTTACCGAATCCGGAGATCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCCT
AACAAACAGTGAGAGAGCAATGCGAGCAGTTGGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTGTGATGA
GCGTGTATCCTCTCGATCACATACAGAAGAGGATTGCACGGAGGAGCTCTTTGACTTCTTGCATGCGAGGGACCA
TTGCGTGGCCCAAACTCTTTAACAACCTGAAATTAAATGTGTGGACTTAATTCACCCCAGTCTTCATCATCTGG
GCATCAGAAATATTTCCCTTATGGTTTTGGATGTACCATTTGTTTCTTATTTGTGTAAGTTACATGAACC
TCATGGGTTTGGCTTAGGCTGGTAGCTTCTATGTAATTCGCAATGATTCCATCTAAATAAAAGTTCTATGATCTG
C

WO 2004/030615

PCT/US2003/028547

240/6881
FIGURE 225

MGLEDEQKMLTESGDPEEEEEEEELVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSHTTEEDCTEELFDFL
HARDHCVAHKLFNNLK

WO 2004/030615

PCT/US2003/028547

241/6881
FIGURE 226

CGCGCCTGAGGAGGAGGAGGAGGCGGGGGCGGCCATGGCTGCTGTGGTGGTGGCGGGCTGCGGGTGGCGCGGGACC
GGCGGTCTGCAGGTGGCCGGTCTCTACCGGGGCCTGTGCGCGGTGCGCAGCCGCGCCCTGGGCCTGGGGCTCGT
GTCACCCGCGCAGCTGCGCGTCTTCCCAGTGCGCCCCGGCTCGGGCCGGCCCGAGGGGGCGCCGACAGCAGCGG
GGTCGGGGCCGAGGCCGAGCTCCAGGCCAACCCTTTCTACGACCGCTACCGCGACAAGATCCAGCTGCTGCGCAG
GTCAGACCCAGCTGCTTTTGTAGTCCCGCCTGGAGAAACGCAGTGAATTTGGAAGCAGCCAGTGGGGCATTCCAG
GCAAGGTGATTTTATCAAATGTGTGGAACAGAAGACAGATGCCTTGGGGAAACAGTCTGTGAACAGAGGATTAC
TAAGGACAAGACTCTCAGTTCAATCTTTAACATTGAGATGGTAAAAAGAAAACTGCAGAAGAAATAAACAGAT
TTGGCAGCAATATTTTGCAGCAAAAGATACAGTCTACGCAGTTATTCCTGCAGAAAAGTTTGATTTGATCTGGAA
CCGGGCTCAGTCTGTCCAACATTTCTATGTGCTCTGCCAAGAAGGGAAGGTTATGAGTTTTTGTAGGACAATG
GACAGGTACTGAACTCCACTTCACTGCACTTATAAATATTCAGACCCGAGGGGAAGCTGCAGCCAGCCAGCTGAT
TTTATATCACTATCCTGAACTTAAGGAAGAAAAGGGCATAGTGCTGATGACTGCAGAAATGGATTCCACATTTCT
GAATGTTGCTGAGGCACAGTGCATCGCCAACCAAGTTCAGCTCTTCTACGCTACTGATCGGAAAGAGACCTACGG
GTTAGTGGAGACCTTTAACCTCAGACCAAATGAGTTCAAATATATGTCTGTCATCGCTGAATTGGAGCAAAGCGG
ACTTGGAGCAGAAGTGAATGTGCCCAGAACCAAAATAAGACTTAGAACTGTACAGGTTGGCCCTTCACCTAGTT
GACTCAGCCCTCGATAGTCTAGAGCCCACCCCTCCTCAGGAAGCTCAAGAGCTCAGCATTATAATGAGCAGTTG
GTAATGAGTTGCCCTATGTGCTTGTGCAAGCAGTCACAGAGATGAGCCCTATTACTTGATATTCAGGAACAAAG
GTACCTGAACATTCTGATAATTATCTCAGCATACTTGAGGTTTCCTTTTTTAAGTGTTCGAGGTTATAACAAGAG
ACAGCCAAGGACCTACAAGACAGTTGACTTGATTTTGCACAGTGTAACAGCGCAGTTGCATTCTGGCCACTTTGA
CCTTATAGCTCCCAAATGATGAGTTTGTGCTCTTTATGAAGTCAAGAGGATAATAAGCTTGAAGACCTGCTGT
AGTTAGATATGGGCTTTAATCCTTCCCAGGCACCAAGTCAGCTGAACAAAAGCATAAGCCAAACATCCTGTTTAA
CTGTAGAATAACCAGATATTCCCATCAGGTAAAGACTTCATCTAGATGATGCCCCCAGAGATGCCTTTAGTGT
AAGTAGCTGGCTTGGGGTATCAGCAAATTTAGGTATAGTTAGATAAACAGGTACAGGGCCTGCATACTATTAA
CCATAGTTTGTGGCACCCGCTTTTCTAACTCCACCTGTTAGAAGCTATGTGTTTGAAGGAATGAATCAGTGCAGT
ATAAATAAAATTCTTTTGTAAAGAG

WO 2004/030615

PCT/US2003/028547

242/6881
FIGURE 227

MAAVVVAAAGGAGPAVLQVAGLYRGLCAVRSRALGLGLVSPAQLRVFPVRPGSGRPEGGADSSGVGAEEAELQANP
FYDRYRDKIQLLRRSDPAAFESRLEKRSEFRKQPVGHSRQGDFIKCVEQKTDALGKQSVNRGFTKDKTLSSIFNI
EMVKEKTAAEIKQIWQQYFAAKDTVYAVIPAEEKFDLIWNRAQSCPTFLCALPRREGYEFFVGQWTGTELHFTALI
NIQTRGEAAASQLILYHYPELKEEKGIVLMTAEMDSTFLNVAEAQCIANQVQLFYATDRKETYGLVETFNLRPNE
FKYMSVIAELEQSGLGAELKCAQNQNKT

WO 2004/030615

PCT/US2003/028547

243/6881
FIGURE 228

ACCTGCCCTCATCCTGGCCCGCGACTGTAAGACCGGACCCACATCCAGACCAATCTTCCTGTCCGGCTGCTGCGA
CGCGGTCCGCAGGTTGCAGGCGGGCGGGCGGGCGCCTGAAGGTTACCGAGTGCATGACGGCCTCAGTTCCCGCG
CTGCCCCGCGCGCTGGCCCGCGACCTCCCCGCGCTCGCCGCCAGCCCTCGGGCCCGGCGGCGGCGGCGGCG
GTGGCGGCGACGGTCGCAGGAGGTGCCGTCTGCCTCCAGGTGCGCGCTTCGCTCCCGGAGCCGCGGAACCTCGGT
CGCGCCATGGCGTCCAACATGGACCGGGAGATGATCCTGGCGGATTTTCAGGCATGTACTGGCATTGAAAACATT
GACGAAGCTATTACATTGCTTGAACAAAATAATTGGGACTTAGTGGCAGCTATCAATGGTGTAAATACCACAGGAA
AATGGCATTCTACAAAGTGAATATGGAGGTGAGACCATAACCAGGACCTGCATTTAATCCAGCAAGTCATCCAGCT
TCAGCTCCTACTTCTCTTCTTCTTCAGCGTTTTGACCTGTAATGCCATCCAGGCAGATTGTAGAAAGGCAACCT
CGGATGCTGGACTTCAGGGTTGAATACAGAGACAGAAATGTTGATGTGGTACTTGAAGACACCTGTACTGTTGGA
GAGATTAAACAGATTCTAGAAAATGAACCTTCAGATACCTGTGTCCAAAATGCTGTTAAAAGGCTGGAAGACGGGA
GATGTGGAAGACAGTACGGTCTTAAATCTCTACACTTGCCAAAAACAACAGTCTTTATGTCCTTACACCAGAT
TTGCCACCACCTTCATCATCTAGTCATGCTGGTGCCCTGCAGGAGTCATTAAATCAAACTTCATGCTGATCATC
ACCCACCGAGAAGTCCAGCGGGAGTACAACCTGAACCTTCTCAGGAAGCAGTACTATTCAAGAGGTAAAGAGAAAT
GTGTATGACCTTACAAGTATCCCCGTTGCCACCAATTATGGGAGGGCTGGCCAACCTTCTGCTACAGACGACTCA
ATGTGTCTTGCTGAATCAGGGCTCTCTTATCCCTGCCATCGACTTACAGTGGGAAGAAGATCTTACCTGCACAG
ACCCGGGAACAGTCGGAAGAACAATCACCGATGTTTCATATGGTTAGTGATAGCGATGGAGATGACTTTGAAGAT
GCTACAGAAATTTGGGGTGGATGATGGAGAAGTATTTGGCATGGCGTCATCTGCCTTGAGAAAATCTCCAATGATG
CCAGAAAACGCAGAAAATGAAGGAGATGCCTTATTACAATTTACAGCAGAGTTTTCTTCAAGATATGGTGATTGC
CATCCTGTATTTTTTATTGGCTCATTAGAAGCTGCTTTTTCAAGAGGCCTTCTATGTGAAAGCCCGAGATAGAAAG
CTTCTTGCTATCTACCTCCACCATGATGAAAGTGTGTTAACCAACGTGTTCTGCTCACAATGCTTTGTGCTGAA
TCCATTGTTTCTTATCTGAGTCAAAATTTTATAACCTGGGCTTGGGATCTGACAAAGGACTCCAACAGAGCAAGA
TTTCTCACTATGTGCAATAGACACTTTGGCAGTGTTGTGGCACAACCATTCGGACTCAAAAAACGGATCAGTTT
CCGCTTTTCTGATTATTATGGGAAAAGCGATCATCTAATGAAGTGTGAAATGTGATACAAGGGAACACAACAGTA
GATGAGTTAATGATGAGACTCATGGCTGCAATGGAGATCTTCACAGCCCAACAACAGGAAGATATAAAGGACGAG
GATGAACGTGAAGCCAGAGAAAAATGTGAAGAGAGAGCAAGATGAGGCCTATCGCCTTTCACTTGAGGCTGACAGA
GCAAAGAGGGAAGCTCACGAGAGAGAGATGGCAGAACAGTTTCGTTTGGAGCAGATTGCAAGAACAAGAAGAG
GAACGTGAGGCCATCCGGCTGTCTTAGAGCAAGCCCTGCCTCCTGAGCCAAAGGAAGAAAATGCTGAGCCTGTG
AGCAAACGCGGATCCGGACCCCCAGTGGCGAGTTCTTGGAGCGGCGTTTCTTGCCAGCAACAAGCTCCAGATT
GTCTTTGATTTTGTAGCTTCCAAAGGATTTCCATGGGATGAGTACAAGTTACTGAGCACCTTTCTTAGGAGAGAC
GTAACCTCAACTGGACCCAAATAAATCATTATTGGAGGTAAAGTTGTTCCCTCAAGAAACCCTTTTCTTGAAGCA
AAAGAGTAAACACGGCCCGAGCGGTGGAACCAGCCATTCTTGACAAGCCAGCAGCCTGCGTCAGGAGAAGGGCTC
CTCGCCAACCCACCCACACGCTCGTCTCACTCAATTCAATGTACACTTCTGCCTCTTGCAAAATTGCTGGAAAA
AGTAATAATAAATATAGCTACTTAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

244/6881
FIGURE 229

CTCTGCCGAGCCTCCTTAAACTCTGCCGTTAAATGGGGGCGGGTTTTTCAACTCAAAAAGCGCTCAATTTTTT
TCTTTTCAAAAAAGCTGATGAGGTCGGAAAAAGGGAGAAGAAACCGGCACCCTCTCTGAGAGGCAACAGAAGC
AGCAATTGTTTCAGCGAAAAAGCAGCAAGGGAGGGAGTGAAGGAAAAAGCAAAAAGGGGGCGACACGCAAGT
GCCTGTAGGGGTGAAAGGAGCAGGGACCGCGATCTAGGGGGGGATCAGCTACAAAAGAACTGTCACCTGGGAGC
GGTGCGGCCAAGGAGGAAGCAGTGCTGCCAGGCTCTGCTCCAGGGCACAGCTGGCTGGCGGGCTGCCCTGTCCGCA
GCAAAGGGGCACAGGCCGGGGACCGGAGAGGTGGCAAAGTGGCACCGGGCGCCGAGGCTGCTGAGCGCTCGCCG
AGACGGCGACCGGACTGGCTGCCCGGAACTGCGGCGACTCTCCCTACTCAGAACTTGGCCTACGTTTCCCAGGA
CTCTCCCCATCTCCAGAGGCCCCCAAAAACCGGGAAAGGAAGGAAAGGACAGCGGGCGGCAGCAGCTCAATGAGT
GCCTACAGCAGAAAGCCTGAACGAGCTCGGTCTAGGCGGGAAAGTTCCCGGGGGGGCTGCCAGTGCAGCCGCAA
TGCTGCCGCGAGCTGCCCGCAGCTCCGGGCTCCGTAGACGCTTTCCGCATCACTCTCCTTCTCGGGCTGCCGG
GAGTCCCGGGACCTGGCGGGGCGGGCATGACGGGCTTCTCGGGGGCCCGCCGACGCCCCGGCAGCCTCCGGAGAC
GCGCGCCGAGCCCGGCTCCACGGCCTCTGAGGCTCGGGCGGGCTGCGGCTGCCTGGCGGGCGGGCTCCGGAGCT
TTCTGAGCGGCATTAGCCACGGCTTGGCCCGGACGCGACCAAAGGCTCTTCTGGAGAAGCCAGAGCACTGGG
CAATCGTTACGACCTGTAACCTGAGGGCCACCGAAGTGTACTCCCGTTTCGCTTTGGCGATCATCTTTAACCC
TCCGGAGCACGTCAGCATCCAGCCACCGCGGGCGCTCTCCAGCAGCGGAGGACCCAGGACTATCCCTTCGGCGAG
ACGGATGGAAACCGAGCCCCCTGGAGGACCTGCCCTGCAAGTTCTGCCTCACACGGCTCAAGTCACCACCGTGAA
CAAGGGACCCTAAAGAATGGCCGAGCCTTGGGGGAACGAGTTGGCGTCCGCAGCTGCCAGGGGGGACCTAGAGCA
ACTTACTAGTTTGTGCAAAATAATGTAAACGTCAATGCACAAAATGGATTTGGAAGGACTGCGCTGCAGGTTAT
GAAACTTGGAATCCCGAGATTGCCAGGAGACTGCTACTTAGAGGTGCTAATCCCGATTTGAAAGACCGAAGTGG
TTTCGCTGTCATTGATGCGGCCAGAGCAGGTTTCTGGACACTTTACAGACTTTGCTGGAGTTTCAAGCTGA
TGTTAACATCGAGGATAATGAAGGGAACCTGCCCTTGCACTTGGCTGCCAAAGAAGGCCACCTCCGGGTGGTGGA
GTTCTGGTGAAGCACACGGCCAGCAATGTGGGGCATCGGAACCATAAGGGGGACACCGCCTGTGATTTGGCCAG
GCTCTATGGGAGGAATGAGGTTGTTAGCCTGATGCAGGCAAACGGGGCTGGGGGAGCCACAAATCTTCAATAAAC
GTGGGGAGGGCTCCCCACGTTGCCTCTACTTTATCAATTAAGTGAAGTCTCCTGACTTTTAAATGTCATTTG
TAAAATACAGTTCTGTCATATGTTAAGCAGCTAAATTTCTGAAACTGCATAAGTGAAATCTTACAACAGGCT
TATGAATATATTTAAGCAACATCTTTTAACTGCAAAATCTGTTCTAACATGTAATTGCAGATAACTTTGACTT
TCTTCTGAATATTTTATCTTTCTTGGCTTTTCCCTTGTCTCCCTTTTGCCAATCTCAACACCCAAGTTGAAGA
CTTTGTTTTTAAATGGTTTGCCTGATGCTTTTGTCTAATTAACACTTTCAAACAGGAAAAAAAAAAAAAA
AAAA

WO 2004/030615

PCT/US2003/028547

245/6881
FIGURE 230

MAEPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDLKDRTGFAVIH
DAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRNHKGD TACDLARLYGRN
EVSLSMQANGAGGATNLQ

WO 2004/030615

PCT/US2003/028547

246/6881
FIGURE 231

AAAACACCAAATGGTGGATGACACCAAGTGCAGCGGGGGGGGGCCCGAGGCCCTGGGATCGGGGAAGTGCGGTGGC
TTCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTTCGCAGCCGTAGACGGGGCCGGGGCCGAGGCCGCGGA
GCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCCCGTACCAAGCTGGGCTGCTTGGTGAAGGACATGAAG
ATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCATTAAAGGAATCAGAGATCATTGACTTTTTCTGGGG
GCCTCTCTCAAGGATGAGGTTTTGAAGATTATGCCAGTGCAGACGCAGACCCGTGCTGGCCAGCGCACCAGGTTT
AAGGCGTTTGTGCTATCGGGGACTACAATGGCCACGTCCGTCTGGGTGTTAAGTGCTCCAAGGAGGTGGCCACC
GCCATCCATGGGGCCATCATCCTGGCCAAGCTCTCCATTGTCCCCGTGCGCAGAGGCTACTGGGGGAACAAGATT
GGCAAGCCCCACACCGTCCCTTGCAAGGTGACAGGCCGCTGCGGCTCTGCACTGGTGCACCTCATCCCTGTACCC
AGGGGCACTGGCATTGTCTCCGCACCTGTGCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTGCACC
TCAGCCTGGGGCTGCACTGCCACCCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATTTCTAAGACCTACAGC
TACCTGACCCCCGACCTCTGGAAGGAGACTGTATTTACCAAGTCTCCCGATCAGGAATTCAGTACCACCTCATC
AAGGCCCACGCCAGAGTCTCCGTGCAGCGGACCCAGGCTCCAGCTGTGGCTACAACATAGGGTTTTTAGACAAGG
AAAATAAAGCGAATTAAGCGT

WO 2004/030615

PCT/US2003/028547

247/6881
FIGURE 232

MGNCGGFRGGFGSGIRGRGRSRRRGRGRGRGARGGKAEDKEWMPVTKLGCLVKDMKIKSLEEIYLFSLPIKESEI
IDFFLGASLKDEVLKIMPVQTQTRAGQRTRFKAFVAIGDYNHVG LGVKCSKEVATAIHGAII LAKLSIVPVRRG
YWG NKIGKPHTVPCKVTGRCGSALVHLIPVPRGTGIVSAPVPKKLLMMAGIDDCCTSAWGCTATLG NFAKATFDA
ISK TYSYLTPDLWKETVFTKSPDQEFTDHLIKAHARVSVQRTQAPAVATT

WO 2004/030615

PCT/US2003/028547

248/6881
FIGURE 233

ATGTCTAAGTCAGAATCTCTTAAAGAGCCCCGAACAGCTGCAGAACTCCTCACTGGAGGGTTGAGCATTGAAGCA
ACCAATGAGAGCCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCACGGACTGTGTGGTCCTGAGAGATCCAAAC
ACTAAGTGCTCCAGGGGCTTTGGGTTTGTACATATGCCACTGTGGAGGAGGTGGATGCAGCCACAAATGCAAGG
CCACACAAGGTGGATGGAAGAGTTGTGGAAACAAAGAGAGCTGTCTCAAGAGAAGATTCCCAAAGACCAGGTGCT
CACTTAACTGTGAAAAAGTTTGAAAAATGGAAGTGATTGAAATCATGACTGACCATGGCAGTGGCAAGAAAAGG
GACTTTGCCTTTGTAACTTTGATGACCATGACTCCGTGGATAAGACTGTCATTTCAGAAATACCATATTGTGAAT
GGCCACAACGTGTAAGTTAGGAAAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGGTCGA
ACAGGCTCCTTGATGCCTAAAGCCCAATGTCTGGCATTTCGAGCCCTCCATGACAGGTTCCCAGCTTTCTGCAAG
GCCATGCTCCTCACGGCCTATGACTGCCTCCTGTTCTGCGCCTGTCAGGTCTTCCACCTCACCCCTCTTCTCAGC
CTATCCAAGCCCATTTCAGTCTTCAGGCGAGCTCTAG

WO 2004/030615

PCT/US2003/028547

249/6881

FIGURE 234

MSKSESLKEPEQLQKLLTGGLSIEATNESLRSHFEQWGLTDCVVL RDPNTKCSRGFGFV TYATVEEVDAATNAR
PHKVDGRVVETKRAVSREDSQRPGAHLTVKKFGKMEVIEIMTDHGSGKKRDFAFVTFDDHDSVDKTVIQKYHIVN
GHNCEVRKALSKQEMASASSQRGRTGSLMPKAQCLAFEPSMTGSQLSCKAMLLTAYDCLLFCACQVFHLTPLLS
LSKPIQSSGEL

WO 2004/030615

PCT/US2003/028547

250/6881
FIGURE 235

CGGTCCCGCACTGGTGCAGCCATGTCCTCTTCCCCGTGGGAGCCTGCGACCCTGCGCCGGGTGTTCTGTGGTGGG
GTTGGCATGACCAAGTTTGTGAAGCCTGGAGCTGAGAATTCAAGAGACTACCCTGACTTGGCAGAAGAAGCAGGC
AAGAAGGCTTTAGCTGATGCACAGATCCCTTATTGAGCAGTGGACCAGGCATGTGTTGGCTATGTTTTTGGTGAC
TCTACCTGTGGGCAGAGGGCTATCTATCACAGTTTGGGAATGACTGGAATTCCTATAATCAATGTCAACAATAAC
TGTGCTACTGGTTCCTACTGCTTTGTTTATGGCCCGCCAGCTGATTGAGGGTGGTGTGGCAGAATGTGTCTTGGCT
CTTGGGTTTGAGAAGATGAGTAAGGGAAGCCTTGAATAAAAAATTTTTCAGATAGAACCATTCCCACTGATAAGCAT
GTTGACCTCCTGATCAATAAGTATGGATTGTCTGCTCACCCAGTTGCTCCTCAGATGTTTGGGTATGCTGGAAAA
GAACATATGGAAAAATATGGAACAAAAATTGAACACTTTGCAAAAAATTGGATGGAAAAATCATAAACATTTCAGTT
AATAACCCGTATTCCCAAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAGTTTTTGATTTT
TTGACTATCTTACAATGTTGTCCCACTTCAGATGGTGTGTCAGCAGCAATTTTGGCCAGTGAAGCATTGTGACAG
AAGTATGGCCTGCAATCCAAAGCTGTGGAAATTTTGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAA
GAAAAAGCATTATTAAATGGTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAAATGCTATGAGAAATCTGGC
CTGACACCAAATGATATTGACGTAATAGAATTCACGATTGCTTTTCTACCAACGAACCTCCTGACTTATGAAGCA
CTCGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAGATAATACATATGGAGGAAAGTGGGTC
ATAAATCCTAGTGGTGGACTGATTTCAAAGGGACACCCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTC
TGCTGGCAGCTGAGAGGGGAAGCCGGAAGAGGCAAGTTTCTGGTGCAAGGTGGCTCTGCAGCATAATTTAGGC
ATTGGAGGAGCTGTGGTTGTAACACTCTACAAGATGGGTTTTCCGGAAGCCGCCAGTCTTTTAGAACTCATCAA
ATTGAAGCTGTTCCAACCAGCTCTGCAAGTGATGGATTTAAGGCAAATCTGTTTTTAAGGAGATTGAGAAGAAA
CTTGAAGAGGAAGGGGAACAGTTTGTGAAGAAATCGGTGGTATTTTTGCCTTCAAGGTGAAAGATGGCCCTGGG
GGTAAAGAGGCCACCTGGGTGGTGGATGTGAAGATGGCAAAGGATCAGTGCTTCCTAACTCAGATAAGAAGGCT
GACTGCACAATCACAATGGCTGACTCAGACTTCCTGGCTTTAATGACTGGTAAATGAATCCTCAGTCGGCCTTC
TTTCAAGGCAAATTGAAAATCACTGGCAACATGGGTCTCGCTATGAAGTTACAAAATCTTCAGCTTCAGCCAGGC
AACGCTAAGCTCTGAAGAATCCCTTTGGCTACTTTTGAAAATCAAGATGAGATATATAGATATATATCCATACA
TTTTATTGTCAGAAATTTAGACTGAACTACACATTGGCAAATAGCGTGGATAGGATTTGTTTCTTAATGGGTGTG
ACCAATCCTGTTTTTCTATGCTCTGGGTGAATAGAGCCTGATGGTATACTACTGCTTTGCGGAATTGCATACAA
CTGTGCATTACAAAGTTAATATGGTAATTATGGTCTGGGGTAAATGAGTTTCAGAATAAAATTAGGAACAGTA
AAATCCAAAGAACTATGTAAACAAAAAAGCTTTTGTTTTGCTTACAAAGTATATTTAAGGATTATTCTGCTGAAG
ATTGAGTTTAAAGATTTTCTTGGGAGAACTAAGTAAGAAACACAATGCCAACAGCTGGCCAGTAATTAGTGTG
TGCATTTCATGTCATTAATCAATTTCTCAATAGTTCTTAAATAGTGAGATTAAAAATCTAAAAATTTTGCATT
TCATGCTATCAGAAACAGTATTTTCTTCCCAAATCAAAATAAAAAGAAATATGATCAGAGCTTGAACACAGGCTTA
TTTTTAAATAAAAAATATTTTTAACATGGGTTTCTTATTGAAAAATCAGTGTATTAGTCATAAAACACCATCAT
TAAGAATAATTGAACAATAAAGTTTGCCTTTCAGATGCAGTTTCAAATTTATAATCTCATTTCATTTATAACGTT
CTCAGTCTTTGTTATAATTTTCTTTTTCATGTAAGTTTAAATATCTGCATTTATCTTTTTTCTAGTTTTTCT
AATACTAATGTTATTTTCTTAAATTCAGTGAGATATAGGATAAAATAATGCTTTGAGAAGAATGTTTAATAGAAA
ATTAAATAACTTTTTCTGGCA

WO 2004/030615

PCT/US2003/028547

251/6881
FIGURE 236

MSSSPWEPATLRRVFVVGVMKTFVKPGAENSRDYPDLAEEAGKKALADAQIPYSAVDQACVGYVFGDSTCGQRA
IYHSLGMTGIP I INVNNNCATGSTALFMARQLIQGGVAECVLALGF EKMSKSLGIKFSDRTIPTDKHVDLLINK
YGLSAHPVAPQMFGYAGKEHMEKYGTKIEHFAKIGWKNHKHSVNNPYSQFQDEYSLDEV MASKEVDFLTILQCC
PTSDGAAAAILASEAFVQKYGLQSKAVEILAQEMMTDLPSSFEEKSIIKMGVFDMSKEAARKCYEKSGLTPNDID
VIELHDCFSTNELLTYEALGLCPEGQGATLVDRGDNTYGGKWVINPSGGLISKGHPLGATGLAQCAELCWQLRGE
AGKRQVP GAKVALQHNLGIGGAVVVTLYKMGFPEAASSFRTHQIEAVPTSSASDGFKANLVFKEIEKKLEEEGEQ
FVKKIGGIFAFKVVDGPGGKEATWVVDVKNGKGSVLPNSDKKADCTITMADSDFLALMTGKMNPQSAFFQGLKI
TGNMGLAMKLQNLQLQPGNAKL

WO 2004/030615

PCT/US2003/028547

252/6881
FIGURE 237

GGCCCTGCGCGCGGCAACATGGCGGGGTCCAGGTGGAGGTCTTGAGGCTATCAGATCGGTATGGCATTGGCGTCC
GGGCCCCGAAGGCGGGCGCTAGCTGGCTCCGGGCAGCTCGGCCCTTGGGGGCTTCGGGGCCCCGAGACGCGGGGCG
TATGAGTGGGGCGTGCGCTCCACGCGGAAGTCGGAGCCTCCTCCCCTGGATAGGGTGTACGAGATCCCTGGACTG
GAGCCCATCACCTTTGCGGGGAAGATGCACCTTCGTGCCCTGGCTGGCGCGGCCGATCTTTCCGCCCTGGGACCGC
GGCTACAAGGACCCAAGGTTCTACCGCTCGCCCCCTCTTCACGAGCATCCGCTGTACAAAGACCAGGCCTGCTAT
ATCTTTACCAACCGTTGCCGCCTTCTCGAGGGGTGTAAAGCAGGCCCTCTGGCTCACCAAGACCAAGTTAATAGAA
GGCCTTCCCGAGAAAGTGCTTAGCCTTGTTGATGATCCAAGGAACCACATAGAGAACCAAGACGAGTGCGTTCTG
AATGTGATCTCTCACGCCCCGTCTCTGGCAGACCACTGAGGAAATCCCCAAGAGAGAGACCTACTGCCCGGTCATC
GTGGACAACCTAATACAGCTGTGTAAATCTCAGATTCTCAAGCATCCTTCTCTGGCCAGGAGGATCTGTGTCCAA
AACTCCACGTTTTCTGCTACCTGGAACCGAGAGTCTCTTCTCCTTCAAGTCCGTGGTTCTGGTGGAGCCCGACTG
AGACTAAGGATCCTCTGCCCCACCATCGCCTCCAGAGAGGAGATTGAAGCTACTAAGAATCATGTTCTAGAGACC
TTCTACCCCATATCACCCATCATCGATCTTCATGAATGCAATATTTATGATGTGAAAAATGACACAGGATTCCAG
GAAGGCTATCCTTACCCCTATCCCCATACCTGTACTTACTGGACAAAGCCAATTTACGACCACACCGCCTTCAA
CCAGATCAGCTGCGGGCCAAGATGATCCTGTTTGTCTTTTGGCAGTGCCCTGGCTCAGGCCCGGCTCCTCTATGGG
AATGATGCCAAGGTCTTGAGCAGCCCGTGGTGGTGCAGAGCGTGGGCACGGATGGACGTGTCTTCCATTTCCCTA
GTGTTTCAACTGAATACCACAGACCTGGACTGTAACGAGGGTGTCAAGAATTTGGCCTGGGTGGACTCAGACCAG
CTCCTCTATCAGCATTTTTGGTGTCTCCCAGTGATCAAAAAGAGAGTGGTTGTGGAACCTGTTGGGCCAGTTGGT
TTCAAGCCAGAGACATTCAGAAAGTTTTAGCTCTATATTTGCATGGTGTGCGTGGAGCGGAGGACCCCTCTGAA
TCCTGAAACCCCTCTTGCTCTCTTCCACGGAAGAGGGCCTGGGCCCCGTGGAGCCTCAGTGCCCGTTTGGCCTG
CTGCTCTCGCTGACAATAAAGAGCCCTTGCGTTGC

WO 2004/030615

PCT/US2003/028547

253/6881
FIGURE 238

MALASGPARRALAGSGQLGLGGFGAPRRGAYEWGVRSTRKSEPPPLDRVYEIPGLEPITFAGKMHFVPWLARPIF
PPWDRGYKDPRFYRSPPLHEHPLYKDQACYIFHHRCRLLEGVKQALWLTGTKLIEGLPEKVLSLVDDPRNHIENQ
DECVLNVISHARLWQTTEEIPKRETYCPVIVDNLIQLCKSQILKHPSLARRICVQNSTFSATWNRESLLLQVRGS
GGARLSTKDPLPTIASREEIEATKNHVLETFYPISPIIDLHECNIYDVKNDTGFQEGYPYPYPHTLYLLDKANLR
PHRLQPDQLRAKMILFAFGSALAQARLLYGNDKVLQPVVVQSVGTDGRVFHFLVFQLNTTDLDCNEGKVLAW
VDSQQLLYQHFWCLPVIKKRVVVEPVGPVGFKPETFRKFLALYLHGAA

WO 2004/030615

PCT/US2003/028547

254/6881
FIGURE 239

CCGCGGCCGGGGCTGACGCTTTGACAGCTGGAAAGAGCGCGGAGCCAGCGCCTGGGGGGGAGGGAGGGGAGCGCG
GCGAGGAGAGCGCCAGCGAGCGAGAGAGCGAGCGAGCGCGCGGGGAGGGGGCCGGGAGCGAGGGGCAGCTCGGGAG
AGCCGGAGCGGTAGCGGCGGCGGCGGCGGCGGCGGCGAGGCTCGGCGCCCTCTTCCCTGCAAAACCATGTTTGCCA
AAGGCAAAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTCGGGAAAAGTTAGCTTTATACGTCTACGAATATTTAC
TGCACGTAGGAGCACAGAAATCTGCACAGACCTTCTTATCGGAGATTTCGATGGGAAAAAACATCACGTTGGGAG
AACCGCCTGGGTTTTTGCACCTCGTGGTGGTGTGTATTTTGGGACCTTTACTGTGCAGCTCCTGAAAGGAGAGACA
CTTGTAACATTCAAGTGAAGCAAAAGCCTTTCATGATTATAGTGCAGCAGCTGCCCCGAGCCCCGCTGCTTGGCA
ACATTCCCCCAACGATGGGATGCCGGGAGGCCCCATCCCGCCAGGTTTCTTTCAGGGTCCTCCGGGGTCACAGC
CCTCGCCGCACGCACAGCCTCCACCTCACAATCCTAGCAGCATGATGGGACCCACAGTCAGCCTCCGGGAGGAG
TTCTGGGACACAGCCATTGCTGCCCAATTCTATGGATCCACACGACAACAAGGCCACCCCAACATGGGAGGAT
CAATGCAGAGAATGAACCTCCCCGAGGCATGGGGCCCATGGGTCCCGGCCACAGAATTACGGCAGCGGCATGA
GACCACCACCCAACTCCCTCGGCCCCGCCATGCCCGGGATTAACATGGGCCCCGGGAGCTGGCAGACCCTGGCCCA
ATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGGGACCCCCTGGTGGTGGCG
GTCTCCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCCAGTGACAACATCTACACAATGATTA
ATCCAGTGCCGCCTGGAGGCAGCCGGTCCAATTCCCGATGGGTCCCGGCTCGGACGGTCCGATGGGCGGCATGG
GTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGACTTCCAAAAAATTCTCCTA
ACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAGCTAGGAGGGAACTTCCTCCACT
CCTTTCAGAACGACAATTATTCTCCAAGCATGACGATGAGTGTGTGATCCCCCTTCTCCGAGACGCTGAGAGAG
CAGGCATTGCAGGCGGGAAGATGCCAGAAATTATGCAAGAAGTGAGGTGTCATTATCCAGGAGCTGGTGGGGAGG
GCATCTCCCTGCTCCCTCAACCCCTCCACCCCATCCACGCCCCCTACCTTTCCCAATTTTAGTTTCATGCAA
TAAAAAGGCCAACTTTTATTCCATAAAACAAAAA

WO 2004/030615

PCT/US2003/028547

255/6881
FIGURE 240

MFAKGKGSAPVSDGQAREKLALYVYEYLLHVGAQKSAQTFLSEIRWEKNITLGEPPGFLHSWWCVFWDLYCAAPE
RRDTCEHSSEAKAFHDYSAAPSPVLGNIPPNDGMPGGPIPPGFFQGPPGSQPSPHAQPPPHNPSSMMGPHSQP
PGGVPGTQPLLPNSMDPTRQQGHPNMGGSMQRMNPPRGMGPMGPGPQNYGSGMRPPPNLGPAMPGINMGPAGR
PWPNPNSANSIPYSSSSPGTYVGPPGGGGPPGTPIMPSPADSTNSSDNIYTMINPVPPGGSRSNFPMPGSDGPM
GGMGMEPHHMNGSLGSGDIDGLPKNSPNNISGISNPPGTPRDDGELGGNFLHSFQNDNYSPSMTMSV

WO 2004/030615

PCT/US2003/028547

256/6881
FIGURE 241

ATGTACGCCTTTGTGCGGTTCTTGAGGACAACGTCTGCTACGCGCTGCCCGTGTGCTGCGTGCGCGACTTCAGC
CCCCGCTCGCGGCTGGATTTTGACAACCAGAAGGTGTACGCCGTGTACCGGGGCCCGGAGGAATTGGGCGCCGGG
CCCGAGAGCCCCCGCGCGCCCCCGCGACTGGGGCGCGCTGTTGCTCCACAAGGCCAGATCCTGGCGCTGGCA
GAAGACAAATCTGACCTTGAAAACAGTGTGATGCAGAAGAAAATAAAAATCCCCAAGCTTTCTCTTAATCATGTA
GAAGAAGATGGAGAGGTTAAAGATTATGGGGAAGAAGATTTACAGCTTAGACACATCAAGGATTGTCTGGGGAAA
TATTGATCTGCAGTCCAAGAAAATCCCAGCTGCCCTTGCCCTGAACTGATTCTCGTTGTCTACACAGAGACCTGA
GGGGCGGAAGCCGAGCGAAGTGGCGCACAAAGAGCATCGAGGCGAGTGGTGGCTCGGCTAGAGAAGCAGAACGGCCT
GAGCCTGGGCCATAGCACGTGTCCGGAAGAGGTCTTCGTGGAGGCCCTGCCAGGCACAGAGGACATGGACAGTCT
AGAAGATGCTGTGGTGCCCCGGGCTCTGTATGAGGAGCTGCTGCGCAACTACCAGCAGCAACAGGAAGAGATGCG
CCACCTCCAGCAGGAGCTGGAGCGGACTCGGAGGCAGCTGGTACAACAGGCCAAGAAGCTCAAGGAGTACGGGGC
ACTTGTGTCTGAAATGAAGGAGCTCCGTGACCTTAACCGGAGGCTCCAGGACGTGCTGCTCCTGAGGCTTGGCAG
CGGTCCCGCCATTGATCTGGAAGAAAGTAAAGTCAGAAATGTCTCGAGCCCGAGCCGGAGTTACGGAGCACTTTCAG
TGAGGAAGCAAATACGTCGTCCTATTACCCCGCTCCTGCGCCTGTGATGGACAAGTATATCCTAGACAATGGCAA
GGTCCATCTGGGAAGCGGGATTGGGTTGATGAGGAGAAATGGCACCAGCTACAAGTAACCCAAGGAGATTCCAA
GTACACGAAGAACTTGGCAGTTATGATTTGGGGAACAGATGTTCTGAAAAACAGAAGCGTCACAGGCGTCGCCAC
AAAAAAAAAGAAAGATGCAGTCCCTAAACCACCCCTCTCGCCTCGCAAATAAGCATCGTCAGAGAGTGTGTTGTA
TGACAGAATAGCACAAAGAACTGTGGATGAACTGAAATTGCACAGAGACTCTCCAAAGTCAACAAGTACATCTG
TGAAAAAATCATGGATATCAATAAATCCTGTAAAAATGAAGAACGAAGGGAAGCAAAATACAATTTGCAATAAAC
TTTGGATTTTTCAT

WO 2004/030615

PCT/US2003/028547

257/6881
FIGURE 242

MDSLEDVVPRALYEELLRNYQQQQEEMRHLQQELERTRRQLVQQAKKLKEYGALVSEMKELRDLNRRLQDVLLL
RLGSGPAIDLEKVKSECLEPEPELRSTFSEEANTSSYYPPAPAPVMDKYILDNGKVHLGSGIWWDEEKWHQLQVTQ
GDSKYTKNLAVMIWGTDLKNRSVTGVATKKKKDAVPKPPLSPRKLSIVRECLYDRIAQETVDETEIAQRLSKVN
KYICEKIMDINKSCKNEERREAKYNLQ

WO 2004/030615

PCT/US2003/028547

258/6881
FIGURE 243

CCTTTCGTTGCCTGATCGCCGCCATCATGGGTCGTATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTAC
CCTATCGACGCAGCTTCCCCACTTGGTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAAACTGGCCA
AGAAGGGCCTTACTCCTTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTTGCACAAGTACGTTTTGTGA
CAGGCAATCTCTACCATTTAATTAAGAAAGCAGTTGCTGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGA
TGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATTCACCGTTTG

WO 2004/030615

PCT/US2003/028547

259/6881
FIGURE 244

CGCCGCCATCATGGGTCTGATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTACCCCTATCGACGCAGCTT
CCCCACTTG GTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAACTGGCCAAGAAGGGCCTTACTCC
TTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTG CACAAGTACGTTTTGTGACAGGCAATAAAATTTT
AAGAATTCTTAAGTCTAAGGGACTTGCTCCTGATCTTCCTGAAGATCTCTACCATTTAATTAAGAAAGCAGTTGC
TGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATT
CACCGTTTGGCTCAATATTATAAGACCAAGCGAGTCTCCCTCCCAGTTGGAAATATGAATCATCTACAGCCTCT
GCCCTGGTCGCATAAATTTGTCTGTGTACTCAAGCAATAAAATGATTGTTTAACTAAAATAAAACAAAAACAAA
ACAAAAAA

WO 2004/030615

PCT/US2003/028547

260/6881
FIGURE 245

AGAAGATGCTTCAAATTCAACCCGAGAAGGATATCATTGTAGAGTTTATCAAAAATGGAGATTTCAAGTATGTCC
GCATGCTGGGGGCACTTTACATGAGGCTGACAGGCACTGCAATTGATTGCTACAAGTACTTGGAACCTTTGTACA
ATGACTATCGAAAAATCAAGAGCCAGAACCAGAAATGGGGAGTTTGAATTGATGCATGTTGATGAGTTTATTGATG
AACTATTGCACAGTGAGAGAGTCTGTGATATCATTCTGCCCCGACTACAGAAACGCTATGTATTAGAGGAAGCTG
AGCAACTGGAGCCTCGAGTTAGTGCTCTGGAAGAGGACATGGATGATGTGGAGTCCAGTGAAGAGGAAGAAGAGG
AGGATGAGAAGTTGGAAAGAGTGCCATCACCTGATCACCGCCGGAGAAGCTACCGAGACTTGGACAAGCCCCGTC
GCTCTCCACACTGCGCTACAGGAGGAGTAGGAGCCGGTCTCCAGAAAGGCGGAGTCCGATCTCCCAAAAGGAGAA
GCCCCCTCCCTCGCCGAGAAAGGCATCGGAGCAAGAGTCCAAGACGTACCGCAGCAGGTCCCAGATCGGCGGC
ACAGATCCCGTTCCAAGTCCCAGGTCATCACCGTAGTCACAGACACAGGAGCCACTCAAAGTCTCCCGAAAGGT
CTAAGAAGAGCCACAAGAAGAGCCGGAGAGGGAATGAGTAATGGACTCAGTTTGGTTTGTAGTCCACATGGCCTCC
TGTGGATATAAGGATATCTGTATGTGGAAGGATTAAGATCTCCCCAGGCAGCTATAAGAATATTTTAGTTTTTT
TCTTATCAAGTTTCTCAACCTTTATTTTAAATGAAGGAGGTGCTGAGTTTGTATCTTTTAAATCATAATCAACA
TCAGTTTTTGACCCAACCTAAGTGTGACTGATTCAAATATGAGAGTATAAAGGATCTGGAGGTTGGGGATATG
ACTGACAAGGAAAGGCTGTGGCCACCTGATGACCTTTCCCTTTTATTAAACCGGACACACCTGTTTCCCATTT
CGCTGTAGTTTGTGTTTTGGTTTGTGTTGGTGGAACTGCTTTGAGAATCCTGGGATTTGTGCTGCTGCTGTTAT
TCAAAGATCAAAGGAGTAAACATAGTTGCTCCTAACTTTTTTCCAGCAGCAGCAAGTGGTAATAAACATGAAAA
CTGGTTTGTAGCAGTTTTGAAAGAATAGAATGCATTCAAATGTAAGGCTGCTTCTGGATCATTAAAGCCAGTTTC
ATCAAACAGTTCAACAGAGAGCAGCACTTAATACCCTTTATACAGCCCATTTTTTCATAGTTTCAATTGTTCTTG
CCCACAAGCTTGAAATCCAGGTTAAGGTATCCAGCCTTTATCATATAAGCATTGACATTATCCAGGCCTAGTCAG
TAGCAGTAGGGTAACGGGATTGAAAAAGATTTGATGGAGAGGAAAGTATCTAATATTAGTCATGGTTTTGACCTA
AATTGCTAGACAGTCTGTGCCATTACAAAAGTCAGAAAATACAGCAGGAAGAGACAGCTTTTAGAGGGGCAGAGAA
TTAGAGGATGGTGGTAGTAATGAAAAAGATGCATTCAAGTTTAAACAAGTTTAAATTGAGACAGCTATGGTATAGCT
AAAAACAAAAGCCCATAAAGTTGGAGATAGGGACCAGAGTTTAAACATAGCGATCTAGGCCAGAATTGACAATGTT
TAAGTAATGGTGGAACTCTGTCAATAAGACTTCCCAGAGTGTTAATATATATATCAGAAATGCACACAACAGAACCAT
AGGCAACACCAACACAGGAAGAAATAGAAGTCACCTATTGAAAACCTGGAATGGCCCATTCAGAAAGACAGGAGAA
TTAGGAGAGAGTGAGTGAAAGAAGCCAAGGGTCAAGAATGCAGAAAGCAAGGAAGGACTAAAAAGCCTCCACGGA
CATCGATAATCAAGAGATTATTAAGATCTTTGCTAGAAGAGTTCCCTTTACCTGTACTTAACTCCCTTAAAAAGAG
AAAAGTGATGGAATGACTTCTGCAACTGTAGTCCCAGCAGGAACTGTGAAGACCAGCTGCCCTGCAGGATCCAGT
TTTTCTTGGGAGGTTGTATCTGGTCATAAGGTAAACATTCTATATATTCTATGCCTGCTCTAGAATTGAAAGACT
TCAGCAGTATTAAAGCATTTTTTAATCTT

WO 2004/030615

PCT/US2003/028547

261/6881
FIGURE 246

MLQIQPEKDIIVEFIKNGDFKYVRMLGALYMRLTGTAIDCYKYLEPLYNDYRKIKSQNRNGEFELMHVDEFIDEL
LHSERVCDIILPRLQKRYVLEEAEQLEPRVSALEEDMDDVESSEEEEEDEKLERVSPDHRRRSYRDLDPKPRS
PTLRYRRSRSRSPRRRSRSPKRRSPSPRRERHRSKSPRRHRSRSDRRHRSRSKSPGHHRSHRHRSHSKSPERSK
KSHKKSRRGNE

WO 2004/030615

PCT/US2003/028547

262/6881
FIGURE 247

GTTTCGGGCCAGATGCGCTCCATCATGGAAGGGCCGCTGAGCAAATGGACTAACGTGATGAAGGGCTGGCAGTACC
GTTGGTTTCGTGCTGGACTACAATGCAGGACTGCTCTCCTACTACACGTCCAAGGACAAAATGATGAGAGGCTCTC
GCAGAGGATGTGTTAGACTCAGAGGAGCTGTGATTGGTATAGACGATGAGGACGACAGCACCTTCACAATAACTG
TTGATCAGAAAACCTTCCATTTCCAGGCCCGTGATGCTGATGAGCGAGAGAAGTGGATCCATGCCCTTAGAAGAAA
CAATTCTTCGACATACTCTCCAGCTTCAAGGTTTGGATTTCAGGATTTGTTCCCTAGTGTCCAAGATTTTGATAAGA
AACTTACAGAAGCTGATGCTTACCTACAAATCTTGATTGAACAATTAAAGCTTTTTGATGACAAGCTTCAAAACT
GCAAAGAAGATGAACAGAGAAAAGAAAATTGAAACTCTCAAAGAGACAACAAATAGCATGGTAGAATCAATTAAAC
ACTGCATTGTGTTGCTGCAGATTGCCAAAGACCAGAGTAATGCCGAGAAGCACGCAGATGGAATGATAAGTACTA
TTAATCCCGTAGATGCAATATATCAACCTAGTCCTTTGGAACCTGTGATCAGCACAAATGCCCTTCCAGACTGTGT
TACCTCCAGAACCTGTTTCAGTTGTGTAAGTCAGAGCAGCGTCCATCTTCCCTACCAGTTGGACCTGTGTTGGCTA
CCTTGGGACATCATCAGACTCCTACACCAATAGTACAGGCAGTGGCCATTACCACCGAGTAGCAGTCTCACTT
CTCCAAGCCACGTGAACCTGTCTCCAAATACAGTCCCAGAGTTCTCTTACTCCAGCAGTGAAGATGAATTTTATG
ATGCTGATGAATTCATCAAAGTGGCTCATCCCCAAAGCGCTTAATAGATTCTTCTGGATCTGCCCTCAGTCCCTGA
CACACAGCAGCTCGGGAAATAGTCTAAAACGCCCAGATACCACAGAATCACTTAATCTTCTCCTGTCCAATGGAA
CAAGTGATGCTGACCTGTTTGATTACATGATGACAGAGATGATGATGCCGAGGCAGGGTCTGTGGAGGAGCACA
AGAGCGTTATCATGCATCTCTTGTGCGAGGTTAGACTTGAATGGATCTTACTAAGGTAGTTCTTCCAACGTTTA
TTCTTGAAAGAAGATCTCTTTTAGAAATGTATGCAGACTTTTTTGACATCCGGACCTGTTTGTGAGCATTAGTG
ACCAGAAGGATCCCAAGGATCGAATGGTTTCAGGTTGTGAAATGGTACCTCTCAGCCTTTCATGCCGGAAGGAAAG
GATCAGTTGCCAAAAGCCATACAAATCCCATTTTGGGCGAGATTTTTCAGTGTCAATTGGACATTACCAATGATA
CTGAAGAGAACACAGAACTAGTTTCAGAAGGACCAGTTCCCTGGGTTTCCAAAACAGTGTAAACATTTGTGGCTG
AGCAGGTTTTCCCATCATCCACCCATTTTCAGCCTTTTATGCTGAGTGTTTTAAACAAGAAGATACAATCAATGCTC
ATATCTGGACCAAATCAAAATTCCTTGGGATGTCAATTGGGGTGCACAACATAGGGCAGGGCTGTGTCTCATGTC
TAGACTATGATGAACATTACATTCTCACATTTCCCAATGGCTATGGAAGTCTATCCTCACAGTGCCCTGGGTGG
AATTAGGAGGAGAATGCAATATTAATTGTTCCAAAACAGGCTATAGTGCAAATATCATCTTCCACACTAAACCTT
TCTATGGGGGCAAGAAGCACAGAATTACTGCCGAGATTTTTTCTCAAATGACAAGAAGTCTTTTTGCTCAATTG
AAGGGGAATGGAATGGTGTGATGTATGCAAAATATGCAACAGGGGAAAATACAGTCTTTGTAGATACCAAGAAGT
TGCCTATAATCAAGAAGAAAGTGAGGAAGTTGGAAGATCAGAACGAGTATGAATCCCGCAGCCTTTGGAAGGATG
TCACTTTCAACTTAAAAATCAGAGACATTGATGCAGCAACTGAAGCAAAGCACAGGCTTGAAGAAAAGACAAAGAG
CAGAAGCCCGAGAAAGGAAGGAGAAGGAAATTCAGTGGGAGACAAGGTTATTTTCATGAAGATGGAGAATGCTGGG
TTTATGATGAACCATTACTGAAACGTCTTGGTGTGCTGCCAAGCATTAGGTTGGAAGATGCAAAGTTTATACCTGAT
GATCAGGGCAGTAGGCATAATTCAGCAACAAACAATCTTCCCTTGGGAGAAACCTGTTTCATTCCAATCTTCTAAT
TACAGTGGTTTCTATCTCAGGGATACTGGACTTTCTGACGCAGATGAACAATTAAGGGGAAAAGCTTCCCTTTTC
CCTCTGTGGCAGTTACGATTTTGACTTCAGTCTGAGAAAACCTTCAGGTTTTGAAAATCAGATGATGTCTTCTC
CTTTTCCAAACACCACACGTTGAAAGCATTATATAATCCAAGTCTGAACTCTGCGCTCTAGTACTGCTGTTAAG
ATACACAACCTTGTTCCTTAGTTTCATATAATCTCGGGATACACACACACACATATATATACACACACATACG
TATACACACACATACATATATATAAATATACCTGATGCCAGATTTTTTTCATAAATATTCTGCCTACTGTAAATA
TGGGTTCTCTGAGTTGTTTTAGAAAATTAGCGCAATGTATTAATAATCAAGTGTTAGGAAATTTTCATGGTCTTAC
CTACAATAACTTTTATTTTGAATTGAACATATTATTAATTTGTATCTAATCCTGGATTACAGTTTAATTAATTAT
TCTTAGTGCTTAAGGCTTCATAAAGTAATTTTCCAACCTTTTTTTTAAAAA

WO 2004/030615

PCT/US2003/028547

263/6881
FIGURE 248

MASIMEGPLSKWTNVMKGWQYRWFVLDYNAGLLSYYTSKDKMMRGSRRGCVRLRGAVIGIDDEDDSTFTITVDQK
TFHFQARDADEREKWIHALEETILRHTLQLQGLDSGFVPSVQDFDKKLTEADAYLQILIEQLKLFDDKLQNCKED
EQRKKIETLKETTNSMVESIKHCIVLLQIAKDQSNAEKHADGMISTINPVD AIYQPSPLEPVISTMPSQTVLPPE
PVQLCKSEQRPSLPGVPLATLGHHQTPTPNSTGSGHSPSSSLTSPSHVNLSPNTVPEFSYSSSEDEFYDADE
FHQSGSSPKRLIDSSGSASVLTHSSSGNSLKRPDTTESLNSSLNGTSDADLFDSDHDDRDDD AEAGSVEEHKSVI
MHLLSQVRLGMDLT KVVLPTFILERRSLLEMYADFFAHPDLFVSI SDQKDPKDRMVQVVKWYLSAFHAGRKGVA
KKPYNPILGEIFQCHWTLPNDTEENTELVSEGPVPWVSKNSVTFVAEQVSHHPPISAFYAECFNKKIQFNAHIWT
KSKFLGMSIGVHNIGQGCVSLDYDEHYILTFPNGYGRSILTPWVELGGECNINCSKTGYSANIIFHTKPFYGG
KKHRITAEIFSPNDKKSFC SIEGEWNGVMYAKYATGENTVFVDTKKLP I I KKKVRKLEDQNEYESRSLWKDVTFN
LKIRDIDAATEAKHRLEERQRAEARERKEKEIQWETRLFHEDGECWVYDEPLLKRLGA AKH

WO 2004/030615

PCT/US2003/028547

264/6881
FIGURE 249A

CCCCGGCTGTGGGCTACAGGCGCAGAGCGGGCCAGGCGCGGAGCTGGCGGCAGTGACAGGAGGCGCGAACCCGCA
GCGCTTACCGCGCGGGCGCCGACCATGGAGCCCCGCGTGTGCTGGCCGTGTGCGCGCTGCTCTTCTCTGCTGTGG
GTGCGCTGAAGGGGCTGGAGTTCGTGCTCATCCACCAGCGCTGGGTGTTTCGTGTGCCTCTTCTCTGCGGCTC
TCGCTTATCTTCGATATCTACTACTACGTGCGCGCCTGGGTGGTGTTCAGCTCAGCAGCGCTCCGCGCCTGCAC
GAGCAGCGCGTGCGGGACATCCAGAAGCAGGTGCGGGAATGGAAGGAGCAGGGTAGCAAGACCTTCATGTGCACG
GGGCGCCCTGGCTGGCTCACTGTCTCACTACGTGTGCGGAAGTACAAGAAGACACACAAAACATCATGATCAAC
CTGATGGACATTCTGGAAGTGGACACCAAGAAACAGATTGTCCGTGTGGAGCCCTTGGTGACCATGGGCCAGGTG
ACTGCCCTGCTGACCTCCATTGGCTGGACTCTCCCCGTGTTCCTGAGCTTGATGACCTCACAGTGGGGGGCTTG
ATCATGGGCACAGGCATCGAGTCATCATCCACAAGTACGGCCTGTTCCAACACATCTGCACTGCTTACGAGCTG
GTCCTGGCTGATGGCAGCTTTGTGCGATGCACTCCGTCCGAAAACCTCAGACCTGTTCTATGCCGTACCTTGGTCC
TGTGGGACGCTGGGTTTCTGGTGGCCGCTGAGATCCGCATCATCCCTGCCAAGAAGTACGTCAAGCTGCGTTTC
GAGCCAGTGCAGGGGCTGGAGGCTATCTGTGCCAAGTTCACCCACGAGTCCAGCGGCAGGAGAACCCTTCGTG
GAAGGGCTGCTCTACTCCCTGGATGAGGCTGTCAATTATGACAGGGGTGATGACAGATGAGGCAGAGCCCAGCAAG
CTGAATAGCATTGGCAATTACTACAAGCCGTGGTTCCTTTAAGCATGTGGAGAAGTATCTGAAGACAAACCGAGAG
GGCCTGGAGTACATTCCCTTGAGACACTACTACCACCGCCACACGCGCAGCATCTTCTGGGAGCTCCAGGACATT
ATCCCTTTGGCAACAACCCCATCTTCCGCTACCTCTTTGGCTGGATGGTGCCTCCCAAGATCTCCCTCCTGAAG
CTGACCCAGGGTGAGACCTGCGCAAGCTGTACGAGCAGCACCACGTGGTGCAGGACATGCTGGTGGCCATGAAG
TGCCTGCAGCAGGCCCTGCACACCTTCCAAAACGACATCCACGTCTACCCCATCTGGCTGTGTCCGTTTCATCCTG
CCCAGCCAGCCAGGCCTAGTGCACCCCCAAAGGAAATGAGGCAGAGCTCTACATCGACATTGGAGCATATGGGGAG
CCGCGTGTGAAACACTTTGAAGCCAGGTCTGTCATGAGGCAGCTGGAGAAGTTTGTCCGCAGCGTGCATGGCTTC
CAGATGCTGTATGCCGACTGCTACATGAACCGGGAGGAGTTCTGGGAGATGTTTGATGGCTCCTTGTACCACAAG
CTGCGAGAGAAGCTGGGTTGCCAGGACGCCTTCCCCGAGGTGTACGACAAGATCTGCAAGGCCGCCAGGCACTGA
GCTGGAGCCCCGCTGGAGAGACAGACACGTGTGAGTGGTCAGGCATCTTCCCTTCACTCAAGCTTGGCTGCTTTC
CTAGATCCACACTTTCAAAGAGAAAACCCCTCCAGAACTCCCACCCTGACAGCCCAACACCACCTTCCCTCTGGCT
TCCAGGGGGCAGCCAGTGGAAATGGAAGAATGTGGGATTTGGAGTCAGACAAGCCTGAGTCCAGTTCCCGGTTT
AGAAGTCAATTAGCTGTGTGACTCTGGGTGAGTCCCTTAACCCCTCTGAGCCCGGGTCTCTTCATTAGTTGAAAGG
GATAGTAATACCTACTTGCAGGTTGTTGTCTGAGTTGAGCACTGGTCACATTGAAGGTGCTGGGTAAGTGGT
AGCTCTTGTGCTTCCCGTTTCAGCGTCACATCTGCACTGGAGCCTGAAAAGGCTCCACATTAGGTACCTGTCGA
CAGCCATGGCTGGAATGATGAAGGGGATACGCTGGAGTTGCCCTGCCATCGCTCCATCAGCCAGCAGGTCCT
CACAGGAGAAGGACAGCTCTTCCCCACCCTGGGATCTCAGGAGGGCAGCCACGGAGTGGGGAGGCCCCAGATGCG
CTGTGCCAAAGCCAGGTCCGAGGGCCAAAGTTCTCCCTGCCATCCTTGGTGCCGCTCTGCCCCCTTCCCTCTCATG
CCTGGGCCTGCAGGCCACCCAGCCACCACTGAGTCCACTCGGAGTGCCCTGTGTTCTGGAAGAAGCATTCCA
GGGTTGAATCTTGTCCAGCCTCAGCCTGGGACACCTAGGTGGAGAGTGGTCTCCGCTCTGAATTGGATCCAG
GGGACCTGGGCTCATTCTTCTGGCTCACCAACCCTGCAGGCCTCATCTTCCCAAACCCACTTTGTCTTGGTG
GGAGTGGGTCCGCGCTGCTCTGCAGCAGGGGCTGGGGAGTGGACAGCATCAGGTGGGAAAGTGGAGTCCACCCTC
ATGTTTCTGTAGGATTCTACCGTGGGGCTGGAAGAAAAGAGCATCGACTTGATTTCTCCAACCACTCATCCCTC
TTTTTCTTCTTCCACCACTCCCCACCCAGCTGTAGTTAATTTAGTGCCCTTACAAATCCTAAGCTCAGAGAAA
GTTCCATTTCGTTCCAGAGGGAAGGGAACCTCCCTAGGTCTTCCCTGGCTTGTATAACGCAAAGCTTGGTTG
TTTATGCAACTCTATCTTAAGAACTGCCCAGCCTCAGCTGAAAACCCGAATCTGAGAAGGAATTGCGTCATGTAA
GGGAAGCTGGAATTAAGGGAGCTGAGCCAGTCATGGTTGTGGCGTGTGAGTCAGGAGACCTAGGTTTCAGCCCT
CTCTACTGTGAGCGAGCTGTGCAACGTGGGCAAGTCATTGTCTCTGAGCTGCAGTTTCTCATCTGTACATCG
CTACAGACAAGACCTCCCTGGAACCTTCTGATTGTCTTAGACACTGTGGTTGCAAAAACCCAGGAAAGCCTCAT
TTGTGTGGAAGTCAGAGGAAAAATGATCCAGTGGACACTTGGGGATTATCTGTCAATTCAAGATCCTTCTTCAA
CCCCAAGGTGAGTCCCATCTCATTTCCAGAAAAGGCTCATACCTGGCTTGAGGGAAGCATCTGTCTTGTCAATC
CAGGTGCCAGATCTCTCAGAGTCATTGAAGGGTGTTCACCCATCCACCCAAAGGCTTGGCACACTGCCAGTGT
CTTAGCAGGGTCTTGTGAGGGCTGGGGGCATCCAGGCACTCAGAAGGCAAAGGAACACCCTACCCATTGGCCT
CTGGAGGGGCGAGAAGAAAGAAATAAACCTCATCTATATTTTACAAAGCATGTGAATTCTGGCATTAGCTCTCA
TAGGAGACCCATGTGCTTCTTCTGCTCAGTGCAAAACTGATGATTCTACTTGCTGTAGATGAATGGTTAACACGAG

WO 2004/030615

PCT/US2003/028547

265/6881
FIGURE 249B

CTAGTTAAACAGTGCCATTGTTTTGCCAGTGAAGCCTCCAACCCTAAGCCACTGGGACGGTGGCCAGAGATGCCA
GCAGCCTCTGTGCGCCCTTAGTCATATAACCAAAATCCAGACCTTATCCACAACCCGGGGCTTGGAAAGGAAGGTA
TTTTGGAATCACACCCTCCGGTTATGTTGCTCCAGTAAAATCTTGCCTGGAAAGAGGCAGTCTTCTTAGCATGGT
GAGCTGAGTTTCATGGCTTTTTTTTTGTAGCCAGTCCTGTCCCTGGCCATCCATGTGATGGTTTTGGATGGAGTTAA
ACTTGATGCCAGTGGGCAGTGCATGTGGAAAGTATCAGAGTAAGGCTCTCCCTCCAGAGCCCTGAGTTTCTTGG
CTGCATGAAGGTTTTCTTTAGAATCAGAATTGTAGCCAGTTTCTTTGGCCAGAAGGATGAATACTTGGATATTAC
TGAAAGGGAGGGGTGGAGATGGGTGTGGCAGTGTATGGTGTGTGATTTTTATTTTCTTCTTTGGTCATGGGGGCC
AAGGAGAAAGGCATGAATCTTCCCTGTCAGGCTCTTACAGCCACAGGCACTGTGTCTACTGTCTGGAAGACATGT
CCCCATGGCTGTGGGGCCGCTGCTTCTGTTTAAATAAAAGTGGCCTGG

WO 2004/030615

PCT/US2003/028547

266/6881
FIGURE 250

GACATCATGGGCTATTTTTAGGGGTTGACTGGTAGCAGATAAGTGTTGAGCTCGGGCTGGATAAGGGCTCAGAGT
TGCACTGAGTGTGGCTGAAGCAGCGAGGCGGGAGTGGAGGTGCGCGGAGTCAGGCAGACAGACAGACACAGCCAG
CCAGCCAGGTTCGGCAGTATAGTCCGAAGTGCAAATCTTATTTTCTTTTACCTTCTCTCTAACTGCCCAGAGCTA
GCGCCTGTGGCTCCCCGGGCTGGTGTTCGGGAGTGTCCAGAGAGCCTGGTCTCCAGCCGCCCCCGGGAGGAGAGC
CCTGCTGCCCAGGCGCTGTTGACAGCGGCGGAAAGCAGCGGTACCCACGCGCCCGCCGGGGGAAGTCGGCGAGCG
GCTGCAGCAGCAAAGAACTTTCCCGGCTGGGAGGACCGGAGACAAGTGGCAGAGTCCCGGAGCCAACTTTTGCAA
GCCTTTCTGCGTCTTAGGCTTCTCCACGGCGGTAAAGACCAGAAGGCGGCGGAGAGCCACGCAAGAGAAGAAGG
ACGTGCGCTCAGCTTCGCTCGCACCGGTTGTTGAACCTGGGCGAGCGCGAGCCGCGGCTGCCGGGCGCCCCCTCC
CCCTAGCAGCGGAGGAGGGGACAAGTCGTCGGAGTCCGGGCGGCCAAGACCCGCGCGCGGCGGCCACTGCAGGG
TCCGCACTGATCCGCTCCGCGGGGAGAGCCGCTGCTCTGGGAAGTGAGTTGCGCTGCGGACTCCGAGGAACCGCT
GCGCACGAAGAGCGCTCAGTGAGTGACCGCGACTTTTCAAAGCCGGGTAGCGCGCGCGAGTCGACAAGTAAGAGT
GCGGGAGGCATCTTAATTAACCTGCGCTCCCTGGAGCGAGCTGGTGAGGAGGGCGCAGCGGGGACGACAGCCAG
CGGGTGCGTGCGCTCTTAGAGAACTTTCCCTGTCAAAGGCTCCGGGGGGCGCGGGTGTCCCCCGCTTGCCACAG
CCCTGTTGCGGCCCCGAAACTTGTGCGCGCAGCCCCAACTAACCTCACGTGAAGTGACGGACTGTTCTATGACTG
CAAAGATGGAAACGACCTTCTATGACGATGCCCTCAACGCCCTCGTTTCTCCGTCGAGAGCGGACCTTATGGCT
ACAGTAACCCCAAGATCCTGAAACAGAGCATGACCCTGAACCTGGCCGACCCAGTGGGGAGCCTGAAGCCGCACC
TCCGCGCAAGAAGTCCGACCTCCTCACCTCGCCCGACGTGGGGCTGCTCAAGCTGGCGTCGCCCAGCTGGAGC
GCCTGATAATCCAGTCCAGCAACGGGCACATCACCACCACGCCGACCCCCACCCAGTTCCTGTGCCCAAGAACG
TGACAGATGAGCAGGAGGGCTTCGCCGAGGGCTTCGTGCGCGCCCTGGCCGAAGTGCACAGCCAGAACACGCTGC
CCAGCGTCACGTGGCGGGCGCAGCCGGTCAACGGGGCAGGCATGGTGGCTCCCGCGGTAGCCTCGGTGGCAGGGG
GCAGCGGCAGCGGCGGCTTCAGCGCCAGCTGCACAGCGAGCCGCGGTCTACGCAAACCTCAGCAACTTCAACC
CAGGCGCGCTGAGCAGCGGCGGGCGGGCGCCCTCCTACGGCGCGGGCGGCTTGGCCTTTCCCGCGCAACCCAGC
AGCAGCAGCAGCCGCCGCAACCTTGCCCCAGCAGATGCCGTGCAGCACCCGCGGCTGCAGGCCCTGAAGGAGG
AGCCTCAGACAGTGCCCGAGATGCCCCGGCGAGACACCGCCCCCTGTCCCCATCGACATGGAGTCCAGGAGCGGA
TCAAGGCGGAGAGGAAGCGCATGAGGAACCGCATCGCTGCCCTCCAAGTGCCGAAAAAGGAAGCTGGAGAGATCG
CCCGGCTGGAGGAAAAAGTGAAAACCTTGAAAGCTCAGAAGCTCGGAGCTGGCGTCCACGGCCAACATGCTCAGGG
AACAGGTGGCAGAGCTTAAACAGAAAGTATGAACACGTTAACAGTGGGTGCCAACTCATGCTAACGCAGCAGT
TGCAAACATTTTGAAGAGAGACCGTGGGGGCTGAGGGGCAACGAAGAAAAAATAACACAGAGAGACAGACTT
GAGAACTTGCAAGTTGCGACGGAGAGAAAAAGAAAGTGTCCGAGAACTAAAGCCAAGGGTATCCAAGTTGGACT
GGGTGCGTCTGACGGCGCCCCAGTGTGCACGAGTGGGAAGGACTTGGCGCGCCCTCCCTTGGCGTGGAGCCA
GGGAGCGGCCGCTGCGGGCTGCCCCGCTTTGCGGACGGGCTGTCCCGCGCGAACGGAACGTTGGACTTTTCGT
TAACATTGACCAAGAAGTGCATGGACCTAACATTGATCTCATTAGTATTAAAGGGGGAGGGGGAGGGGGTTA
CAAAGTGAATAGAGACTGTAGATTGCTTCTGTAGTACTCCTTAAGAACACAAAGCGGGGGAGGGTTGGGGAGG
GGCGGCAGGAGGGAGGTTTGTGAGAGCGAGGCTGAGCCTACAGATGAAGTCTTCTGGCCTGCCTTCGTTAACTG
TGTATGTACATATATATATTTTTTAAATTTGATGAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAG
TTATTTCTTGTGTTGTTGTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGAGTTT
ACCATTGTATAAAGTATATAATTTTTTATGTTTGTCTGAAAAATCCAGAAAGGATATTTAAGAAAAATAC
AATAAAGTATTGGAAGTACTCCCTAACCTCTTTTCTGCATCATCTGTAGATACTAGCTATCTAGGTGGAGTTG
AAAGAGTTAAGAATGTCGATTAAATCACTCTCAGTGCTTCTTACTATTAAGCAGTAAAAAGTGTCTCTATTAG
ACTTTAGAAATAAATGTACCTGATGTACCTGATGCTATGGTCAGGTTATACTCCTCCTCCCCAGCTATCTATAT
GGAATTGCTTACCAAAGGATAGTGCGATGTTTTCAGGAGGCTGGAGGAAGGGGGGTTGCAGTGAGAGGGACAGCC
CACTGAGAAGTCAAACATTTCAAAGTTGGATTGTATCAAGTGGCATGTGCTGTGACCATTTATAATGTTAGTAG
AAATTTTACAATAGGTGCTTATTCTCAAAGCAGGAATTGGTGGCAGATTTTACAAAAGATGTATCCTTCCAATTT
GGAATCTTCTTTGACAATTCCTAGATAAAAAGATGGCCTTTGCTTATGAATATTTATAACAGCATTCTTGTC
CAATAAATGTATTCAAATACC

PCT/US2003/028547

FIGURE 251A

[illegible]

WO 2004/030615

PCT/US2003/028547

268/6881
FIGURE 251B

CCATTGTTAACTCACAGGCCTCATAAAACATAGGCTGTTGGCTATTATTCTCCAACCCTTGATCTAGAGAATTTT
AAACATTAGAATTTTGTGTTTACATTTGTTAAGCTTTACGTCATCTTCAAATGACACCAAACTCAGAATTATGAT
CTGCATTTAAGCCAATTTTAAATATAAATAAGCAGTCAATGCTGCCTCATTTATTGAAATTCAGTAGATTTTAGT
TTATTTCTTAGTAGTCAGAGAATTGATTTATAGCTATTACCAAACATTCTTACTAACGTTTCCTTATATCTAAA
TCAGATTGATTCTATATTTTGCTTTGTTTGTAATCAATAGCCAATGAAGAATAAGGAGTATTGGAAGAAGCAGTG
AGTCAGCTTTAGGTGACCTGGTTCCTTGTCTCAACTTTGTGATTGGGGAGATACAGTTTACTTTCCCTGAGCCTT
AATTCCTGTGTAAGTGAAGTCTAACTTAACTTCTTAATGTCCTTCCAGAACTAAAATTTTATTGTTTCACTTAAT
CGTTGGACTACTCTTGTGAAGTTTATATTTTGAGTTAATACAGTTTCCAAATTAACATACATTTAAAAAAAAG
GGTAGTATTTTCCATTTCTCTGTGTGCACTTAGGATAAACAGTGAAGTATAGCTTATAAAACAATTAGTTTGAG
GGCTGAGAGTGAAGAGGAACATACCAAAAGTCAGGAAACCTGAGCTCTTACCCTAACCTGTGTTACCAACTTTG
CTGTGTGACCTTAATCAAAACACATAACCTGGACCCCATGCTCCTCACCAGTAAATCAAGGGCCTGAATTTTATG
GCTTAGTATTTCCCTTCCAAGCTCCGAAGTTGCGTGATTCTGTGAAAGGCAGTGATTGATTCCCTTGTACTCATCT
TCCTTTTGACCTGTTTCCCTCATGATATATTGGGGAACAAATACTAAAAAGTGTTTTTATAGCTTTCTTGATTG
ACATTTCCCTATAATACTGATGAATTTGGGTGATGGAAAGTAATGGAAATGTTAAAGTTCTGCTCTCAAACTCT
GAGTCTCCTTGCCCTGTGTGCCAATGTTTAAACCATTTTGCTAATCTAAGCCATATTGCGAGGATCTCAAGGATG
ATACTTGTCAAGAGTTTGGGGCCTTGAGAGCACAGTTTTCAAAATAATACTTAGTATTTTCTGACTATAGAGTAC
ATTTGTCTTGTAAGTATATTTTAAATACAGAGAAGTGTGAAGTACAAATATCTCAGTGCTACTATTTAAAAAA
ACACAATTAGTATATAAATCCTTCCCCATTTTGTGACAGTATAATTTTAGTATGTTAACTTGGTTACTTCTTT
CTCTCTTCTCCATCATTTTCCCTGCTTCTTTTTCTTTTGTGATATTCTTAAACAATTTTGAACCCACAGGTA
CCCACATTGCTGGCACTACCAGCCTTGGGCTACTACCGAGGATAATGGAGCCAGGGCCTGTAGAAGCACAGAGG
AAGTCTAGAAGTGAAGGGGCTATGATACAGGAAGTTCAGGAGGCAGAGTCTCAAAGGAACACCTGCCTTTAATA
ATGTTTACAGAAGTGGAGAAAGGACTAAAGGACTTAAAGACATGCAGGTGTCTTCATCCTGATTCTGTCTTTGTT
ATTGCACAATGACTATAAAATAATGACCTAATTTTTTTTTTTCTGGCTTGGCTAATGGAAATCGACACTAGCG
CTTCCCCAGTATTAGACTTAATCTAATTCAAAGTAACATTCAAGAAAAGAAAAACAGTGGAACAGGATCAGTA
AGCTCAGACTCTCCATCTCCATTATTTTAGCCTTGACCATTCTTCTCTAATCCTTTTAAATTATCTTCAGTTTCC
AGTTCAAGTTACATTGCTTCAGTTACAGTTTGTGTTGACCTGTATTACAGAGCTGCATTATGATTCTTGTGGGCC
TAGATAGTTTGGCATCTTAGACCCCTTCTTCCATACAAAATTAAGTATGATTTTACAATTGTATCTGTATGA
AATGAATGTATTAATATTTTAGATTAAACATTTTGTGTTAGAAGTTCAGTTTCTTATGAGGCTAAAAAAAT
TAAACATTTTGTGGGCTTCTAAAAAAGTGGGCTTAGGTACTGTGCCTAATGGATAAGTTGGCATTGCCTG
TATTCTGAAGGGCATCATTGGAAAAATAGCAGTCATTATTCTGTCCCTTCTCCACCACAGTCCCTTGGAGA
AGCCTTTGCCACTCCATCCAGGAGCACTGCAGTTTCCACGGTTATAGATCTATAGACTTGAACCTTACTTCCCTCC
CAACCTAACGAAAACCTCACAAAGGATTACTTGGGACCATTCATCCTCAAAAAAGATAGGAGGCAGTGTTTGTGTT
AGTCTTCAGATATTTTGTGTTTGGTCAGTCCCTAATCTGTGATTTTGAAGTCTGTCACACTTGAAGGGAAAC
ATCCTACTACCTTTCTTCTCCTCCTATTTCCCAAAACCCTTTCCCTCATCATCACTCCCTGCATTCTTACTTCT
CAGCATATAAATAACAAGACCCTTCTTCTATTTTGTGTTGAAGCTAGGCCTGTAAATAGAGATGGACAGACCA
TGCATGTTTCCATGAAGCTATTTAATGCTGCTCCAGTCTTCTGTCCATACCATTCCCTTCCCTGCCCTAGGAGT
GGGGTTGAGGTCTGTGACATGCAGACTGTAAGCACAGTCAGAACCCTCTGCAGCTCTCAACCCAACAGAGGAGCT
GTGGCTTCAACATGCCAACCTGAGCAGGTCTCCTCTGCATTACCTTCCCTCCATTTCTTCTTCTGGGTCTGATG
AGGTGAGCTGGAGGAACCAATAGTCAGGATGCCCTGGAATTGATGTTGCTCTGTTTTGTGCTCACAAAACAGCCA
TGTAACACATGAGCACCTGAGTTGAAGCCATCCAGTCGCAAGTCAGCAGACAGCAGTTGATGGAATTTCTCAGTAG
AAATTCAGTAAGGGTGCCCAAATTTTATTTTTTTTTTACCTATACTCTACCAATATATGGTATTTAGGAAAAC
TCTTTTATCCAAGCACAAAGAAAAGCACACATTTTTTATAATCATCTGCTTCATCAGGGTAAATAAATAATTTA
ACAAATTTGATCAGCATCTCTAGTTTACCAGTACTTTAATATTAGTTTCTTACAAATTAATGTATTTTGCAATA
TTTCCAGAAAATCACTGTGGGAGAATAATGTAATATACTTTAGGATATATTTCCCTGACCTTTTCTTAAATGGCTT
CATGTGCTATTTCCCCCAAATCTGCTTTCTCTATTTTCTTTTTTATTTAACCTATAATTATACTTTCTAGTATAT
TCTGAGTCTATCTTCAAGCCACCTTACATTTTCTGGAACAAGGGAGGGAATAAATAGTTGCCTCCACTAAAT
CAGGAAAAAATAAATAATATCCAGGGGAGCTGTGATTATGCCAAGAGCTCTAAACAGAAGTTGAGAAGGTAAAA
ATTAAGTTGTAGTATCTGAGTTGTTTTATTTTCTTCTTGGTGTGTTATGAAGGTATTCATAAGAACCTTAATT

WO 2004/030615

PCT/US2003/028547

269/6881
FIGURE 251C

TCAGGGGAAAAAATGCCTGATTTGCTATTTTTGACATTTCTCGTCTCTTAAGAAGTCAGTTAAATATGTTTTC
ATAGTTTATATTCCTGTTTCATAGATTACTGTGAAACATGTATTTAAACCTATGAATTATAAAATAGTATTTAGA
TTCTAGCGTGAGTTAAATAGATTAGTCATATATCTTTTAGATTTGTGGATTTGACATGTAAATTATGTGTTGTGT
ATAAGTAAGTTAGTTACTAAACATATGGCATGGTTATTGATAAACTTGTTGCTATTTTTTTCCAAATGCTATCAG
TGTTTGTGGACTTTTAAAAATTAGTTTGAATTTTGAATGTTCTGTGATAAAATGTAATTTCAACTATTTTGTAC
ATTTAAATATGCCATGTTGTATATGTCTGTATTTAAAAATGTTGTAAATACCTGCATTTTAAGAATTATGAAAGA
TTTTCTCAAAAATGACAGAACTCTCCATACTTAATTGTGACACATTATAAGATATCTGATTTTAAGCTTTTGGA
TTTTGTTCTAAAAATTAAGTTTAAACATGCTGAAAATTCATAAAAATAAAATTTTGAAAATAAA

WO 2004/030615

PCT/US2003/028547

270/6881
FIGURE 252

MHETNQGEFITSDSQEALFSKSSRGCLQNEKQDETLSSSEITLWTEKQSNQDKKSIELNDQKFNELIKNCNKHDG
RGIIVDARQLPSPEPCEIQKNLNDNEMLFHSCQMVEESHEEEELKPPEQEIEIDRNIIQEEEEKQAIPEFFEGRQA
KTPERYLKIRNYILDQWEICKPKYLNKTSVRPGLKNCQDVNCIGRIHTYLELIGAINFGCEQAVYNRPQTVDKVR
IRDRKDAVEAYQLAQRLQSMRTRRRRVDPWGNWCDAKDLEGQTFEHLSAEELAKRREEEEKGRPVKSLKVP RPTK
SSFDPFQLIPCNFFSEEKQEPFQVKVASEALLIMDLHAHVSMAEVIGLLGGRYSEVDKVVEVCAAEP CNSLSTGL
QCEMDPVSQTQASETLAVRGFSVIGWYHSHPAFDENPSLRDIDTQAKYQSYFSRGGAKFIGMIVSPYNRRNPLPY
SQITCLVISEEISPDGSYRLPYKFEVQQMLEEPQWGLVFEKTRWIIIEKYRLSHSSVPMQKIFRRDSDLTCLQKLL
ECMRKTL SKVTNCFMAEEFLTEIENLFLSNYKSNQENGVTENCTKELLM

WO 2004/030615

PCT/US2003/028547

271/6881
FIGURE 253

CTCTCTCTGGTCCGTGCCTCCAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCAC
GTGCAGCCTATTTCGCTGCACTAACTGTGCCCCGATGCGTGCCCAAGGACAAGGCCATTAAGACATTTCGTCATTCTGA
AACATAGTGAAGGCCGAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTG
TATGTGAAGCTACATTACTGTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCCG
AAGGACCGAACACCCCCATCCCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGA
GCTGAGTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTT

WO 2004/030615

PCT/US2003/028547

272/6881
FIGURE 254A

ATGGCACAAACGGGCAAATGCTCTGAAAAACGGATAAAATAAAATGCTGGTCACAGATGAGAACATCAGTCTAGCA
GAGCTTGCGAAGGCAGCAGGGAGGAGAAAACCTCTGAGCTGTGTTTTGCCAGTGTCCACAGAGGGTTAGGAGGA
CCCAATGAAGGAATGACCCTGAAATGTGAACAGGGCGAAGAACTAGGCCCCAGCTCCCTGCAGAGAAGATACATC
AAAGCCCCACATGAGGATTTTTATAGCTCCACATTGGACAAGCTTCCTCTTCTGAGATAGAGCCTACAGGGAAG
GGACAGATTTGGGGCAAGGAGAGGAGTCTGAAAGAGATGGGGTACGCCGTAGTGAAAGCTGGAGTGAGAGCCTTC
GTATTGCAAGGCGGGGACTCGGGCGCTGTTGGCAGCTGGCGACGCGGGGCGAAGCCGCGGCTGGCGGCGCCTGGC
CAGTCCCGCATCCGCCGCGTGCACCCGAGGTTGCGTGCCTCCGAAGCCGGGGTGTGCGCCTAGCTGCCCCGGC
CCCGTGCACCGCGGGCGCCTCGCGCAGGACTTCGCGCAGCTCGCAAGCCTGGGGTCTGCGACAGAAAAGGAGCG
GGGCTGCTCGGGCTGCCCAAAGGGTCATGGTTATTAAGGAAGAAAACACAGAATGGGCCCTTGTATGGACTCTAT
TACCAAGTGCCATTGGACACGCAGGCAGTGTACTGGGAGACAGTCTGGTGTGCTCAGAGGTATTGCCACGGCCT
GAAGTTCTCTCTTGGCCGAGCTGCCCCACTCTGCTGCAATCTTCTGGGGAGGGCTTCACCTGCCACTGCCTC
CTGCATGCCAGCATCGCCTGCTGCAGACTGCAGAGCTGGGGTGCCAAAGACCAGTCCCTCTCAGGGGGATGAAGAG
AAAGACCCTCCGAAGAGCCACCCTTATTCTGTGGAGACCCCATATGGCTTTCATTTAGACCTGGACTTCCTCAAG
TATGTGGATGACATCGAGAAGGGAAACACTATCAAAAGAATTCTATCCACAGAAGGGCCAAGCAGGCCAAATTT
AGCACTCTGCCCCGAAACTTCAGCCTTCCTGACAGTGGGGCTCGCCCCCTGCAGCCCCGCCCTCCAAAACCTGG
TCTCCCGTGGTGCCAAGGGAGGCATCACTTGGGACACAGGAGCAAAACAGTCAACACCGCTTGGTAAATGCCCCC
CAGGCCTCAACAAGCAGGAGTGAGGTGAGCTACCACAGGAAGGCTCTGTTGGCAGAGGCCACCAGACAGTTGGAA
GCTGCTGAGCCAGAGGATGCCGAGCTCACTTTTGGGAGTGGACGGCCCCAGCTCTTGAGAGCATCCAGCATGCCT
GCCACGCTGCTGCACAGCAGGGCTTCTGAGGAGCCAGGCCTGAGCCTGGGGCCCCCTGCCCTCCTGCCCTCCCT
CCCCTTCAGGGTGAAGGCAGTGTCTGTGATGGCACCTTTGAACCTGCAGAAGGATTGGCAGGTTCCACAGCTCC
AGCCCACGAGCATCAACTCGGATTCCAGAGCTGGTCCAGGAGGGAGCTGAGCCTCCAGAGGGTGTGGTGAAGGTT
CCAAATCACCTCCCTCTCCAGGCCCTCCTTCTCATTCCAGAATGTGCTTGTAGTTCTAGAGGACAAGGAAGAT
GAACACAATGCCAGAGAAGCAGAGGTGTTGTTACCCCTGGCTCCCCTACGCCAAGCCGCCACCTCTGCCATCA
CCCATCCCTGAGAATGAGCTCTCTCTGGAAGAAATCGAGCTCAACATCAGCGAGATTCCACCCCCGCCACCTGTA
GAGGTGGACATGAGAAGCATTGGCATCAGGGTAACTGAGGAAAGCCTGGGCCTTGCCAGGGTGGATCCAGGCAGC
ATCTCCAGCCTGAAACAGCAGGTCTCGGCCCTGGAGGGAGAGTTGTCTGGAAGAACCGAGGAAGTGGCACAGGTC
AGAACTGCTCTCCAGCAGCAGGAAGAGGAAATCAAAGCTAGGGAGCAAAGAATTCGAGAGCTGGAGTTCACTGTA
GCCCCAAGTGAAGGACAGTTTACCAAGAGAACGCCAAAGACACTCAGGGCCAGACGGACGTGATGGTGAACACT
GACCCTGTCCATGGACTCTTGACCAGGGAGTCTGTGTATAAGGGCATTGAAGTCAACCTTCTAGGCAGCATGGAG
TCTGAAAGCTGGGGGCACCGAGGAGAGGAGAAATGGCCTCCTATGGGGGCCAGATGGTCATAAACAAGGGAATCAG
AGCCAGCAGAACGTGTGCTTCTGCCCCAGCTGTCACTGCCACAGGGACCCGAGCAGGTCCTTACCTCCTCTGTA
CATAGCTTCTCTCACTGAACTCAGGATTGAAGAAGCAGGCACTGAACAGGAAGGAGGCCCTCAGGGAGGAACC
AGGGGAGCAGGAGGCTTCTGTGGGGCAGCGACAGAAAGACTCCCCCAGCAGGGAGGGAGGAGACCAGTTCCAAT
CTCCAGGGAAGGAGCACCCGGGAAGGCCACCAAGCTCGCCAACGGATGCCACTATTGGGCAGTATGTGAAGAAG
ATCCAGGAGCTCCTGCAGGAGCAGTGGAACTGCCTGGAGCATGGGTACCCGAGCTGGCCAGCGCCATCAAGCAG
CCAGCCTCCAAGCTCAGCAGCATCCAGAGCCAGCTGCTGAGCTCCCTCAACCTGCTGCTGTGCGGCTACTCGGCC
CAGGCTCACCCACCAAGGAGCCACCGGCTCCTCCTCCTCCCCGCCAGTGGAGATCTCCCCATCGACCAGCCTT
AAATCCATAATGAAAAGAAAGACTATGGCTTCCGTGCAGGAGGTAATGGGACCAAAAAGAACCTTCAGTTTGT
GGGGTTAACGGTGGGTATGAGACCACCTCAAGTGAGGAGACCAGCGGTGAGGACAGCACCCAGAGGACTTGTCT
GACAGCGAGGCAGAGAAGAGTGTGACGGCCCAGATCACAAGCATGTCAAAGATGCCATCTCACCTGCGAGGCT
GGGCAGGGCATCCCTGAGGGCACCTGCCATGCTGCCAGGAAAGTGGGCCTGGGGAAGAAGTCCCCACTCCAAG
GCCGAGAGCCGGAAGTCGTCTAGCCCCGCCGTGGTGGCCTCCTACCTCCACGAGGTCCAGCCTCACTCCCCACAC
TTCTGAAACTGCTTGTCAACTTGGCCGATCACAACGGGAACACGGCCCTTCACTACAGCGTGTCCACTCCAAC
TTCTCCATCGTGAAGCTGCTGCTGGAGACAGGCGTCTGCAATGTGGACCATCAGAACAAGCTGGCTACACTGCC
GTAATGATCACTCCCTTGGCTTCCGCAGAGACCAATGAAGACATGGCTGTTGTCTGGAAGCTCTTAAGAGAAGGA
AATGTGAACATTCAAGCTACTCAGGGAGGCCAGACTGCGCTGATGCTGGGAGTCAGCCACGACAGGGAGGACATG
GTTCAAGCGCTGCTTAGCTGCCAGGCAGATGTCAATCTGCAGGACCAGATGGATCCTCGGCCCTCATGGTGGCC
TGTCACCATGGCAACGTGGACCTGGTGGGCTGCTCCTGGCACACCCAGCCTGCGACAGCAGCCTGACTGACAAG

WO 2004/030615

PCT/US2003/028547

273/6881
FIGURE 254B

GCTGGCCGCACAGCTTTGTCCATCGCTCTGAAGTCACCCACCCATATGGAAATTGCTGGGCTTCTGAGAGCCCAC
GCGGAGCAGGGCAGGTCCCTGGGGCTGTAG

WO 2004/030615

PCT/US2003/028547

274/6881
FIGURE 255

MASVQEVMGPKRTFSLLGLTVGMRPPQVRRPAVRTAPQRTCLTARQRRSVTAQITSMKMPISPARLGRASLRAP
AMLPRKVGLGKKSPTRPRDINPQKNFLMHAGH

WO 2004/030615

PCT/US2003/028547

275/6881
FIGURE 256A

GCGGCGGCCGCGGAGTATCCTGGAGCTGCAGACAGTGCGGGCTGCGCCAGTCCCGGCTGTCCTCGCCGCGACC
CCTCCTCAGCCCTGGGCGCGCGCACGCTGGGGCCCCGCGGGGCTGGCCGCTAGCGAGCCTGCCGGTCGACCCCA
GCCAGCGCAGCGACGGGGCGCTGCCTGGCCCAGGCGCACACGGAAGTGCCTTCTCTGAAGTAGCTTTGGAAAGT
AGAGAAGAAAAATCCAGTTTGTCTTCTGGAGAACACTGGACAGCTGAATAAATGCAGTATCTAAATATAAAGAGG
ACTGCAATGCCATGGCTTTCTGTGCTAAAATGAGGAGCTCCAAGAAGACTGAGGTGAACCTGGAGGCCCCTGAGC
CAGGGGTGGAAGTGATCTTCTATCTGTGCGACAGGGAGCCCCCTCCGGCTGGGCAGTGGAGAGTACACAGCAGAGG
AACTGTGCATCAGGGCTGCACAGGCATGCCGTATCTCTCCTCTTTGTCAACCTCTTTGCCCTGTATGACGAGA
ACACCAAGCTCTGGTATGCTCCAAATCGCACCATCACCGTTGATGACAAGATGTCCCTCCGGCTCCACTACCGGA
TGAGGTTCTATTTACCAATTGGCATGGAACCAACGACAATGAGCAGTCAGTGTGGCGTCATTCTCCAAAGAAGC
AGAAAAATGGCTACGAGAAAAAAGATTCCAGATGCAACCCCTCTCCTTGATGCCAGCTCACTGGAGTATCTGT
TTGCTCAGGGACAGTATGATTTGGTGAAATGCCTGGCTCCTATTGAGACCCCAAGACCGAGCAGGATGGACATG
ATATTGAGAACGAGTGTCTAGGGATGGCTGTCTGGCCATCTCACACTATGCCATGATGAAGAAGATGCAGTTGC
CAGAACTGCCCAAGGACATCAGCTACAAGCGATATATTCCAGAAACATTGAATAAGTCCATCAGACAGAGGAACC
TTCTCACCAGGATGCGGATAAATAATGTTTTCAAGGATTTCTTAAAGGAATTTAACAACAAGACCATTTGTGACA
GCAGCGTGTCCACGCATGACCTGAAGGTGAAATACTTGGCTACCTTGGAACCTTTGACAAAACATTACGGTGCTG
AAATATTTGAGACTTCCATGTTACTGATTTTCATCAGAAAATGAGATGAATTGGTTTCATTGCAATGACGGTGGA
ACGTTCTCTACTACGAAGTGATGGTGACTGGGAATCTTGGAAATCCAGTGGAGGCATAAACCAATGTTGTTCTG
TTGAAAAGGAAAAAATAAATGAAGCGGAAAAAAGTGGAAATAAACACAAGAAGGATGAGGAGAAAAACAAGA
TCCGGGAAGAGTGGAACAATTTTTCTTACTTCCCTGAAATCACTCACATTGTAATAAAGGAGTCTGTGGTCAGCA
TTAACAAGCAGGACAACAAGAAAAATGGAAGTGAAGCTCTCTTCCACGAGGAGGCCCTGTCTTTGTGTCCCTGG
TAGATGGCTACTTCCGGCTCACAGCAGATGCCATCATTACCTCTGCACCGACGTGGCCCCCGCTTGATCGTCC
ACAACATACAGAATGGCTGTCTGTCATGGTCCAATCTGTACAGAATACGCCATCAATAAATTGCGGCAAGAAGGAAGCG
AGGAGGGGATGTACGTGCTGAGGTGGAGCTGCACCGACTTTGACAACATCCTCATGACCGTCACCTGCTTTGAGA
AGTCTGAGCAGGTGCAGGGTGCCAGAGCAGTTCAAGAACTTTGAGATCGAGGTGCAGAAGGGCCGCTACAGTC
TGCACGGTTCGGACCGCAGCTTCCCCAGCTTGGGAGACCTCATGAGCCACCTCAAGAAGCAGATCCTGCGCACGG
ATAACATCAGCTTCATGCTAAAACGCTGCTGCCAGCCCAAGCCCCGAGAAATCTCCAACCTGCTGGTGGCTACTA
AGAAAGCCCAGGAGTGGCAGCCCGTCTACCCCATGAGCCAGCTGAGTTTCGATCGGATCCTCAAGAAGGATCTGG
TGCAGGGCGAGCACCTTGGGAGAGGCACGAGAACACACATCTATTCTGGGACCCTGATGGATTACAAGGATGACG
AAGAACTTCTGAAGAGAAGAAGATAAAAGTGATCTCAAAGTCTTAGACCCAGCCACAGGGATATTTCCCTGG
CCTTCTTCGAGGCAGCATGATGAGACAGGTCTCCACAAACACATCGTGTACCTCATGGCGTCTGTGTCC
GCGACGTGGAGAATCATGTTGGAAGAGTTTGTGGAAGGGGGTCTCTGATCTCTTCAATGCACCGGAAAAAGCG
ATGTCTTACCACACCATGGAATTCAAAGTTGCCAAACAGCTGGCCAGTGCCCTGAGCTACTTGGAGGATAAAG
ACCTGGTCCATGGAATGTGTGTACTAAAAACCTCCTCCTGGCCCGTGAGGGCATCGACAGTGAGTGTGGCCAT
TCATCAAGCTCAGTGACCCCGGCATCCCCATTACGGTGCTGTCTAGGCAAGAATGCATTGAACGAATCCCATGGA
TTGCTCCTGAGTGTGTTGAGGACTCCAAGAACCTGAGTGTGGCTGCTGACAAGTGGAGCTTTGGAACACGCTCT
GGGAAATCTGCTACAATGGCGAGATCCCTTGAAAGACAAGACGCTGATTGAGAAAAGAGAGATTCTATGAAAGCC
GGTGCAGGCCAGTGACACCATCATGTAAGGAGCTGGCTGACCTCATGACCCGCTGCATGAACATGACCCCAATC
AGAGGCCCTTTCTTCCGAGCCATCATGAGAGACATTAATAAGCTTGAAGAGCAGAATCCAGATATTGTTTCAGAAA
AAAAACCAGCAACTGAAGTGGACCCACACATTTTGAAAAAGCGCTTCTTAAAGAGGATCCGTGACTTGGGAGAGG
GCCACTTTGGGAAGGTTGAGCTCTGCAGGTATGACCCCGAAGGGGACAATACAGGGGAGCAGGTGGCTGTTAAAT
CTCTGAAGCCTGAGAGTGGAGGTAACCACATAGCTGATCTGAAAAAGGAAATCGAGATCTTAAGGAACCTCTATC
ATGAGAACATTGTGAAGTACAAAGGAATCTGCACAGAAGACGGAGGAAATGGTATTAAGCTCATCATGGAATTTT
TGCTTCGGGAAGCCTTAAGGAATATCTTCCAAAGAATAAGAACAAAATAAACCTCAAACAGCAGCTAAAATATG
CCGTTTCAGATTTGTAAGGGGATGGACTATTTGGGTTCTCGGCAATACGTTACCGGGACTTGGCAGCAAGAAATG
TCCTTGTGAGAGTGAACACCAAGTGAATAATTGGAGACTTCGGTTTAAACCAAGCAATTGAAACCGATAAGGAGT
ATTACACCGTCAAGGATGACCGGGACAGCCCTGTGTTTTGGTATGCTCCAGAATGTTTAATGCAATCTAAATTTT
ATATTGCCCTCTGACGTCTGGTCTTTTGGAGTCACTCTGCATGAGCTGCTGACTTACTGTGATTGAGATTCTAGTC
CCATGGCTTTGTCTGAAAATGATAGGCCCAACCCATGGCCAGATGACAGTCACAAGACTTGTGAATACGTTAA

WO 2004/030615

PCT/US2003/028547

276/6881
FIGURE 256B

AAGAAGGAAAAACGCCGTGCCGTGCCCCACCTAACTGTCCAGATGAGGTTTATCAACTTATGAGGAAATGCTGGGAAT
TCCAACCATCCAATCGGACAAGCTTTTCAAGACCTTATTGAAGGATTTGAAGCACTTTTAAAATAAGAAGCATGAA
TAACATTTAAATTCCACAGATTATCAAGTCCTTCTCCTGCAACAAATGCCCAAGTCATTTTTTAAAAATTTCTAA
TGAAAGAAGTTTGTGTTCTGTCCAAAAAGTCACTGAACTCATACTTCAGTACATATACATGTATAAGGCACACTG
TAGTGCTTAATATGTGTAAGGACTTCCTCTTTAAATTTGGTACCAGTAACTTAGTGACACATAATGACAACCAAA
ATATTTGAAAGCACTTAAGCACTCCTCCTTGTGGAAAGAATATACCACCATTTTATCTGGCTAGTTCACCATCAC
AACTGCATTACCAAAAAGGGGATTTTTGAAAACGAGGAGTTGACCAAAATAATATCTGAAGATGATTGCTTTTCCC
TGCTGCCAGCTGATCTGAAATGTTTTGCTGGCACATTAATCATAGATAAAGAAAGATTGATGGACTTAGCCCTCA
AATTTTCAGTATCTATACAGTACTAGACCATGCATTCTTAAATATTAGATACCAGGTAGTATATATTGTTTCTGT
ACAAAAATGACTGTATTCTCTCACCAGTAGGACTTAACTTTGTTTCTCCAGTGGCTTAGCTCCTGTTTCTTTGG
GTGATCACTAGCACCCATTTTTGAGAAAGCTGGTTCTACATGGGGGGATAGCTGTGGAATAGATAATTTGCTGCA
TGTTAATTCTCAAGAACTAAGCCTGTGCCAGTGCTTTCCTAAGCAGTATACCTTTAATCAGAAGTCAATCCCAGA
ACCTGGATGCTATTACACATGCTTTTAAGAAACGTCAATGTATATCCTTTTATAACTCTACCACCTTTGGGGCAAG
CTATTCCAGCACTGGTTTTGAATGCTGTATGCAACCAGTCTGAATACCACATACGCTGCACTGTTCTTAGAGGGT
TTCCATACTTACCACCGATCTACAAGGGTTGATCCCTGTTTTTACCATCAATCATCACCTGTGGTGCAACACTT
GAAAGACCCGGCTAGAGGCACTATGGACTTCAGGATCCACTAGACAGTTTTTCAGTTTGCTTGGAGGTAGCTGGGT
AATCAAAAATGTTTAGTCATTGATTCAATGTGAACGATTACGGTCTTTATGACCAAGAGTCTGAAAATCTTTTTG
TTATGCTGTTTAGTATTCGTTTGATATTGTTACTTTTCACCTGTTGAGCCCAAATTCAGGATTGGTTTCAGTGCCA
GCAATGAAGTTGCCATTTAAATTTGTTTCATAGCCTACATCACCAGGTCTCTGTGTCAAACCTGTGGCCACTCTA
TATGCACTTTGTTTACTCTTTATACAAATAAATATACTAAAGACTTT

WO 2004/030615

PCT/US2003/028547

277/6881
FIGURE 257

CTCTTCATAAGCCGGCGCTCGGCGAGTTCTCCCAGGAGAAGGCCATGTTTCAGTTTCGAGCGCCAAGATCGTGAAAC
CCAACGGCGAGAAGCCGGAGGAGTTTCGAGTCCGGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTCAGAAC
TCAAGGCTCAGCTCAGAGAGCTGAATATTACGGCAGCCAAGGAAATTGAAGTTGGTGGTGGTCGGAAAGCTATCA
TAATACTTGTTCCCGTTACTCAACTGAAATCTTTCCAGAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAA
AGTTCAGTGGGAAGCATGTCGTCTTTATCGCTCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCTGTACAA
AAAATAAGCAAAAGCGTCCCAGGAGCAGCACTGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCC
CAAGTGAAATTGTGGGCAAGAAAATCCGCGTCAAACCTAGATGGCAGCCGGCTCATAAAGGTTTCATTTGGACAAAG
CACAACAGAACAATGTGGAACACAAGGTTGAAACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTA
ATTGTGAATTCCCAGAGTTTCAATAGTAAACAAAATGACTAAATAAAAATATATATATTCATAGT

WO 2004/030615

PCT/US2003/028547

278/6881
FIGURE 258

MFSSSAKIVKPNGEKPEEFESGISQALLELEMNSELKAQLRELNITAAKEIEVGGGRKAIILVPVTQLKSFQKI
QIRLVSELEKKFSGKHVVFIQRRILPKPTRKSCTKNKQKRPRSSTVTAVHDAILEDLVFPSEIVGKKIRVKLDG
SRLIKVHLDKAQQNNVEHKVETFSGVYKKLMGKDVNCEFPEFQS

WO 2004/030615

PCT/US2003/028547

279/6881
FIGURE 259

GGAGAAGGCCATGTTTCAGTTCGAGCGCCAAGATCGTGAAACCCAACGGCGAGAAGCCGGAGGAGTTCGAGTCCGG
CATCTCCCAGGAAATTGAAGTTGGTGGTGGTCGAAAGCTATCATAATACTTGTTCCCGTTACTCAACTGAAATC
TTTCCAGAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAAAGTTCAGTGGGAAGCATGTCGTCTTTATCGC
TCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCTGTACAAAAAATAAGCAAAAGCGTCCCAGGAGCAGCAC
TGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCCCAAGTGAAATTGTGGGCAAGAAAATCCGCGT
CAAAC TAGATGGCAGCCGGCTCATAAAGGTTCAATTTGGACAAAGCACACAGAACAATGTGGAACACAAGGTTGA
AACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTAATTGTGAATTCCCAGAGTTTCAATAGTAAAC
AAAAATGACTAAATAAAAAATATATATATTCATAGTAAAAAAAAAAAAAAAAAATCTC

WO 2004/030615

PCT/US2003/028547

280/6881
FIGURE 260

GGGGGTGGGAAGAGCTGAAGCAGGCGCTCTTGGCTCGGCGCGGCCCGCTGCAATCCGTGGAGGAACGCGCCGCCG
AGCCACCATCATGCCTGGGCACCTTACAGGAAGGCTTCGGCTGCGTGGTCACCAACCGATTTCGACCAGTTATTTGA
CGACGAATCGGACCCCTTCGAGGTGCTGAAGGCAGCAGAGAACAAGAAAAAGAGCCGGCGGGGGCGGCGTTGG
GGGCCCTGGGGCCAAGAGCGCAGCTCAGGCCGCGGCCAGACCAACTCCAACGCGGCAGGCAAACAGCTGCGCAA
GGAGTCCCAGAAAGACCGCAAGAACCCGCTGCCCCCAGCGTTGGCGTGGTTGACAAGAAAGAGGAGACGCAGCC
GCCCCGTGGCGCTTAAGAAAGAAGGAATAAGACGAGTTGGAAGAAGACCTGATCAACAACCTTCAGGGTGAAGGGAA
AATAATTGATAGAAGACCAGAAAGGCGACCACCTCGTGAACGAAGATTTCGAAAAGCCACTTGAAGAAAAGGGTGA
AGGAGGCGAATTTTCAGTTGATAGACCGATTATTGACCGACCTATTTCGAGGTCTGGTGGTCTTGGAAAGAGGTCTG
AGGGGGCCGTGGACGTGGAATGGGCCGAGGAGATGGATTTGATTCTCGTGGCAAACGTGAATTTGATAGGCATAG
TGGAAGTGATAGATCTGGCCTGAAGCACGAGGACAAACGTGGAGGTAGCGGATCTCACAACCTGGGGAACCTGTCAA
AGACGAATTAACCTGACTTGGATCAATCAAATGTGACTGAGGAAACACCTGAAGGTGAAGAACATCATCCAGTGGC
AGACACTGAAAATAAGGAGAATGAAGTTGAAGAGGTAAAAGAGGAGGGTCCAAAAGAGATGACTTTGGATGAGTG
GAAGGCTATTCAAATAAGGACCGGGCAAAAGTAGAATTTAATATCCGAAAACCAAATGAAGGTGCTGATGGGCA
GTGGAAGAAGGGATTTGTTCTTCATAAATCAAAGAGTGAAGAGGCTCATGCTGAAGATTTCGGTTATGGACCATCA
TTTCCGGAAGCCAGCAAATGATATAACGTCTCAGCTGGAGATCAATTTGGAGACCTTGGCCGCCCAGGACGTGG
CGGCAGGGGAGGACGAGGTGGACGTGGGCGTGGTGGGCGCCCAAACCGTGGCAGCAGGACCGACAAGTCAAGTGC
TTCTGCTCCTGATGTGGATGACCCAGAGGCATTCCAGCTCTGGCTTAACTGGATGCCATAAGACAACCCTGGTT
CCTTTGTGAACCCCTTCTGTTCAAAGCTTTTGCATGCTTAAGGATTCCAAACGACTAAGAAATTAAGAAAAAAG
ACTGTCATTATACCATTCACACCTAAAGACTGAATTTTATCTGTTTTAAATGAACCTTCTCCCGCTACACAGA
AGTAACAAATATGGTAGTCAGTTTTGTATTTAGAAATGTATTGGTAGCAGGGATGTTTTCATATTTTCAGAGAT
TATGCATTCTTCATGAATACTTTTGTATTGCTGCTTGCAAATATGCATTTCCAAACTTGAAATATAGGTGTGAAC
AGTGTGTACCAAGTTTAAAGCTTTCACCTTCAATTTGTGTTTTTAATTAAGGACTTAGAAGTCCCCCAATTACAAA
CTGGTTTTTAAATATTGGACATACTGGTTTTAATACCTGCTTTGCATATTCACACATSGTCAACTGGGACATGTTA
AACTTTGATTTGTCAAATTTTATGCTGTGTGGAATACTAATAATATGATTTTAACTTAGTTTTAATATTTTCAT
ITTTGGGGGAAAAATCTTTTTTCACTTCTCATGATAGCTGTTATATATATATGCTAAATCTTATATACAGAAATA
TCAGTACTTGAACAAATTCAAAGCACATTTGGTTTTATTAACCCTTGCTCCTTGCATGGCTCATTAGGTTCAAATT
ATACTAATTTACATTTTCAGCTATATTTACTTTTTAAATGCTTGAGTTTCCATTTTAAATCTAACTAGACA
TCTTAATTGGTGAAAGTTGTTTTAACTACTTATTGTTGGTAGGCACATCGTGTCAAGTGAAGTAGTTTTATAGGT
ATGGGTTTTTCTCCCCCTTACCAGGGTGGGTGGAATAAGTTGATTTGGCCAATGTGTAATATTTAACTGTTC
TGTAATAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

281/6881
FIGURE 261

MPGHLQEGFGCVVTNRFDQLFDDSDPFVFLKAAENKKKEAGGGVGGPGAKSAAQAAAQTSNAAGKQLRKESQ
KDRKNPLPPSVGVVDKKEETQPPVALKKEGIRRVGRRPDQQLQGEGKIIDRRPERRPPRERRFEKPLEEKGE
FSVDRPIIDRPIRGRGGLGRGRGGRGRGMGRGDGFSRGKREFDRHSGSDRSGLKHEDKRGGSGSHNWGT
VDELTDLDQSNVTEETPEGEEHHPVADTENKENEVEEVKEEGPKEMTLDEWKAIQNKDRAKVEFNIRKP
NEGADGQWKKGFVLHKSKEEHAEDSVMDDHHFRKPANDITSQLEINFGDLGRPGRGGRGGRGGRGGR
PNRGSRTDKSSASAPDVDDPEAFPALA

WO 2004/030615

PCT/US2003/028547

282/6881
FIGURE 262

ACCTTTAAGCGTCACGGGTGGGGCTGCAGCTTCTGGACCTAGGACTTTGAACATGTCGCGCCTGAAGCGGATAGC
GGGGCAGGATCTCCGCGCTGGTTTTCAAAGCAGGTGGAAGAGACTGCGGTACCTCGGTACCCCAAGGGCTGTTGAA
GGCAGCGAGGAAGAGCGGCCAGTTAAACCTGTGCGGTAGAAACCTCAGTGAAGTGCCGCAGTGTGTCTGGAGAAT
AAATGTGGATATCCCTGAGGAAGCTAATCAGAATCTTTCGTTTGGTGCTACTGAAAGATGGTGGGAGCAGACAGA
TTTGACCAAATAATAATATCAAACAATAAACTTCAGTCACCTTACAGATGACCTGCGACTCTTGCTGCACTGAC
TGTTCTTGATATACATGATAATCAGTTGACATCCCTTCCTTCTGCTATAAGAGAGCTAGAAAACTTTCAGAACT
TAATGTCAGCCATAATAAACTGAAAATACTCCCTGAAGAAATTACAAACCTAAGAAACCTGAAGTGCTGTATCT
CCAGCATAATGAATTAACCTGCATATCAGAGGGATTGAACTTCCAAATTTAGAAGATTTAGATCTTTCAA
CAATCATCTTACAACGTTCCTGCTAGTTTTCTTCTGCTCCAGTCTGGTGCGACTCAATCTTTCTAGTAATGA
ACTGAAGAGTTTGCCAGCAGAAATAAATAGAATGAAAAGGTTGAAGCATTTGGATTGTAATTCAAATCTCTTGA
AACTATACCTCCTGAATTGGCTGGCATGGAATCAGTAGAATTGCTTTATTTGCGGAGGAATAAATTACGTTTTCT
ACCAGAATTTCTTCTGTAGTCTATTGAAGGAATTGCACGTAGGTGAAAACAGATTGAAATGTTAGAGGCAGA
ACATCTTAAACATCTGAATTCATTTCTGTGCTAGACCTGAGGGATAACAAGTTAAAATCTGTTCCAGATGAAAT
TATACTACTACGGTCCTTGGAAGGGCTTGACCTAAGCAACAATGATATTAGTAGTCTTCCCTATTATTGGGGAA
CCTTCATTTGAAATTTTGGCATTAGAAGGAAATCCTTTGAGAACAATTCGAAGAGAAATTATAAGTAAAGGAAC
ACAAGAAGTCCTAAAATATCTACGAAGCAAGATCAAAGATGATGGACCTAGCCAAAGTGAGTCTGCTACTGAGAC
TGCCATGACACTACCAAGTGAATCCAGAGTCAATATACATGCCATCATTACATTAATAATATTAGACTATAGTGA
TAAACAAGCAACTTTGATTCTGATGAGGTGTTTGATGCAGTAAAAAGCAACATCGTCACTTCTATTAACTTCAG
TAAGAATCAACTATGTGAAATTCAAAAAGGATGGTAGAAGTGAAGGAAATGGTTTCTGATGTCGATCTCAGTTT
TAATAAACTTTCTTTATATCCTTGAGTTATGTGTGCTTCAGAAATTGACTTTTTTAGATCTCAGGAACAATTT
TTTAAATCTTTGCCAGAAGAAATGGAATCACTGGTAAGACTGCAACGATCAATCTTTCTTTAATAGGTTTAA
AATGCTACCTGAAGTTCTATATCGTATCTTCACACTTGAACAATCTGATTAGTAATAATCAGGTTGGATCTGT
GGACCCTCAGAAAATGAAGATGATGGAAAATCTGACCACGTGAGACCTTCAAATAATGACCTCTTACAAATTCC
ACCAGAGCTCGGTAATTGTGTAACTTAAGAACATTACTATTGGATGGAAATCCATTCCGAGTTCTCGAGCAGC
CATATTAATGAAAGGAACAGCTGCTATACTTGAATATTTGAGAGACCGAATTCCTACTTAACATGGAGTTGCTTT
ATAACCCTTGTCATGTATTATTAACCCTGGTTAATTCAGGAGGATGTAACATTTGTTTTAGTATCATCTTAAA
AGGTGATTATTGTAATTGATCTTGTAGTTTCCAGTATCACCTACCCGTTGGTATAATTAGCCTGGGCCATATTC
ACTGCCAGTAAATATTTTACATTTTATTTAAGATTTTGTAAAGGTGTTGTGTACATTTGTAATGGTGATAACC
ACAATGTGTTCTATACATTTGTTCTAAATGTTTTGCTTATGATTTATCCTGCTAACTTTTATTTTCTTATAGCAAG
CAGTTTTTTCAAATAATGAATTTTATTTAATGTGGTTCAGTATTATAATAACAAAGCATTTTTGTAGAACTGGTT
TTTTTCTCATTTATTTTGTATTCCATACAATGTGACCAATTGACTTGAATATGACTAGCCAGTTTCTATGTTT
TTGTTAGATATAAAATTAATCGAATTTTGTGTAATACTGTTCTTTGGCATTAAAAAATAAGACCTTCTTATCT
TGGGCCACATGTCAAAAAGAAAAAGGAAACAAAAATATATTAATAAAGACTTTTTCATTACCCATGATAGGACTT
TTGTGATATGGCTAATCTCAGTACACATTTCAACTTAAACCTTTTTATTTACAGCACCATAATTTTAAATTTA
CTTGCAATCTTGGTAAGACTAAACTTGCAGTGTTTTTCTAAAAGGGAATTTGATAGGTAACTTGATTTAATAAA
AATTAATATCATTTTTGTTTACACCAAAATATCAGAAGTAGGTTGATTAGTCATTATAACACTTACCATATGA
TTCTATTAAGAAGTCAATTCAGTAGCATGTATATCAATTTATATAGATAGGTAGATAGCTTTTGGATGATTGAGG
CATGCTTATATTATGAAAAAATTGCTAATAAAGATAAATACTACATGTTTCAGAATAAAAGTTACATTTTTTC

WO 2004/030615

PCT/US2003/028547

283/6881
FIGURE 263

MSRLKRIAGQDLRAGFKAGGRDCGTSVPQGLLKAARKSGQLNLSGRNLSEVPQCVWRINVDIPEEANQNLSFGAT
ERWWEQTDLTCLIISNNKLQSLTDDLRLLPALTVLDIHDNQLTSLPSAIRELENLQKLNVSHNKLIKILPEEITNL
RNLKCLYLQHNETLCISEGFEQLSNLEDLDLSNNHLTTVPASFSSSLVRLNLSSNELKSLPAEINRMKRLKHL
DCNSNLEETIPPELAGMESLELLYLRRNKLRFLPEFPSCSLLKELHVGENQIEMLEAEHLKHLNSILVLDLRDNK
LKSVPDEIILLRSLERLDLSNNDISSLPYSLGNLHLKFLALEGNPLRTIRREIISKGTQEVLYLRSKIKDDGPS
QSEATETAMTLPSES RVNIHAIITLKILDYSDKQATLIPDEVF DAVKSNIVTSINFSKNQLCEIPKRMVELKEM
VSDVDLSFNKLSFISLELCVLQKLTFDLRNNFLNSLPEEMESLVRLQTINLSFNRFKMLPEVLYRIFTLETILI
SNNQVGSVDPQKMKMMENLTTLDLQNNDLLQIPPELGNCVNLRTLLLDGNPFRVPRAAILMKGTAAILLEYLRDRI
PT

WO 2004/030615

PCT/US2003/028547

284/6881
FIGURE 264

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCACGAAA
TCACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACAAAAGCCACGAAGTATCTGAAAGATGTCACTT
TACAGAAACAGTGTGTACCATTCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCT
GGACACAAGGTCGGTGGCCCCAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTG
AACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCC
GGACCTACAGAGCTCATGGTCGGATTAAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAA
AGGAACAGATTGTTCTAAACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAAC
AAAAACTTATGGCACGGGAGTAAATTCAGCATTAAATAAATGTAATTAAAAGGAAAAATAAAAAATAAAATAA
ATAAATAAATAAATAAAAAAAAAAAAAAAAAAAG

WO 2004/030615

PCT/US2003/028547

285/6881
FIGURE 265

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCACGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACAAAAAGCCACGAAGTATCTGAAAGATGTCACCTTTACAGAAACAGTGTGTACCATTCGACGTTAC
AATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCCAAAAAGAGTGCT
GAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCGGATTAAACCA
TACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCTAAACCAGAAGAGGAG
GTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAACTTATGGCACGGGAGTAAATTCAGCAT
TAAATAAATGTAATTAAAAGG

WO 2004/030615

PCT/US2003/028547

286/6881
FIGURE 266

MVRYSLDPENPTKSCSRGSNLRVHFKNTRETAQAIGMYIQGTKYLDVTLQKQCIPFRHYNGGVGRCAQAKQ
WGWTQGRWPKKSAEFLHVLKNTESNAELKGRFSGH

WO 2004/030615

PCT/US2003/028547

287/6881
FIGURE 267

CGGGAAGGATTGAATACGAGACGCTGTCTGCTTGCCTTAAGACAGCTAGCTGAATTGCTGATTAACTTTTAA
AATACCCAGCTTGGTTTATTTTTCTTAGAATCTGTTGCTAAGACTGGGGACGCTGTTTCTTTACAAAGGGAAA
TCTAAGTTAATTTCAAGGCATTGAAATCGGGGAAAGACTATTATTGCATTTTGGGAATTGAGAAAGGAGCTTCAG
ATGAAGATATTA AAAAGGCTTACCGAAAACAAGCCCTCAAATTTTCATCCGGACAAGAACAATCTCCTCAGGCAG
AGGAAAAATTTAAAGAGGTCGCAGAAGCTTATGAAGTATTGAGTGATCCTAAAAAGAGAGAAATATATGATCAGT
TTGGGGAGGAAGGGTTGAAAGGAGGAGCAGGAGGTACTGATGGACAAGGAGGTACCTTCCGGTACACCTTTCATG
GCGATCCTCATGCTACATTTGCTGCATTTTTCGGAGGGTCCAACCCCTTTGAAATTTTCTTTGGAAGACGAATGG
GTGGTGGTAGAGATTCTGAAGAAATGGAATAGATGGTGATCCTTTTAGTGCCCTTTGGTTTCAGCATGAATGGAT
ATCCAAGAGACAGGAATTCTGTGGGGCCATCCCGCCTCAAACAAGATCCTCCAGTTATTCATGAACTTAGAGTAT
CACTTGAAGAGATATATAGTGGTTGTACCAAACGGATGAAGATTTCTCGAAAAAGGCTAAACGCTGATGGAAGGA
GTTACAGATCTGAGGACAAAATTCTTACCATTGAGATTAAAAAAGGGTGGAAGAAGGCACCAAAATTACTTTTC
CAAGAGAAGGAGATGAAACACCAAATAGTATTCCAGCAGACATTGTTTTTATCATTAAAGACAAAGATCATCCAA
AATTTAAAGGGATGGATCAAATATAATTTTATACTGCTAAAATTAGTTTTACGAGAGGCATTGTGTGGCTGCTCAA
TTAATGTACCAACACTGGATGGAAGAAACATACCTATGTCAGTAAATGATATTGTGAAACCCGGAATGAGGAGAA
GAATTATTGGATATGGGCTGCCATTTCCAAAAATCCTGACCAACGTGGTGACCTTCTAATAGAATTTGAGGTGT
CCTTCCCAGATACTATATCTTCTTCATCCAAAGAAGTACTTAGGAAACATCTTCCTGCCTCATAGAAATGAAGAAC
TTTGTTACACATATTTTGATAAGGCACTGAAATATAAAAGGACTGGTAGTTTACTGATGTAGATGTGAATTCTG
TATAAAGATGTGTAAATTGTTTTGAGGGTTCATTAAATTGCAT

WO 2004/030615

PCT/US2003/028547

288/6881
FIGURE 268

MGKDYCYILGIEKGASDEDIKKAYRKQALKFHPDKNKSPQAEEKFKEVAEAYEVLSDPKKREIYDQFGEEGLKGG
AGGTDGQGGTFRYTFHGDPHATFAAFFGGSNPFEIFFGRRMGGGRDSEEMEIDGDPFSAFGFSMNGYPRDRNSVG
PSRLKQDPPVIHEL RVSL EEIYSGCTKRMKISRKRLNADGRSYRSEDKILTIEIKKGWKEGTKITFPREGDETPN
SIPADIVFI IKDKDHPKF KRDGSNIIYTAKISLREALCGCSINVPTLDGRNIPMSVNDIVKPGMRRRIIGYGLPF
PKNPDQRGDLLEFEVSFPDTISSSSKEVLRKHLPAS

WO 2004/030615

PCT/US2003/028547

289/6881
FIGURE 269

GCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTCGCCGCGCTCGCCCCGGGCTACTCCTGCGCG
CCACAATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCCTTCTCCACTTGACCAGGCTGGCGCTCT
CCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGC GCGCCGGGAGTCGGGCTGGTCCGGGACG
GCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCA
AGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGAC
CCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTA
TTGATGGCGCCGTGGGCTGCATTCTCTGTGTCCCAAGAAGTATCTCTCCCAACTTGGGCTGTCCCAACCCCTC
GGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGG
ACCAGGACGGCCTCCTTGTTAAGGAGCTGGGATTGATGCCTCCGAGGTGGAGTTGACGAGAAAACAATGAATTGA
TTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGATCCCTGTTTTTGAATGGAGCCTCGCATCCGATACAACCCCTT
TACAAGGCCAGAAATGTATTGTTCAAACAACCTTCATGGTCCAGTGCTCAAAGACCTGTGGAAGTGGTATCTCCA
CACGAGTTACCAATGACAACCCCTGAGTGCCGCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCCTTGTGGAC
AGCCAGTGATACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAAGTCAGGTTTA
CTTACGCTGGATGTTTGAGTGTAAGAAATACCGGCCCAAGTACTGCGGTTCTGCGTGAGCGGCCGATGCTGCA
CGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAAGCTCATGA
TGATCCAGTCCTGCAAATGCAACTACAAGTCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCA
ATGACATTACAAAATTTAGGGACTAAATGCTACCTGGGTTTTCCAGGGCACACCTAGACAAACAAGGGAGAAGAGT
GTCAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGATGGGACTCATTGTAGAAAGGAAGCCTTG
CTCATTCTTGAGGAGCATTAAAGGTATTTGAAACTGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACG
ATTGGAGAATACTTTGCTTCATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACT
TTCTGTTTTCTGTTTGTAATTTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCTTTTGGGGTTCTACAGTCG
TAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTTCGTCCTTTGACAAAAGTAAATGGGAGGGCAT
TCCATCCCTTCTGTAAGGGGGACACTCCATGAGTGTCTGTGAGAGGCAGCTATCTGCACTCTAAACTGCAACAG
AAATCAGGTGTTTTAAGACTGAATGTTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACT
GGAATAATTTGTAAATGATTTTAATTTTATATTTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATAAG
AAATATTTACCT

WO 2004/030615

PCT/US2003/028547

290/6881
FIGURE 270

MSSRIARALALVVTLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCCKVCAKQLNEDCSKTQPCDHTKG
LECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRL
VKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKSSLKRIPVFGMEPRIRYNPLQ
GQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGPVYSSLKKGKKCSKTKKSPEPVRFTY
AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEGETFSKNVMMIQSCKCNYNCPHANEAAFPFYRLFND
IHKFRD

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

292/6881
FIGURE 272

MVNP GSSSQPPPVTAGSLSWKRCAGCGGKIADRFLLYAMDSYWHSRCLKSCCQAQLG DIGTSCYTKSGMILCRN
DYIRLFGNSGACSACGQSIPASELVMRAQGNVYHLKCFTCSTCRNRLVPGDRFHYINGSLFCEHDRPTALINGHL
NSLQSNPLLPDQKVC

WO 2004/030615

PCT/US2003/028547

293/6881
FIGURE 273

AGCGATGCGGGCTGGGCCGAGTGGGTGCTCTGGTGCCGGCGTTTGGGCTACGGTTGTTGTTGGCGACTGTGCTTCA
AGCGGTGTCTGCTTTTGGGGCAGAGTTTTTCATCGGAGGCATGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTG
CAGCTCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCCAGGAGGA
AGCACAATTTGAAACCAAAAAGCTGTATGCAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCC
TCAAGTCCAAGCTTTTGTAGGAGTGATAAACCCAAACTGTTTCAGAGGACTGCAAATCAAGTATGTCCGTGGTTC
AGACCCTGTATTAAAGCTTTTGGACGACAATGGGAACATTGCTGAAGAACTGAGCATTCTCAAATGGAACACAGA
CAGTGTAGAAGAATTCCTGAGTGAAAAGTTGGAACGCATATAAATCTTGCTTAAATTTTGTCCCTATCCTTTTGT
ACCTTATCAAATGAAATATTACAGCACCTAGAAAATAATTTAGTTTTTGCTTGCTTCCATTGATCAGTCTTTTACT
TGAGGCATTAAATATCTAATTAAATCGTGAAATGGCAGTATAGTCCATGATATCTAAGGAGTTGGCAAGCTTAAC
AAAACCCATTTTTTATAAATGTCCATCCTCCTGCATTTGTTGATACCACTAACAAAATGCTTTGTAACAGACTTG
CGGTAAATTATGCAAATGATAGTTTGTGATAATTGGTCCAGTTTTACGAACAACAGATTTCTAAATTAGAGAGGT
TAACAAGACAGATGATTACTATGCCTCATGTGCTGTGTGCTCTTTGAAAGGAATGACAGCAGACTACAAAGCAAA
TAAGATATACTGAGCCTCAACAGATTGCCTGCTCCTCAGAGTCTCTCCTATTTTTGTATTACCCAGCTTTCTTTT
TAATACAAATGTTATTTATAGTTTACAATGAATGCACTGCATAAAAACCTTTGTAGCTTCATTATTGTAAACATA
TTCAAGATCCTACAGTAAGAGTGAAACATTCACAAAGATTGCGTTAATGAAGACTACACAGAAAACCTTTCTAG
GGATTTGTGTGGATCAGATACATACTTGGCAAATTTTTGAGTTTTACATTCTTACAGAAAAGTCCATTTAAAAGT
GATCATTTGTAAGACCAAAATATAAATAAAAAGTTTCAAAAATCTATCTGAATTTGGAATTCCTCTGGTTTGTT
TTTCATGTTTAAAATGATGTTTTTCAATGCATTTTTTTCATGTAAGCCCTTTTTTTAGCCAAAATGTAAAAATG
GCTGTAATATTTAAACTTATAACATCTTATTGTTGGTAATAGTGCTTTATATTTGTCTGATTTTATTTTCAA
GTTTTTTCATTTATGAACACATTTTCATTGGTATATTATTTAAGGAATATCTCTTGATATAGAATTTTATATTA
AAAATGATTTTTCTTTGGC

WO 2004/030615

PCT/US2003/028547

294/6881

FIGURE 274

MAAGPSGCLVPAFGLRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQEEA
QFETKKLYAGAILEVCGENWEGSLKSKLLLGVINPNCSEDCKSSMSVVQTLYLKLLDDNGNIAEELSILKWNTDS
VEEFLSEKLRI

WO 2004/030615

PCT/US2003/028547

295/6881
FIGURE 275

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCATGAAA
TCACACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCAC
TTTACAGAAACAGTGCATACCATTCCGACGTTACAATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGG
CTGGACACAAGGTCGGTGGCCCCAAAAGAGTGCTGAATTTTTGCTGCACATGTTTAAAAACGCAGAGGGTAATAC
TGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCG
CCGGACCTACAGAGCTCATGGTCGGATTAACCTACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGA
AAAGGAACAGATTGTTCTAAACCAGAAAAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAA
ACAAAACTTATGGCCCAGGAAATTCAGCATTAAATAAATGTAATTAAAAGGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAG

WO 2004/030615

PCT/US2003/028547

296/6881
FIGURE 276

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACCTTGACCCGGAGAACCCCATGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGGACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCACCTTACAGAAACAGTGCATACCATTCCGACGTTAC
AATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCCAAAAGAGTGCT
GAATTTTTGCTGCACATGTTTTAAAAACGCAGAGGGTAATACTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCGCCGGACCTACAGAGCTCATGGTCGGATTAACTCA
TACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGAAAAGGAACAGATTGTTCCCTAAACCAGAAAAGGAG
GTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAACTTATGGCCCCGAAGTAAATTCAGCAT
TAAATAAATGTAATTAAAAGG

WO 2004/030615

PCT/US2003/028547

297/6881
FIGURE 277

CTTTTTCACAACGGGTTTGTGCGCAGAACACAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAAAGAA
AAGACTCATATCAACATTGTGTCATTGGACACGTAGATTCTGGGCAAGTCCACCACTTCTGGCCATCTGATCTAC
AAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTC
AAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA
TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTCATCAAAAACATGATTACA
GGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGTGGTGAATTGGAAGCTGGTATCTCCAAG
AATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAACATAATTGTTGATGTTAACAAA
ATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAG
AAAATTGGCTACAACCCCAACACAGTAGCATTGTGTGCCAATTTCTGGTTAGAATGGTGACAACATGCTGGAGCCA
AGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCATGCTGCTT
GAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAAGTACAAGCCCTTGCCTGCTCCTCCAGGATGTCTAC
AAAATTGGTGGTATTGGTACTGTTCTTGTGCGCGAGTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACC
TTTGCTCCAGTCAGCGTTACAACAGAAGTAAATCTGTGCGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCT
GGGGACAATATGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCATCGTGGCAACGTTGCTGGTGACAGC
AAAAATGACCCACCAATGGAAGCAGCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGT
CGCTTTACTGTTTCATGATATGAGACAGACACTTGGCGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGA
GCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCA
CTCTTAATCAGTGGTGGGAAGAACGGTCTCAGAAGTGTGTTGTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGAC
TGGTTAATGATAATAATGCAACATAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACCACCTTGGTTTTCTT
TTTCGATGCAGCAGTTTTAAGTTATTAGTTTTTAAATCAGTACTTTTTTAAATGGAAACAACCTTGACCAAAAAT
TTGTCACAGAATTTTGTGAGACCCATTAAAAAGTTTAAATGAG

WO 2004/030615

PCT/US2003/028547

298/6881
FIGURE 278

MLEPSANMPWFKGWKVTHKDGNASGTMLEALDCILPPTRPTDKPLRLPLQDVYKIGGIGTVLVGRVETGILKPG
MVRTFAPVSVTTEVKSVEMHHEALNEALPGDNMGFNVKNVSVKDVHRGNVAGDSKNDPPMEAAGKPMCVESFSDY
PPLGRFTVHDMRQTLAVGVKAVDKKAAGAGKVTKSAQKAQKAK

WO 2004/030615

PCT/US2003/028547

299/6881
FIGURE 279

CACAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTG
GACACGTAGATTCGGGCAAGTCCACCACTTCTGGCCATCTGATCTACAAATGCGGTGGCATCGACAAAAGAACAA
TTGAAAAATTGCAGAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGA
AAGCTGAGCGTGAACTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTA
TCATTGATGCCCTTCTGGCATATACACTGGGTGTGAAACAACATAATTGTTGATGTTAACAAAATGGATTCCACTG
AGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAGGGTGACAACATGC
TGGAGCCAAGTGCTAACAATGCCTTGGTTCAAGGGATGGAAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCA
TGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAAGTGAAGCCGGCCAAATAAGCTCTGGCTA
TGCACCTGTATTGGATTGCCACACAGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCG
TTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTTCCTGG
CAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTACTGTTTCATGATATGAGACAGAC
ACTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAA
AGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGG

WO 2004/030615

PCT/US2003/028547

300/6881
FIGURE 280

GCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAGTCCACCACT
TCTGGCCATCTGATCTACAAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAGAGGCTGCTGAG
ATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATT
GATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTC
ATCAAAAACATGATTACAGGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGTGGTGAATTT
GAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAATA
ATTGTTGATGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAA
ATCAGCACTTACATTAAGAAAATTGGCTACAACCCCAACACAGTAGCATTGTGCCAAATTCTTGAAGTCTGGTG
ATGCTGCCATTGCTGATATGGTTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTC
GCTTTACTGTTTATGATATGAGACAGACACTTGCGGTGGGTG

WO 2004/030615

PCT/US2003/028547

301/6881
FIGURE 281

GTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACCTTTGCTCCAGTCAGCGTTACAACAGAAGTAAAAATCT
GTCGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCTGGGGACAATATGGGCTTCAATGTCAAGAATGTGTCT
GTCAAGGATGTTTCATCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACT
GCTCAGGTGATTATCCTGAACCATCCGGGCCAAATAAGCTCTGGCTATGCACCTGTATTGGATTGCCACACAGCT
CACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCT
AAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCA
GACTATCCACCTTTGGGTCGCTTTACTGTTTCATGATATGAGACAGACACTTGCGGTGGGTGTCATCAAAGCAGTG
GACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCC
CTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTA
AGTTTAGTAGTAAATTTTGTGGACCACTTTGGTT

WO 2004/030615

PCT/US2003/028547

302/6881
FIGURE 282

GTTACTCAAAGACTACCTACTGCGTGGTGCTCCAAGTGAAATTCGTGAAGAATTAGAAAAGCAGCTTTATTCTTG
TATTGCTCTCAAAGTCACAGCAAATCAAATGGAAATGGAACATTCTTTGATACTAAATAACCTAAAAACATTATT
GTGGAAGAAAATTTTCTACACTAATGACTCTTAGTTCATTTGGACATAATTACCATTTTAAGAAAACCTGCCACTT
TTAAAGAACAATTTTGAGCATTAAAAAAAATGGCTTCAAATTCGGGCCAGTTACACAAAACCTCTTCCCCCAG
GCCTGAGAAGCCATCAGTATGTGATCACTGAAGTAATGGCAGGTGTAGGATCAACAGGTCCCCAAGATGTCATTC
CTGCCCTTTTAGAAGCCCTGTTACATCTCCGAAGTACATTCAATTGTGTAACATTTTGGACTGACTTTAAAAACCA
ATGCTGTGAAAAGCTTCATTCCATAAACATCAACAGTGAGTGATTTGTAGATTTACCTTAGCCAAAAATACCAATG
CTGGAAGCATTGTGTTTGCATTGAAGCTGCTGTTCAACAAGAAAATTTATAAATTTACTAATGTCTTAGCATGGT
AAAGTTTGCACATTAACAGAAATTAAGACTGCAAAGCAGGTTAAACTTGCTTCTTTATAAAAACAGATGTTGGGTT
AATAGCATGGTTTACTGTATTAAAGACTTATACACCCATTTTAAACCTCATTACAGACATCAAGTTATGTGTAGCT
TCACAATGGTTCAAGTGGCTTACTTCAAGAAATCTTATACCTGACAGTACACCAATTTTATTGACTAAAAATGGA
TGAATTTTCTTAAAGATTCAAAGGGCCCATCTTAGTATCACGCAGCTGACTGAGCCCTTCAAAAACCTGACATCTTA
AGGCCCAATCAAGATCCACATATCTGATTTTGAAGTATGTGAAAGTGGGACTGTAAGTGCAAGACTAAAAATAAA
TTATAGCAGACTTTTTAGTAATAACTTTCCATTTTCAAACAGTATATCCTGTGGGCCAAAGGGCTATTTCTTAA
GAGGCATGTAAATGTATTTATTTATCTAATGTTTTTCCCCATGTAAACTTGATATACAAGGTTTAGTATTTGC
TCCTCTTTCATATTATTTTACACGTATACTCAGATTTGGCATGTACCTTCAACATCTCCATAAAATTAACAC
CTTTTGGAGAAAAGAACCCTATTTTCTGCTCAAAGGTTTCGCCTACCTAAAGTGGACATGTTAAAAATCTATG
TGACCATCACTGGACAGCTTTCTCTCAAACCTTTCTTCAACGCCATGGATTAGCACCAGTTTGTGTTACTTTAA
GGTACTTTTCCCATTCATCATCTGGTTATATAAATGGATGGAAGAAATATTTCCCACTGATGGTTGGTCTGTG
CTTGCCAAATTTTTAGGGAGAGCTGTTTCATCATACAACATAAGGGATAATGACTCCTGTCAGGTAAACAGAAGC
CCAAGAAATAACAACCTTTTTTCTTAAAAAGTTAGTTACACTTGTTTTCTTGGAGAAAAAACCTGTCAACTCCT
TTGCTTTTCCAAATATTTTCAGGGTATTTCTATAAGGTTTATAAGAAATAAGAGCTTAACACAGAAATAGTTGCT
GTTTATAAGTTTATTATCTATATCTGAAAAATCATAGAAATTGCTGGGTTTAGCTCTCAGCAGCCCGCTCCTG
AGCTCTGAGGAAGCTTGCTTTCTTTTGGAGCTACCCGATCCTTCTTCTGAGCAAGGGACATTTTGGGACGGTTCCA
CCTACAAAAGATAGGAATATATATTTTAAACTATAACTGAAGAGAATAGAATATTTAATTTAAATTTTAATA
AAATTTAATTTTGTAGAGAAATATTTAAGACTTTGCAATCAGAAGGTTAAATAATCCAAGTTCAATATACATTTAC
TTATGTATGATCTTAAGCTAACTTTCCCAAACCCCACTTCTGTGATGTCCTACTACCATAGGGCCAAAGTCAA
ATAGAAGACATGTTAGATTTCAGTAATACCACTTCTAGGTATTTGCCCAAATGTTTTGAAATCAGTTTGTCCAAGA
GAGTGGCACTCCCATGTTTCATTGCAGCACTATATATTAATAGCAACAGATAAATGGATAAAGGAAATGTGGTATA
CATATACATAATGGATTATTACCCAGTCTTTAAAAATGATGGAAATCTGTCAATTTGCAACATGAATGAAGTGGA
GAATATTGTGCTCAGTGAATAAGCCAGGCACAAAAGACAAATCTTCAATTCATATAGAAATCTAAAACAATG
GAACTCACAGAAGCAGAGAGCAGAATGGTGGTTACAGAGGCTGGTGGGTGCAAAGAAATGGGCAGATGATAGTCAA
GTATAAAATCTCCAACAGGAGGAGTATGATTTTGTGTTTATGTTCTATTGCACAGCATGATGAATATAGAATATCG
TACATTTCACAATTAAGAGAATAAATTTCAAATGTTGTTGCCACAAAGTGTTAAGTATTTGAGGTGAATATGTTA
AATACATTGATTTAATTACTATACATTTGATTTGTGGCCATCACATCACTTTATGCTTACATGTTTCAATTAAGTA
TTACTTTCTATTCCATTTAAAGATCAAACATGAAAGATCAACAAAAGCAACTTGTGAGCCAATAAAAAAATGC
AGTAACCACTACTTAGACTGTACTAGGATAGAAAGAACCACTCAGTAGTGTCTGAGGCTAACACATTTCCATCA
CCACAGTTACTTTTGCAAACCTGGTTCCCTTCGCTTCTGCCACATCACGCAGAGCTAGTGATCGAGTTTGACAA
TTACACCAACAGTCTGCCCCAGTGGAACCATTTCCCAACCTGTTTTCTTGAAAAGACAAAAAAGACGACAT
ACCTCTTCTTTTTAACTTCTTTCTTGGGCTTCTTTTCATAGACTGGATTCTCTCGTATAGCAGCATGAGCTTTCT
TATACATCTCCTCCATCTGAAACAAAGGAAAGCAAACAGTACTTGGTTTCAATTCATGTGCCCTACTATATTAAT
GCAACCATAACTTATCTTGTCTTCTAAGCCAGATTCTCAAAGGAACTAACTAAATCAATGTTGGTAAACACT
TTAACTTCTAAATGTAACCTCACCTTTTCTAACAATTTCCCAATTTTCACTTATGCAATGTGAATTATCACTAC
AGAACTCCATCTTACTCAAGAAAAAATCAGGCCAGGTGTGGTGGTTCATGCCTGTAATCTCAAGCACTTTGGGA
GTCTGAAGTGGGAGGATCACTTACGCCAGGAGTTTGAGACCAGCTAAGGCAACACAGTGAGACCTGTCTCCATA
AAAAAATAATTAGCCAGGTGGCAATTATTAATGGTGGCATGCACCTGTAGTCCCAGCTACAGGACTACACGTGA
GTCCAGGAGGTCAAGGCTGCAGTGGCACAATCACAGCTCACTGGACCCAGCCTAGATGACAGAATGAGACCTCA
TCTCTACCAAAATTAATAAAAAAAAAAAAAAAAAAATTAGCAGGG

WO 2004/030615

PCT/US2003/028547

303/6881
FIGURE 283

MFFSPCKLDIQGLVFAPLSYYFHTYTQIWHVPFNISIKLNTFWRKEPLFSAQRFRLPKVEHVKNLCDHHWTAFSQ
NFPSTPWISTSFVYFKVLFPPFIWL

WO 2004/030615

PCT/US2003/028547

304/6881
FIGURE 284

CCTAGCGCCGCTGGGCCTGCAGGTCTCTGTCGAGCAGCGGACGCCGGTCTCTGTTCCGCAGGATGGGGTTTGTTA
AAGTTGTTAAGAATAAGGCCTACTTTAAGAGATACCAAGTGAAATTTAGAAGACGACGAGAGGGTAAAACTGATT
ATTATGCTCGGAAACGCTTGGTGATACAAGATAAAAAATAAATACAACACACCCAAATACAGGATGATAGTTTCGTG
TGACAAACAGAGATATCATTGTGTCAGATTGCTTATGCCCCGTATAGAGGGGGATATGATAGTCTGCGCAGCGTATG
CACACGAACTGCCAAATATGGTGTGAAGGTTGGCCTGACAAATTATGCTGCAGCATATTGTACTGGCCTGCTGC
TGGCCCGCAGGCTTCTCAATAGGTTTGGCATGGACAAGATCTATGAAGGCCAAGTGGAGGTGACTGGTGATGAAT
ACAATGTGGAAAGCATTGATGGTCAGCCAGGTGCCTTCACCTGCTATTTGGATGCAGGCCTTGCCAGAACTACCA
CTGGCAATAAAGTTTTTGGTGCCCTGAAGGGAGCTGTGGATGGAGGCTTGTCTATCCCTCACAGTACCAAACGAT
TCCCTGGTTATGATTCTGAAAGCAAGGAATTTAATGCAGAAGTACATCGGAAGCACATCATGGGCCAGAATGTTG
CAGATTACATGCGCTACTTAATGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACA
GCGTAACTCCAGACATGATGGAGGAGATGTATAAGAAAGCTCATGCTGCTATACGAGAGAATCCAGTCTATGAAA
AGAAGCCCAAGAAAGAAGTTAAAAAGAAGAGGTGGAACCGTCCCAAAATGTCCCTTGCTCAGAAAGAAGGATCGGG
TAGCTCAAAAGAAGGCAAGCTTCCTCAGAGCTCAGGAGCGGGCTGCTGAGAGCTAAACCCAGCAATTTTCTATGA
TTTTTTCAGATATAGATAATAAACTTATGAACAGCAACTAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

305/6881
FIGURE 285

MGFVKVVKNKAYFKRYQVKFRRRREGKTDYYARKRLVIQDKNKYNTPKYRMIVRVNTRDIICQIAYARIEGDMIV
CAAYAHELPKYGVKVGLTNYAAAYCTGLLLARRLLNRFGMDKIYEGQVEVTGDEYNVESIDGQPGAFTCYLDAGL
ARTTTGNKVFGALKGAVDGGLSIPHSTKRFPGYDSESKEFNAEVHRKHIMGQNVADYMYLMEEDEDAYKKQFSQ
YIKNSVTPDMMEEMYKKAHAAI RENPVYEKKPKKEVKKKRWNRPKMSLAQKKDRVAQKKASFLRAQERAAES

WO 2004/030615

PCT/US2003/028547

306/6881
FIGURE 286

ATGGTAATGTTAAGACAAATCTTGGGAGAAACATTTATCAATTCCAATACCTCTCTCCACCCCAATACTGTATG
CTCTTGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACAGTGTA ACTCCAGACATG
ATGGAGGAGATGTATAAGAAAGCTCATGCTGCTGTACCAGAGAATCCGGTCTATGAAAAGAAGCCCAAGAAAGAA
GTTAAAAAGAAGAGGTGGAACCGTTCCAAAATGTCCCTTGCTCAGAAGAAGGATTGGGTAGCTCAAAAGAAGGCA
AGCTTCCTCAGAGCTTAG

WO 2004/030615

PCT/US2003/028547

307/6881
FIGURE 287

MVNVKTNLGRNIYQFQYLSPPQYCMLEDEDEAYKKQFSQYIKNSVTPDMMEEMYKKAHAAPENPVYEKKPKKE
VKKKRWNRSKMSLAQKKDWVAQKKASFLRA

WO 2004/030615

PCT/US2003/028547

308/6881
FIGURE 288

GCTGACTCCAGTGTCCCGAGAGGCGCCGCTTCTTCCGCTTTCTCGTCAGGCTCCTGCAACCCAGGCATGAACCA
AGGTTTCTGAACTACTGGGCGGGAGCCAACGTCTCTTCTTTCTCCCGCTCTGGCGGAGGCTTTGTCTGCTGCGGGC
TGGGCCCCAGGGTGTCCCCCATGGCGGGGCGCGGGTGGAGGTCGATGGCAGCATCATGGAAGGGGGCGGCCAGA
TCCTGAGAGTCTCTACGGCCTTGAGCTGTCTCCTAGGCCCTCCCCCTGCGGGTGCAGAAGATCCGAGCCGGCCGGA
GCACGCCAGGCCTGAGGCCTCAACATTTATCTGGACTGGAAATGATTCGAGATTGTGTGATGGGCAACTGGAGG
GGGCAGAAATTGGCTCAACAGAAATAACCTTTACACCAGAGAAGATCAAAGGTGGAATCCACACAGCAGATACCA
AGACAGCAGGGAGTGTGTGCCTCTTGATGCAGGTCTCAATGCCGTGTGTTCTCTTTGCTGCTTCTCCATCAGAAC
TTCATTTGAAAGGTGGAACATAATGCTGAAATGGCACCACAGATCGATTATACAGTGATGGTCTTCAAGCCAATTG
TTGAAAAATTTGGTTTTCATATTTAATTGTGACATTAAAAACAAGGGGATATTACCCAAAAGGGGGTGGTGAAGTGA
TTGTTTCGAATGTCACCAGTTAAACAATTGAACCCATAAAATTTAACTGAGCGTGGCTGTGTGACTAAGATATATG
GAAGAGCTTTCGTTGCTGGTGTGTTTGCCATTAAAGTAGCAAAAGATATGGCAGCGGCAGCAGTTAGATGCATCA
GAAAGGAGATCCGGGATTTGTATGTTAACATCCAGCCTGTTCAAGAACCTAAAGACCAAGCATTGGAATGGAA
ATGGAATAATAATTATTGCTGAGACCTCCACTGGCTGTTTGTGTTGCTGGATCATCGCTTGGTAAACGAGGTGTAA
ATGCAGACAAAGTTGGAATTGAAGCTGCCGAAATGCTATTAGCAAAATCTTAGACATGGTGGTACTGTGGATGAGT
ATCTGCAAGACCAGCTGATTGTTTTCATGGCATTAGCCAATGGAGTTTCCAGAATAAAAAACAGGACCAGTTACAC
TCCATACGCAAACCGCGATACATTTGCTGAACAAATAGCAAAGGCTAAATTTATTGTGAAGAAATCAGAAGATG
AAGAAGACGCCGCTAAAGATACTTATATTATTGAATGCCAAGGAATTGGGATGACAAATCCAAATCTATAGAGTA
TTTGCCTCTTAAATGATACCTCATTGATATATTGCACTATTTCAATAACTATAAAATAATGACTAGGAAGTAA
CTTATTAAAGGCTATGACTTAAATTTGAAGATGAAGTACAGTGTTCTAGGTTTGCTGAGAAGGCTTCATTAAATT
AATCTCACTTTGAATATCTCCTGAGAGATGGACAATGAAATATCAGTTGGTGGATATGTGTGATAGCTGATTCA
ATATTGAAGTATTGAAATAAAATATTCTTTACACCTGAG

WO 2004/030615

PCT/US2003/028547

309/6881
FIGURE 289

MAGPRVEVDGSIMEGGGQILRVSTALSCLLGLPLRVQKIRAGRSTPGLRPQHLSGLEMIRDLC DGQLEGAEIGST
EITFTPEKIKGGIHTADTKTAGSVCLLMQVSMPCVLFAASPSELHLKGGTNAEMAPQIDYTMVFKPIVEKFGFI
FNCDIKTRGYYPKGGGEVIVRMSPVKQLNPINLTERGCVTKIYGRAFVAGVLPFKVAKDMAAAVRCIRKEIRDL
YVNIQPVQEPKDQAFGNNGIIIIAETSTGCLFAGSSLGKRGVNADKVGIEAAEMLLANLRHGGTVDEYLQDQLI
VFMALANGVSRIKTGPVTLHTQTAIHFAEQIAKAKFIVKKSEDEEDAADTYIECQGIGMTNPNL

WO 2004/030615

PCT/US2003/028547

310/6881
FIGURE 290

GCTTTTCCTTGCTACCTGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACTTAAAGGGAACTTT
CACAAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGATGTCCTTAAGTTCCTTGACGACAGGAACCCACTT
AGGTGGCACC AATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAA
TCTGAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGGTCGTGCTATTGTTGCCATTGAAAACCCCTGCTGATGTCAG
TGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAATTTGCTGCTGCCACTGGAGCCACTCCAATTGC
TGGCCGCTTCACTCCTGGAACCTTCACTAACC GGATCCAGGCAGCCTTCCGGGAGCCACGGCTTGTTGTGGTTAC
TGACCCCAGGGCTGACCACCAGCCTCTCACAGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACAC
AGATTCTCCTCTGTGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAACCTCACTCAGTGGGTTTGATGTG
GTGGATGCTGGCTCGGGAAGTTCTGCGCATGTGTGGCACCATTTCCTGTAACACCCATGGGAGGTCATGCCTGA
TCTGTACTTCGACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAGAAGGCAGTGACCAAGGA
GGAATTT CAGGGTGAATGGACTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGA
AGGTGTACAGGTGCCCTCTGTGCCTATT CAGCAATTCCTACTGAAGACTGGAGCGCTCAGCCTGCCACGGAAGA
CTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGACTGGTCTTTAAGCTGTTCTTGC
ATAGGCTCTTAAGCAGCATGGAAAAATGGTTGATGGAAAAATAACATCAGTTTCT

WO 2004/030615

PCT/US2003/028547

311/6881
FIGURE 291

MSGALDVLQMKEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAGRAIVAIENPADVSV
ISSRNTGQRAVLKFAAATGATPIAGRFTPGTFTNRIQAAFREPRLVVTDPRADHQPLTEASYVNLPTIALCNTD
SPLCYVDIAIPCNNKGTHSVGLMWWMLAREVLRMCGTISRHPWEVMPDLYFDRDP EEIEKEEQAAAEKAVTKEE
FQGEWTAPAPEFTATQPEVADWSEGVQVPSVPIQQFTEDWSAQPATDWSAAPT AQATEWVGATTDWS

WO 2004/030615

PCT/US2003/028547

312/6881
FIGURE 292

GGCACGAGGAAGAATCAGGAGCTTAGGATGTATTAACACCAACTCATTAAATATACTAACCGGACAATGTTCTACA
AACAAATTCTACATTGTAAAGGACTGGATTGGCACAAAATAAAATAATTTTATTTTATTTCAGCTTATAATATGACT
CGATGGAGGAAAATTTGATAAGCATGAGAGAAGACCATTCTTTTCATGTTTCGTTACAGAATGGAAGCTTCTTGCC
TAGAGCTGGCCTTGGAAGGGGAACGTCTATGTAAATCAGGAGACTGCCGCGCTGGCGTGTCATTCTTTGAAGCTG
CAGTTCAAGTTGGAACCTGAAGACCTAAAAACACTTAGCGCTATTTACAGCCAGTTGGGCAATGCTTATTTCTATT
TGCATGATTATGCCAAAGCATTAGAATATCACCATCATGATTTAACCCCTTGCAAGGACTATTGGAGACCAGCTGG
GGGAAGCGAAAGCTAGTGGTAATCTGGGAAACACCTTAAAGTTCTTGGGAATTTTGACGAAGCCATAGTTTGT
GTCAGCGACACCTAGATATTTCCAGAGAGCTTAATGACAAGGTGGGAGAAGCAAGAGCACTTTACAATCTTGGGA
ATGTGTATCATGCCAAAGGGAAAAGTTTGGTTGCCCTGGTCCCCAGGATGTAGGAGAATTTCCAGAAGAAGTGA
GAGATGCTCTGCAGGCAGCCGTGGATTTTTATGAGGAAAACCTATCATTAGTGACTGCTTTGGGTGACCGAGCGG
CACAAGGACGTGCCCTTTGGAAATCTTGGAAACACACATTACCTCCTTGGCAACTTCAGGGATGCAGTTATAGCTC
ATGAGCAGCGTCTCCTTATTGCAAAAGAATTTGGAGATAAAGCAGCTGAAAGAAGAGCATATAGCAACCTTGGAA
ATGCATATATATTTCTTGGTGAATTTGAACTGCCTCGGAATACTACAAGAAGACACTACTGTTGGCCCGACAGC
TTAAAGACCGAGCTGTAGAAGCACAGTCTTGTTACAGTCTTGGAAATACATATACTTTACTTCAAGACTATGAAA
AGGCCATTGATTATCATCTGAAGCACTTAGCAATTGCTCAAGAGCTGAATGATAGAATTGGTGAAGGAAGAGCAT
GTTGGAGCTTAGGAAATGCATACACAGCACTAGGAAATCATGATCAAGCAATGCATTTTGCTGAAAAGCACTTGG
AAATTTCAAGAGAGGTTGGGGATAAAAGTGGTGAACCTAACAGCACGACTTAATCTCTCAGACCTTCAAATGGTTC
TTGGTCTGAGCTACAGCACAAATAACTCCATAATGTCTGAAAATACTGAAATTGATAGCAGTTTGAATGGTGTAC
TCCCCAAGTTGGGACGCCCGCATAGTATGGAAAATATGGAACCTTATGAAGTTAACACCAGAAAAGGTACAGAACT
GGAACAGTGAAATTCTTGCTAAGCAAAAACCTCTTATTGCCAAACCTTCTGCAAAGCTACTCTTTGTCAACAGAC
TGAAGGGGAAAAAATACAAAACGAATTCCTCCACTAAAGTTCTCCAAGATGCCAGTAATTCTATTGACCACCGAA
TTCCAAATTTCTCAGAGGAAAATCAGTGCAGATACTATTGGAGATGAAGGGTTCTTTGACTTATTAAGCCGATTC
AAAGCAATAGGATGGATGATCAGAGATGTTGCTTACAAGAAAAGAACTGCCATACAGCTTCAACAACAACCTCTT
CCACTCCCCCTAAAATGATGCTAAAAACATCATCTGTTCCCTGTGGTATCCCCAACACGGATGAGTTTGTAGATC
TTCTTGCCAGCTCACAGAGTCGCCGTCTGGATGACCAGAGGGCTAGTTTCAGTAATTTGCCAGGGCTTCGTCTAA
CACAAAACAGCCAGTCGGTACTTAGCCACCTGATGACTAATGACAACAAAGAGGCTGATGAAGATTCTTTGACA
TCCTTGTAATAATGTCAAGGATCCAGATTAGATGATCAAAGATGTGCTCCACCACCTGCTACCACAAAGGGTCCGA
CAGTACCAGATGAAGACTTTTTTCAGCCTTATTTTACGGTCCCAGGGAAAGAGAATGGATGAACAGAGAGTTCCTT
TACAAAGAGATCAAAACAGAGACACTGACTTTGGGCTAAAGGACTTTTTTGCAAAATAATGCTTTGTGGAGTTTA
AAAATTCAGGGAAAAAATCGGCAGACCATTTAGTTACTATGGATTTATTTTTTTTCTTTCAAACACGGTAAGGAA
ACAATCTATTACTTTTTTCTTAAAGGAGAATTTATAGCACTGTAATACAGCTTAAAAATATTTTAGAATGATG
TAAATAGTTAA

WO 2004/030615

PCT/US2003/028547

313/6881
FIGURE 293

MREDHSFHVRYRMEASCLELALALEGERLCKSGDCRAGVSFFEAAVQVGTEDLKTLSTAIYSQLG NAYFYLHDYAKAL
EYHHHDLTLARTIGDQLGEAKASGNLGNTLKV LGNFDEAIVCCQRHLDISRELNDKVGEARALYNLGNVYHAKGK
SFGCPGPQDVGEFPEEVRDALQAAVD FYEENLSLVTALGDRAAQGRAFGNLGNTHYLLGNFRDAVIAHEQRLLIA
KEFGDKAAERRAYSNLGNAYIFLGEFETASEYYKKTLLARQLKDRAVEAQSCYSLGNTYTLLQDYEK AIDYHLK
HLAIAQELNDRIGEGRACWSLGNAYTALGNHDQAMHFAEKHLEISREVGDKSGELTARLNLSDLQMVLGLSYSTN
NSIMSENTEIDSSLNGVLPKLGRRHSMENMELMKLTPEKVQNWNSEILAKQKPLIAKPSAKLLFVNRLKGKKYKT
NSSTKVLQDASNSIDHRIPNSQRKISADTIGDEGFFDLLSRFQSNRMDDQRCCLQEKNCHTASTTTSSTPPKMML
KTSSVPVSPNTDEFD LLLASSQSRRLDDQRASF SNLPGRLRTQNSQSVLSHLM TNDNKEADEDFFDILVKCQGS
RLDDQRCAPPPATTGPTVPDEDDFFSLILRSQGKRMDEQRVLLQRDQNRD TDFGLKDFLQNNALLEFKNSGKKS A
DH

WO 2004/030615

PCT/US2003/028547

314/6881
FIGURE 294

AAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCACGAAATCATGCAAATC
AAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACAACACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACG
AAAAGCCACGAAGTATCTGAAAGATGTCACCTTTACAGAAACAGTGTGTACCATTCCGACGTTACAATGGTGGAGT
TGGCAGGTGTGCGCAGGCCCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGA
TTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCG
GATTAAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGAAAAGGAACAGATTGTTCTAAACC
AGAAGAGGAGGTTGCCCAGAAGAAAAGGATATCCCAGAAGAACTGAAGAAACAAAACTTATGGCACGGGAGTA
AATTCAGCAT

WO 2004/030615

PCT/US2003/028547

315/6881
FIGURE 295

GCAGGCTCTGCCTGTGGCCACTAGCAGAGAAGCTGCTGTCCTTCCACCACCAGCACCAGGACCACCTGCTCCAAGA
CCAGCCTCCTGGGGGGACCAGGCACCCGGCCTTCACTGGCACCACAGGGAGCCGTCCTCAGCAGCGTCAACATGTC
AAGGCCACAGCAGCAGAGCCATTTACTTGCACCGGAAGGAGTACTCCAGAACCTCACCTCAGAGCCCACCTCCT
GCAGCACAGGGTGGAGCACTTGATGACATGCAAGCAGGGGAGTCAGAGAGTCCAGGGGCCCCGAGGATGCCTTGCA
GAAGCTGTTTCGAGATGGATGCACAGGGCCGGGTGTGGAGCCAAGACTTGATCCTGCAGGTTCAGGGACGGCTGGCT
GCAGCTGCTGGACATTGAGACCAAGGAGGAGCTGGACTCTTACCGCCTAGACAGCATCCAGGCCATGAATGTGGC
GCTCAACACATGTTCTTACAACCTCCATCCTGTCCATCACCGTGCAGGAGCCGGGCTGCCAGGCACTAGCACTCT
GCTCTTCCAGTGCCAGGAAGTGGGGGCAGAGCGACTGAAGACCAGCCTGCAGAAGGCTCTGGAGGAAGAGCTGGA
GCAAAGACCTCGACTTGGAGGCCCTCAGCCAGGCCAGGACAGATGGAGGGGGCTGCTATGGAAAGGCCGCTCCC
TATGGAGCAGGCACGCTATCTGGAGCCGGGGATCCCTCCAGAACAGCCCCACCAGAGGACCCTAGAGCACAGCCT
CCCACCATCCCCAAGGCCCTGCCACGCCACACAGTGCCCGAGAACCAAGTGCCTTTACTCTGCCTCCTCCAAG
GCGTCTCTTCCCCGAGGACCCAGAGAGGGACGAGGAAGTGCTGAACCATGTCCTAAGGGACATTGAGCTGTT
CATGGGAAAGCTGGAGAAGGCCAGGCAAGACCAGCAGGAAGAAGAAATTTGGGAAAAAACAAGGACCAGGG
AGGTCTCACCCAGGCACAGTACATTGACTGCTTCCAGAAGATCAAGCACAGCTTCAACCTCCTGGGAAGGCTGGC
CACCTGGCTGAAGGAGACAAGTGCCCTGAGCTCGTACACATCCTCTTCAAGTCCCTGAACCTTATCCTGGCCAG
GTGCCCTGAGGCTGGCCTAGCAGCCCAAGTGATCTACCCCTCCTCACCCCTAAAGCTATCAACCTGCTACAGTC
CTGTCTAAGCCACCTGAGAGTAACCTTTGGATGGGGTTGGGCCCAGCCTGGACCACTAGCCGGGCGGACTGGAC
AGGCGATGAGCCCTGCCCTACCAACCCACATTCTCAGATGACTGGCAACTTCCAGAGCCCTCCAGCCAAGCACC
CTTAGGATACCAGGACCCTGTTTCCCTTCGGCGGGGAAGTCATAGGTTAGGGAGCACCTCACACTTTCCTCAGGA
GAAGACACACAACCATGACCCTCAGCCTGGGGACCCCAACTCCAGGCCCTCCAGCCCCAACCTGCCAGCCAGC
CCTGAAAATGCAAGTCTTGTACGAGTTTGAAGCTAGGAACCCACGGGAAGTACTGTGGTCCAGGGAGAGAAGCT
GGAGGTTCTGGACCACAGCAAGCGGTGGTGGCTGGTGAAGAATGAGGCGGGACGGAGCGGCTACATTCCAAGCAA
CATCCTGGAGCCCTACAGCCGGGGACCCCTGGGACCCAGGGCCAGTCACCCTCTCGGGTTCCAATGCTTCGACT
TAGCTCGAGGCCTGAAGAGGTCACAGACTGGCTGCAGGCAGAGAACTTCTCCACTGCCACGGTGAGGACACTTGG
GTCCCTGACGGGGAGCCAGCTACTTCGCATAAGACCTGGGGAGCTACAGATGCTATGTCCACAGGAGGCCCCACG
AATCCTGTCCCGCTGGAGGCTGTCAGAAGGATGCTGGGGATAAGCCCTTAGGCACCAGCTTAGACACCTCCAAG
AACCAGGCCCCGCTGATGCAAGATGGCAGATCTGATACCCATTAGAGCCCCGAGAATTCCTCTTCTGGATCCAG
TTTGCAGCAAACCCACACCCAGCTCACACAGCAAAAACAATGGACAGGCCCCAGAGGCTGAAGCAAACAGTGTC
CCTTCTGGCTGTGTTGGAGCCTCCCCAGTAACCACCTATTTATTTTACCTCTTTCCCAAACCTGGAGCATTATG
CCTAGGCTTGTCAAGAATCTGTTCACTCCCTCTCCTTCTCAATAAAAGCATCTTCAAGCTTGT

WO 2004/030615

PCT/US2003/028547

316/6881
FIGURE 296

GGGAGAAAGCCTGTTGCGTGGAAGATAAGGCGGCGCGGAAGTGGACACAGGGTGGGCTGGAGCTCAGATCTAAC
TGGACTCTCGCTCCTGCTGGCTGGACATGGAGGATTTGGAGGAAGATGTAAGGTTTATTGTGGATGAGACCTTGG
ACTTTGGGGGGCTGTCAACATCTGACAGCCGTGAGGAGGAAGACATAACAGTGTTGGTGACTCCAGAGAAACCAC
TTCGACGGGGCCTCTCCACCGAAGTGACCCAAATGCAGTGGCACCTGCCCCCAGGGTGTGAGGCTCAGCCTAG
GCCCCCTCAGTCCAGAGAAGCTGGAGGAGATCCTCGATGAGGCCAACCGGCTGGCCGCTCAGCTGGAGCAGTGTG
CCCTGCAGGATCGGGAGAGCGCAGGCGAGGGCCTGGGGCCTCGCCGAGTGAAGCCCAGTCCTCGGCGGGAGACCT
TTGTGCTGAAGGATAGTCCTGTCCGAGACCTGCTGCCACTGTGAACCTCTTTGACGCGGAGCACCCCCCTCCCCAA
GCAGCCTGACGCCTCGACTCCGGAGTAATGATAGGAAGGGGTGAGTCAGGGCTCTCCGGGGCTACATCTGGAAAGA
GGCCCTCCAACATGAAGAGGGAGTCACCCACTTGCAATCTGTTCCCTGCATCCAAAAGCCCAGCATCTTCTCCTC
TTACCCGATCGACTCCCCCAGTCCGGGGGAGAGCCGGGCCAGTGGGAGAGCAGCAGCCAGCCCACCCACCCCCA
TCAGATCCGTCTGGCCCCACAGCCTTCTACCAGCAACTCTCAACGCCTGCCCCGGCCGAGGGAGCAGCTGCTA
AATCTTCCAGTCAACTGCCCATTCCCTCGGCCATCCCCAGGCCTGCCAGCCGAATGCCACTCACCAGCCGGAGTG
TGCCACCTGGCAGAGGTGCCCTACCTCCGGATTCTCTGTCAACTCGAAAAGGGCTTCCAAGACCAAGCACTGCAG
GACACAGAGTGCGGGAAAGTGGACACAAGGTTCTGTTTCCAGCGACTAAATCTTCTGTGTCATGGGTGCCACTC
GCAGCAATCTGCAGCCCCCAGGAAAGTGGCAGTCCCAGGACCTACCAGGTAAAGAGATCAGGACAGCAAGCAAG
ACTTCAGTAGCAAACCACTACAGTCAGTACCTGGACTCGCCTCTACCCAGCAGACCCTGACTCCAGCAGATTCTG
GCCCAGGGACAGGAGGAAGAGATGCCACCAGGGCTGGTCTCCCAGGAGTAGAGACCATGGGAAATGGGGTGGATT
AGGATTGAGCTGGAGAAGACTTAAACTCTCTGGGTTGAAAGAAGATTAGGGGAAAAAGAGGTACCTTCCAGCAGT
GAAATGAACAAATAGAAGATGAGAAGTACAGGCAAGTGGTTTGTCTTTATCCACCCCCACTGTTGTGGTCAGCCC
CAGAGAATTTTATCTTCTTCCCTTGGCATTGGTTCACTGGACATTTCCACGTGAGCGGCCTCCGTAGCTAACCTCC
CTGCCCTCTGAGGAGCCATCTTCTGAATCGCATTCTCTACTGGACTCTGGCCTGCTTGGAGAGGTGGCAGCAGG
CACCTGGTCTTCAGAAATTGTTTCTGTGAATTCTGTGACTCCTAATAGGCCAGTTTGTGATAAGCTTACTCTAT
GAGTCTTCATTTTTCTAAAATAAAGTGAATGTATTTTTAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

317/6881
FIGURE 297

MEDLEEDVRFIVDETLDGGLSPSDSREEEDITVLVTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLE
EILDEANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFLVKDSPVRDLLPTVNSLTRSTPSPSSLTPRLRS
NDRKGSVRALRATSGKRPSNMKRESPTCNLFPASKSPASSPLTRSTPPVRGRAGPSGRAAASPPTPIRSVLAPQP
STSNSQRLPRPQGAAAKSSQLPIPSAIPRPASRMPLTSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGH
KVPVSQRLNLPVMGATRNLQPPRKVAVPGPTR

WO 2004/030615

PCT/US2003/028547

318/6881
FIGURE 298

GCAGTGCGGCGGTACAGGCTGAGTGCTGCGGCGCGATCCTTGCTTCCCTGAGCGTTGGCCCCGGGAGGAAAGAAG
ATGGTGCTGGATCTGGATTTGTTTCGGGTGGATAAAGGAGGGGACCCAGCCCTCATCCGAGAGACGCAGGAGAAG
CGCTTCAAGGACCCGGGACTAGTGGACCAGCTGGTGAAGGCAGACAGCGAGTGGCGACGATGTAGATTTTCGGGCA
GACAACTTGAACAAGCTGAAGAACCTATGCAGCAAGACAATCGGAGAGAAAAATGAAGAAAAAGAGCCAGTGGGA
GATGATGAGTCTGTCCCAGAGAATGTGCTGAGTTTCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAAGTC
TCACAAATCAAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACGCGGAGCGGATAAAAGTTGGAA
GCAGAGCGGTTTGAAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCCTTCTGTACCCATCAGTAACGATGAGGAT
GTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTG
ATGGTAGATGGCTTTGAAGGCGAAAAGGGGGCCGTGGTGGCTGGGAGTCGAGGGTACTTCTTGAAGGGGGTCCCTG
GTGTTCCCTGGAACAGGCTCTCATCCAGTATGCCCTTCGCACCTTGGGAAGTCGGGGCTACATTCCCATTATACC
CCCTTTTTTCATGAGGAAGGAGGTCAATGCAGGAGGTGGCACAGCTCAGCCAGTTTGATGAAGAACTTTATAAGGTG
ATTGGCAAAGGCAGTGAAAAGTCTGATGACAACCTCCTATGATGAGAAGTACCTGATTGCCACCTCAGAGCAGCCC
ATTGCTGCCCTGCACCGGGATGAGTGGCTCCGGCCGGAGGACCTGCCCATCAAGTATGCTGGCCTGTCTACCTGC
TTCCGTCAGGAGGTGGGCTCCCATGGCCGTGACACCCGTGGCATCTTCCGAGTCCATCAGTTTGAGAAGATTGAA
CAGTTTGTGTACTCATACCCCATGACAACAAGTCATGGGAGATGTTTGAAGAGATGATTACCACCGCAGAGGAG
TTCTACCAGTCCCTGGGGATTCTTTACCACATTGTGAATATTGTCTCAGGTTCTTTGAATCATGCTGCCAGTAAG
AAGCTTGACCTGGAGGCCTGGTTTCCGGGCTCAGGAGCCTTCCGTGAGTTGGTCTCCTGTTCTAATTGCACGGAT
TACCAGGCTCGCCGGCTTCGAATCCGATATGGGCAAACCAAGAAGATGATGGACAAGGTGGAGTTTGTCCATATG
CTCAATGCTACCATGTGCGCCACTACCCGTACCATCTGCGCCATCCTGGAGAACTACCAGACAGAGAAGGGCATC
ACTGTGCCTGAGAAATTGAAGGAGTTCAATGCCGCCAGGACTGCAAGAACTGATCCCCTTTGTGAAGCCTGCGCCC
ATTGAGCAGGAGCCATCAAAGAAGCAGAAGAAGCAACATGAGGGCAGCAAAAAGAAAGCAGCAGCAAGAGACGTC
ACCCTAGAAAACAGGCTGCAGAACATGGAGGTACCGATGCTTGAACATTCTGCTCCCTATTGCGCAGGCTTT
CATTTCTGTCTGCTGAGATCTCAGAGCCTGCCAACAGCAGGGAAGCCAAGCACCCATTATCCCCCTGCCCCCA
TCTGACTGCGTAGCTGAGAGGGGAACAGTGCCATGTACCACACAGATGTTCTGTCTCCTCGCATGGGCATAGGG
ACCCATCATTGATGACTGATGAAACCATGTAATAAAGCATCTCTGGGGAGGGCTTAGGACTCTTCTCAGTCTTC
TTCCCCGGGCTTGAACCCCGAAAAA

WO 2004/030615

PCT/US2003/028547

319/6881
FIGURE 299

MVLDDLDFRVDKGGDPALIRETQEKRFKDPGLVDQLVKADSEWRRCRFRADNLNKLKNLCSKTIGKMKKKKEPVG
DDESVPENVL SFDDL TADALANLKV SQIKKVRL IDEAILKCD AERIKLEAERFENLREIGNLLHPSVPI SNDED
VDNKVERIWGDCTVRKKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGVLVFLEQALI QYALRTLGSRGYIPIYT
PFFMRKEVMQEVAQLSQFDEELYKVIGKGSEKSDDNSYDEKYLIATSEQPIAALHRDEWLRPEDLP IKYAGLSTC
FRQEVGSHGRDTRGIFRVHQFEKIEQFVYSSPHDNKSWEMFEEMITTAEEFYQSLGIPYHIVNIVSGSLNHAASK
KLDLEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGTKKMMDKVEFVHMLNATMCATTRTICAILENYQTEKGI
TVPEKLKEFMPPGLQELIPFVKPAPIEQEPSKKQKKQHEGSKKKAAARDVTLENRLQNMEVTD A

WO 2004/030615

PCT/US2003/028547

320/6881
FIGURE 300

CAGAGTGCCCTTTCTCCCCGCCTCTTCCCCCTCCCGGGAGCTGCCAGTACTTGACGTGGCGTCACCGCCCTCTAC
CCTCGCTTTGCGTGCGTGTTTGCCTACAGCGGAGGTGGCGGCGCGGGCAGGTCGGAGCTCGGAGCTGCTGCTTCT
GGTTCTCTTGTGGCCACCGTCGCTGTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTC
AGAAGCCGACGCAGCTCGACGCAGGGGCCGGCAGGAGGTGGGCGATCGCGTGTCGGAGGGCGCCGCGCGGGCAG
GCGGGCGGGCGCCAGAGGGGGAAGAGGCGGGGGCGGCGGGTCAGCCGCTGGCCGGGCCGGCGGGGGAATGTCGA
TGCCTGACGCGATGCCGCTGCCCGGGGTGGGGAGGAGCTGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGT
ACTCCTTCATGGCCACCGTCACCAAGGCGCCCAAGAAGCAATCCAGTTTGCTGATGACATGCAGGAGTTCACCA
AATTCCCCACCAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCTCCACTGACAGCTACAGTTCAG
CTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGCAAACCAACTCCAAGGGCAGCA
GCAATTTCTGTGTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGT
CTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAATAGTGGGCTGTACAC
ACATCACAGCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTA
ACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTGCTTGAAGGGCG
AGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGG
ATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTAAGAAGATCCGAGGCATTGTGG
AAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACG
TCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGA
GGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTG
CTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGG
ATGGGTTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGA
ATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAG
AAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCACT
GGCCAGATGGCAAACGAGTTGTCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCACCT
TTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGCGGATACA
AGCAGGATGTGTACTTGCTTCTTAAGAAAATGGATGAATACGTTGCCAGCTTGCACTGCCATCATTTGATGCCC
ACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAACAAAATGGGCCATTCAAACCTAATTATT
ACAGATACTAATGGACCATACTACCAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTTTAAGAT
AACTTTTATTTTCTTCTTACTCCTTTCTCTTGATTTTTTCTTATAATTTTCTTCTTGTTTTTTTCATCTCATT
TCCAAGTTCTGCAGACCACACAGGAACCTTGCTTCATGGCTCTTTAGATGAAATAGAAGTTCAGGGTCCCTCACTC
TAGTCACTAAAGAAGGATTTTACTCCCCAGCCAGAAAGGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAG
TCTTAATTAGGTACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGC
CTTAAAGAGGCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGTACCTAC
CCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCTGCGTAAAG
GTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGT
ATAGCCCTTCTCCACTCCACCAGACTTGCTCATTTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAGTTTA
ATTTTGTCTCTAGGATTTATTTCTGTTGTCCAAAAA

WO 2004/030615

PCT/US2003/028547

321/6881
FIGURE 301

MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMA TVTKAPKKQIQFADDMQEFTKFPTKTGRRSLRSISQSSTDSY
SSAASYTSSDDEVSPREKQQTNSKGSSNFCVKNIKQAEFGRREIEIAEQDMSALISLRKRAQGEKPLAGAKIVG
CTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDGWQANM
ILDDGGDLTHWVYKKYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILDG
LKRTTDMVFGGKQVVVCGYGEVKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVIRQVDVITCTG
NKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQVDHVIWPDGKRVLLEGRLLNLSCTV
PTFVLSITATTQALALIELYNAPEGRYKQDVYLLPKKMDEYVASLHLP SFD AHLTELTDDQAKYLGLNKNGPFPK
NYYRY

WO 2004/030615

PCT/US2003/028547

322/6881
FIGURE 302A

GCTTATGGCGGCGCTGGAGAGGGGGCGCTGAGCTGTTGGGTATGAAGTGTAACAGAACAGACTTTACCACCTGAA
ACTGCTGCTTCAAGTTCAGATCAGGCAAGGAACAAACCTCGTAACAACCTAACAGACCAAAGAGTACACTTA
AGTTGAAGACACAACACTTGTCTGAAACAAGAAGTTTGTGCCACTCAACAGCTTTGAAAGAGCACTTCCCAAC
GCTGCTAGTAGTCTTTGTTTTCTTCAGTGCTGTACTGTGAGATTGCCCGGTACAGCAGCAGTTGTATTCTTTATT
AGCTTGGTAGATCATTTTCTCTCGCTCTTTTTTTTAATACTAGCAACTTTCATCCTTTGAAACGTGTGCTGAAAA
AGAAGAATCAGCAAATACTACTGAAAGTGCAATATTTGAGTATCACTGCGAGATGAGCTTTGATCCAAACCTTCT
CCACAACAATGGACATAATGGGTACCCTAATGGTACTTCAGCAGCACTGCGTGAAACTGGGGTTATTGAAAAACT
GTTAACCTCTTACGGATTTATTTCAGTGTTTCAAGCTCAAGCTAGACTTTTTCTTCCACTGTTTACAGTATAATGG
CAACCTGCAAGACTTAAAGTAGGAGATGATGTTGAATTTGAAGTATCATCGGACCGACGGACTGGGAAACCCAT
TGCTGTTAAACTGGTGAAGATAAAACAAGAAATCCTCCCTGAAGAACGAATGAATGGACAAGTTGTGTGCGCTGT
TCCTCACAACCTTAGAGAGTAAATCTCCAGCTGCCCGGGTCAGAGTCCAACAGGGAAGTGTATGCTACGAACGTAA
TGGGGAAGTGTTTTATCTGACTTACACCCCTGAAGATGTCGAAGGGAACGTTTCAGCTGGAACTGGAGATAAAAT
AAACTTTGTAATTGATAACAATAAACATACTGGTGCTGTAAGTGCTCGCAACATTATGCTGTTGAAAAAGAAACA
AGCCCGCTGTCAGGGAGTAGTTTTGTGCCATGAAGGAGGCATTTGGCTTTATTGAAAGAGGTGATGTTGTAAGA
GATATTCTTTCACTATAGTGAATTTAAGGGTGACTTAGAAACCTTACAGCCTGGCGATGATGTGGAATTCACAA
CAAGGACAGAAATGGTAAAGAAGTTGCAACAGATGTCAGACTATTGCCCTCAAGGAACAGTCATTTTTGAAGATAT
CAGCATTGAACATTTTGAAGGAAGTGAACCAAAGTTATCCCAAAGTACCCAGTAAAAACCAGAATGACCCATT
GCCAGGACGCATCAAAGTTGACTTTGTGATCCCTAAAGAACTTCCCTTTGGAGACAAAGATACGAAATCCAAGGT
GACCCTGCTGGAAGGTGACCATGTTAGGTTTAAATTTCAACAGACCGACGTGACAAATTAGAGCGAGCAACCAA
TATAGAAGTTCTGTCAAATACATTTTCAGTTCACTAATGAAGCCGAGAAATGGGTGTGATTGCTGCCATGAGAGA
TGGTTTTGGTTTTATCAAGTGTGTGGATCGTGATGTTTCGTATGTTCTTCCACTTCAGTGAAATCTGGATGGGAA
CCAGCTCCATATTGCAGATGAAGTAGAGTTTACTGTGGTTCTTGATATGCTCTCTGCTCAAAGAAATCATGCTAT
TAGGATTAAAAACTTCCCAAGGGCACGGTTTCATTTCACTCCATTTCAGATCACCGTTTTCTGGGCACGGTAGA
AAAAGAAGCCACTTTTCCAACTCTAAACCCTAGCCCAAATAAAGGCAAAGAGAAGGAGGCTGAGGATGGCAT
TATTGCTTATGATGACTGTGGGGTGAAGTACTATTGCTTTTCAAGCCAAGGATGTGGAAGGATCTACTTCTCC
TCAAATAGGAGATAAGGTTGAATTTAGTATTAGTGACAAACAGAGGCCCTGGACAGCAGGTGCAACTTGTGTGCG
ACTTTTAGGTCGTAATTTCTAACTCCAAGAGGCTCTTGGGTTATGTGGCAACTCTGAAGGATAATTTGGATTAT
TGAAACAGCCAATCATGATAAGGAAATCTTTTCCATTACAGTGAGTTCTCTGGTGATGTTGATAGCCTGGAAC
GGGGGACATGGTCGAGTATAGCTTGTCCAAAGGCAAAGGCAACAAAGTCAGTGCAAAAAAGTGAACAAAACACA
CTCAGTGAATGGCATTACTGAGGAAGCTGATCCACCATTACTCTGGCAAAGTAATTCGCCCCCTGAGGAGTGT
TGATCCAACACAGACTGAGTACCAAGGAATGATTGAGATTGTGGAGGAGGGCGATATGAAAGGTGAGGTCTATCC
ATTTGGCATCGTTGGGATGGCCAAACAAGGGGATTGCTGCGAAAGGGGAGAGCGTCAAGTTCCAATTGTGTGT
CCTGGGCCAAAATGCACAACTATGGCTTACAACATCACACCCCTGCGCAGGGCCACAGTGAATGTGTGAAAGA
TCAGTTTGGCTTCATTAATATGAAGTAGGAGATAGCAAGAAGCTCTTTTCCATGTGAAAGAAGTTTCAGGATGG
CATTGAGCTACAGGCAGGAGATGAGGTGGAGTTCTCAGTGATTCTTAATCAGCGCACTGGCAAGTGCAGCGCCTG
TAATGTTTGGCGAGTCTGTGAGGGCCCCAAGGCTGTTGCAGCTCCTCGACCTGATCGGTTGGTCAATCGCTTGAA
GAATATCACTCTGGATGATGCCAGTGCTCCTCGCCTAATGGTTCTTCGTCAGCCAAGGGGACCAGATAACTCAAT
GGGGTTTTGGTGCAGAAAGAAAGATCCGTCAAGCTGGTGTCACTGACTAAACCATCCACAAAGCACACCATTAAT
CCACTATGATCAAGTTGGGGGGAATCTGGTGAAGGGTTCTGAATATCTCCCTCTTCATCCCTCCCGAAATCTGGA
ATACTTATTCTATTGAGCTATTACACCAGTTTTAACACCTTCCTCGTGTTATGTTTAAAAAATAAATAAATTTA
AGAAAACCATTTTTAAATAATGCACAGTTGCAGCCTGGAAAAACTTAAGGTGGCGCCTTATAGTATCAATTTTAGG
AGCTTTATTTGGTGCATTTAACGCAACTGGTAATTGCAGAATCCACTTTGCCGTGTGAAGTGAAAAATATAGACT
GTTATCTTGTGGCCCTATGAAATCTGCACCTTTTCATTATATACTCTACCTTCATTAATTACTTCTGGCAAGAT
GTTCTGCCTTAGCACTCAGTTGCATTCTTTTCTTTTCTTCTGTTTCAATTATGCTTTAATTCTGAGGACCATAT
GAGGGTAGAATATATTATCTTTTAAAAATTACAAAAATTTGTATAGGCAAACCATTTCTTAAAGTTGATGGCCAA
ATTTTAAATGTTATTTTTCATATCATTTATAATCTTGTACAAATCCACTTAAAGAAGTTTGGTTATATTTTCAGT
GAAATTTTCTTCCAGAGTAGGTTTTTTTTCTGGGTTGGGGGGTAACTTTACTACAATTAGTAAGTATGGTGCA
GAATTTTCATGCAAATGAGGAGTGCCAGCAGTGTGATAATTTAAACATATTTAAACAAAAACAAAAAAATGAATG

WO 2004/030615

PCT/US2003/028547

323/6881
FIGURE 302B

CACAACTTGCTGCTGCTTAGATCACTGCAGCTTCTAGGACCCGGTTTCTTTTACTGATTTAAAAACAAAACAAA
AAAAAATAAAAAAGTTTGTGCCTGAAATGAATCTTGTTTTTTTTTTATAAGTAGCCGCCTGGTTACTGTGTCCTGTA
AAATACAGACACTTGACCCTTGGTGTAGCTTCTGTTCAACTTTATATCACGGGAATGGATGGGTCTGATTTCTTG
GCCCTCTTCTTGAATTGGCCATATACAGGGTCCCTGGCCAGTGGACTGAAGGCTTTGTCTAAGATGACAAGGGTC
AGCTCAGGGGATGTGGGGGAGGGCGGTTTTATCTTCCCCCTTGTCGTTTGAGGTTTTGATCTCTGGGTAAAGAGG
CCGTTTATCTTTGTAAACACGAAACATTTTGTCTTCTCCAGTTTTCTGTTAATGGCGAAAGAATGGAAGCGAAT
AAAGTTTTACTGATTTTTTGAGACACT

WO 2004/030615

PCT/US2003/028547

324/6881
FIGURE 303

MSFDPNLLHNNNGHNGYPNGTSAALRETGVIEKLLTSYGF IQCSERQARLFFHCSQYNGNLQDLKVGDDVEFEVSS
DRRTGKPIAVKLVKIKQEILPEERMNGQVVCAPHNLESKSPAAPGQSPTGSVCYERNGEV FYLTYPEDVEGNV
QLETGDKINFVIDNNKHTGAVSARNIMLLKKKQARCQGVVCAMKEAFGFIERGDVVKEIFFHYSEFKGDLETLP
GDDVEFTIKDRNGKEVATDVRLLPQGT VIFEDISIEHFEGTVTKVIPKVP SKNQNDPLPGRIKVD FVIPKELPFG
DKDTKSKVTLLLEGDHVRFNISTDRRKLERATNIEVLSNTFQFTNEAREMGVIAAMRDGFGFIKCVDRDVRMFFH
FSEILDGNQLHIADEVEFTVVPDMLSAQRNHAIKIKLPKGTVSFHS HSDHRFLGTVEKEATFSNP KTTSPNKGK
EKEAEDGIIAYDDCGVKLTIAFAQKDVEGSTSPQIGDKVEFSISDKQRPGQVATCVRL LGRNSNSKRL LGYVAT
LKDNFGFIETANHDKEIFFHYSEFSGDVDSLELGDMVEYSLSKGKGNKVS AEKVNKTHSVNGITEADPTIYSGK
VIRPLRSVDPTQTEYQGMIEIVEEGDMKGEVYPFGIVGMANKGDCLQKGESVKFQLCVLGQNAQT MAYNITPLRR
ATVECVKDQFGFINYEVGDSKKLFFHVKEVQDGI ELQAGDEVEFSVILNQRTGKCSACNVWRVCEGPKAVAAPRP
DRLVNRLKNITLDDASAPRLMVL RQPRGPDNSMGFGAERKIRQAGVID

WO 2004/030615

PCT/US2003/028547

325/6881
FIGURE 304

GCTGAAGATGGGGAGCCACTCTCAAATCATGCTGGATAACACCTACATGAAAAAGTGTGACGAGAACATCCTGTG
GCTGGACTACAAGAACATCTGCAAGGTGATGGAAGTGGGCAGCAAGATCTACGTGGATGATGGGCTTATTTCTCT
CCAGGTAAAGCAGAAAGGTGCTGACTTCCTGGTGACGGAGGTGGAACTGGTGGTTCCTCGGGCAGCAAGAAGGG
TGTGAACCTTCCTGGGGCTGCTGTGGACTTGCTGTGTGTCAGAGGACATCCAGGACCTGAATTTTGGGGTCGA
GCAGGATGTGATATGGTGTGTTGCGTCGTTTCATCCGCAAGGCATCTGATGTCCATGAAGTTAGGGAGGCCCTGGG
AGAGAAGGGAAAGAAAACACTCCACCCTCCACCTTCCATTTTCCCCCACTACTGCAGCACCTCCGGGCCTGTTGC
TATAGAGCCTACCTGTATATCAATAAACACAGCTTGAAG

WO 2004/030615

PCT/US2003/028547

326/6881
FIGURE 305

MGATLKIMLDNTYMKKCDENILWLDYKNICKVMEVGSKIYVDDGLISLQVKQKGADFLVTEVETGGSSGSKKGVN
LPGAAVDLPAVSEDIQDLNFGVEQDVMVFASFIRKASDVHEVREALGEKGKKTLLHPPPSIFPHYCSTSGPVAIE
PTCISINNS

WO 2004/030615

PCT/US2003/028547

327/6881
FIGURE 306

AGAAGAAGCTGGCCAAGGATATGGGAGCAACCACCAATGGACCAGAAGTCTCTCTGGGCAGGTGTAGTGGTCTTGC
TGCTTCTCCAGGGAGGATCTGCCTACAAACTGGTTTGCTACTTTACCAACTGGTCCCAGGACCGGCAGGAACCAG
GAAAATTCACCCCTGAGAATATTGACCCCTTCCTATGCTCTCATCTCATCTATTCAATTCGCCAGCATCGAAAAACA
ACAAGGTTATCATCAAGGACAAGAGTGAAGTGATGCTCTACCAGACCATCAACAGTCTCAAAAACCAAGAATCCCA
AACTGAAAATTCTCTTGTCCATTGGAGGGTACCTGTTTGTTCCAAAGGGTTCCACCCTATGGTGGATTCTTCTA
CATCACGCTTGGAATTCATTAACCTCCATAATCCTGTTTCTGAGGAACCATAACTTTGATGGACTGGATGTAAGCT
GGATCTACCCAGATCAGAAAGAAAACACTCATTTCACTGTGCTGATTGATGAGTTAGCAGAAAGCCTTTTCAGAAGG
ACTTCACAAAATCCACCAAGGAAAGGCTTCTCTTGACTGCGGGCGTATCTGCAGGGAGGCAAATGATTGATAACA
GCTATCAAGTTGAGAACTGGCAAAGATCTGGATTTCATCAACCTCCTGTCTTTGACTTCCATGGGTCTTGGG
AAAAGCCCTTATCACTGGCCACAACAGCCCTCTGAGCAAGGGGTGGCAGGACAGAGGGCCAAGCTCCTACTACA
ATGTGGAATATGCTGTGGGGTACTGGATACATAAGGGAATGCCATCAGAGAAGGTGGTCATGGGCATCCCCACAT
ATGGGCACCTCTTACACTGGCCTCTGCAGAAACCACCGTGGGGGCCCCCTGCCTCTGGCCCTGGAGCTGCTGGAC
CCATCACAGAGTCTTCAGGCTTCCTGGCCTATTATGAGATCTGCCAGTTCCTGAAAGGAGCCAAGATCACGCGCC
TCCAGGATCAGCAGGTTCCCTACGCAGTCAAGGGGAACAGTGGGTGGGCTATGATGATGTGAAGAGTATGGAGA
CCAAGGTTCACTTCTTAAAGAATTTAAACCTGGGAGGAGCCATGATCTGGTCTATTGACATGGATGACTTCACTG
GCAATCCTGCAACCAGGGCCCTTACCCTCTTGTCCAAGCAGTCAAGAGAAGCCTTGGCTCCTTTGAAGGATTA
ACTTACAGAGAAGCAGGCAAGATGACCTTGCTGCCTGGGGCCTGCTCTCTCCAGGAATTCTCATGTGGGATTCC
CCTTGCCAGGCTGGCCTTTGGATCTCTCTTCCAAGCCTTTCTGACTTCCTCTTAGATCATAGATTGGACCTGGT
TTTGTCTTCTGCTGAGCTGTTGACTTGTTGCCCTGAAGTACAATAAAAAAATTCATTTTGCTCCAGTA

WO 2004/030615

PCT/US2003/028547

328/6881
FIGURE 307

MDQKSLWAGVVVLLLLQGGSAYKLV CYFTNWSQDRQEPGKFTPENIDPFLCSHLIYSFASIENNKV I IKDKSEVM
LYQTINSLKTKNPKLKILLSIGGYLFGSKGFHPMVDSSSRLEFINSIILFLRNHNFDGLDVSWIYPDQKENTHF
TVLIHELAEAFQKDFTKSTKERLLLTAGVSAGRQ MIDNSYQVEKLAKDLDFINLLSFDFHGSWEKPLITGHNSPL
SKGWQDRGPSSYYNVEYAVGYWIHKGMPSEKVVMGIPTYGHSFTLASAETTVGAPASGPGAAGPITESSGFLAYY
EICQFLKGAKITRLQDQQVPYAVKGNQWVG YDDVKSMETKVQFLKNLNLGGAMIWSIDMDDFTGKSCNQGPYPLV
QAVKRSLGSL

WO 2004/030615

PCT/US2003/028547

329/6881
FIGURE 308

GGGGAGACTTGTGAGCGGCCATCTTGGTCCTGCCCTGACAGATTCTCCTATCGGGGTCACAGGGACGCTAAGATT
GCTACCTGGACTTTTCGTTGACCATGCTGTCCCGGTGGTACTTTCCGCCGCCGCCACAGCGGCCCCCTCTCTGAA
GAATGCAGCCTTCCTAGGTCCAGGGGTATTGCAGGCAACAAGGACCTTTCATACAGGGCAGCCACACCTTGTCCC
TGTACCACCTCTTCCTGAATACGGAGGAAAAGTTTCGTTATGGACTGATCCCTGAGGAATTCTTCAGTTTCTTTA
TCCTAAAACCTGGTGTAAACAGGACCCTATGTACTCGGAACCTGGGCTTATCTTGTACGCTTTATCCAAAGAAATATA
TGTGATTAGCGCAGAGACCTTCACTGCCCTATCAGTACTAGGTGTAATGGTCTATGGAATTAATAAATATGGTCC
CTTTGTTGCAGACTTTGCTGATAAACTCAATGAGCAAAAACCTTGCCCAACTAGAAGAGGCGAAGCAGGCTTCCAT
CCAACACATCCAGAATGCAATTGATACGGAGAAGTCACAACAGGCACTGGTTCAGAAGCGCCATTACCTTTTTGA
TGTGCAAAGGAATAACATTGCTATGGCTTTGGAAGTTACTTACCGGGAACGACTGTATAGAGTATATAAGGAAGT
AAAGAATCGCCTGGACTATCATATATCTGTGCAGAACATGATGCGTCGAAAGGAACAAGAACACATGATAAATTG
GGTGGAGAAGCACGTGGTGCAAAGCATCTCCACACAGCAGGAAAAGGAGACAATTGCCAAGTGCAATTGCGGACCT
AAAGCTGCTGGCAAAGAAGGCTCAAGCACAGCCAGTTATGTAATGTATCTATCCCAATTGAGACAGCTAGAAAC
AGTTGACTGACTAAATGGAACTAGTCTATTTGACAAAGTCTTCTGTGTTGGTGTCTACTGAAGTTATAGTTTA
CCCTTCCTAAAAATGAAAAGTTTGTTCATATAGTGAGAGAACGAAATCTCTATCGGCCAGTCAGATGTTTCTCA
TCCTTCTTGCTCTGCCTTTGAGTTGTTCCGTGATCACTTCTGAATAAGCAGTTTGCCTTTATAAAAACTTGCTGC
CTGACTAAAGATTAACAGGTTATAGTTTAAATTTGTAATTAATTCTACCATCTTGCAATAAAGTGACAATTGAAT
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

330/6881
FIGURE 309

MLSRVVL SAAATAAPSLKNA AFLGPGVLQATR TFHTGQPHLVPVPPLPEYGGKVRYGLIPEEFFQFLYPKTGVTG
PYVLGTGLILYALSKEIYVISAETFTALSVLGVMVYGIKKYGPVFADFADKLINEQKLAQLEEAQASIQHIONAI
DTEKSQQALVQKRHYLFDVQRNNIAMALEVTYRERLYRVYKEVKNRLDYHISVQNMRRKEQEHMINWVEKHVVQ
SISTQQEKETIAKCIADLKL LAKKAQAQPVM

WO 2004/030615

PCT/US2003/028547

331/6881
FIGURE 310

GC GGGGAGCCGGCCCGGAGCGCAGTTTCCAGTGGGGCCGGGGTTTACCCGGGGCCCTCTCTGTTTGAACCGAACC
CGACAAATGGGCGCATGACGATGGAGAGCAGGGAAATGGACTGCTATCTCCGTCGCCTCAAACAGGAGCTGATGT
CCATGAAGGAGGTGGGTGATGGCTTACAGGATCAGATGAACTGCATGATGGGTGCACTGCAAGAACTGAAGCTCC
TCCAGGTGCAGACAGCACTGGAACAGCTGGAGATCTCTGGAGGGGGTCCCTGTGCCAGGCAGCCCTGAAGGTCCCA
GGACCCAGTGCGAGCACCCCTTGTTGGGAGGGTGGCAGAGGTCTTGCCAGGCCCACAGTCTGTTCCCCCTCCAGTC
AACCTTCTCTTGGCAGCAGCACCAAGTTTCCATCCCATAGGAGTGTCTGTGGAAGGGATTAGCCCCCTTGCCCA
GGACACAGCCACATCAAAGCTGTGCTCAGCAGGGGCCAGAGCGAGTGGAACCGGATGACTGGACCTCCACGTTGA
TGTCCCGGGGCCGGAATCGACAGCCTCTGGTGTTAGGGGACAACGTTTTTGCAGACCTGGTGGGCAATTGGCTAG
ACTTGCCAGAAGTGGAGAAGGGTGGGGAGAAGGGTGAGACTGGGGGGGCACGTGAACCCAAAGGAGAGAAAGGCC
AGCCCCAGGAGCTGGGCCCGCAGGTTCGCCCTGACAGCAAACATCTTTAAGAAGTTCTTGCGTAGTGTGCGGCCTG
ACCGTGACCGGCTGCTGAAGGAGAAGCCAGGCTGGGTGACACCCATGGTCCCTGAGTCCCGAACCGGCCGCTCAC
AGAAGGTCAAGAAGCGGAGCCTTTCCAAGGGCTCTGGACATTTCCCTTCCCAGGCACCGGGGAGCACAGGCGAG
GGGAGAATCCCCCACAAGCTGCCCCAAGGCCCTGGAGCACTCACCTCAGGATTGATATTAACACAGCTGTTT
GGGTCTGAATCCTAGAGACAGAAAGTTGACTGAGCCTGAAAGGGCCAGGTCCCAGTGCTGGGCCCCCTGGGGAGGA
GGGAGGGTGGGCGGTATGGCTCTCGAAAGCCCACTCCAAGTTCCTTTCCCCCAGAAAGCGGGGAGAAGCCAGAG
TTCTTGGCTCAGGACTGAAGGGAAGGTGGTTGGGAGAGGCTGTCTTGGGGGCTAGCTGGTGGAGGAGGTAAGAGT
AGCTGGAGAGTGAGCTGTGCGTGTGTGTGTGTGTGTGTCATGTGTGTGTCTGTCTGGCATGCATGCACTCACTT
TGGGGCTGGAGGTGACAGTAGGTGAGGGCAGAGGAGGAGATCAGAAAAATCCCTCTGACATCTCCACTGCCCCAA
AGACCTCCGTTGAACATTCTGTATGGAAAAGAGCCCTGGAGCATCAGGTTCCCCAGATAGGCCCCCAAATAAAGA
CCTGTCTATGGCTCTCCAA

WO 2004/030615

PCT/US2003/028547

332/6881
FIGURE 311

MTMESREMDCYLRRLKQELMSMKEVGDGLQDOMNCMMGALQEIKLLQVQTALQLEISGGGPVPGSPEGPRTQCE
HPCWEGGRGPARPTVCSPSSQPSLGSSTKFFSHRSVCGRDLAPLPRTQPHQSCAQGGPERVEPDDWTSTLMSRGR
NRQPLVLGDNVFA DLVGNWLDLPELEKGGEKGETGGAREPKGEKGQPQELGRRFALTANIFKKFLRSVRPDRDL
LKEKPGWVTPMVPESRTGRSQVKKRSLSKGS GHFFPFGTGEHRRGENPPTSCPKALEHSPSGFDINTAVWV

WO 2004/030615

PCT/US2003/028547

333/6881
FIGURE 312A

GGCACGAGGCTGGGGCGCAGAGCAGCGGGGAGGAGGCGGACACGTGGCAACAGCGGTAGCAGCCCCGGGCGCGG
GCAGCAACAGCGGGCGGCGGCATCGGCCCGAGCCGCCGGCCGCCCTCCCACCCTCCCGCCCCGCGGCAGCCCTAGC
TCCCTCCACTTGGCTCCCCTGGTCCCCTCGCTCGGCCGGGAGCTGCTCTGTGCTTTTCTCTGATTCTCCAGC
GACAGGACCCGGCGCGGGGCACTGAGCACC GCCACCAATGGGAAGGGGGTTGGACGTGATAAGTATGAGCCTGCA
GCTGTTTCAGAACAAAGGTGATAAAAAGGGCAAAAAGGGCAAAAAGACAGGGACATGGATGAAGTGAAGAAAGAA
GTTTCTATGGATGATCATAAACTTAGCCTTGATGAACCTTCATCGTAAATATGGAACAGACTTGAGCCGGGGATTA
ACATCTGCTCGTGCAGCTGAGATCCTGGCGCGAGATGGTCCCAACGCCCTCACTCCCCCTCCCACTACTCCTGAA
TGGATCAAGTTTTGTGCGGCAGCTCTTTGGGGGGTTCTCAATGTTACTGTGGATTGGAGCGATTCTTTGTTTCTTG
GCTTATAGCATCCAAGCTGTACAGAAGAGGAACCTCAAAACGATAATCTGTACCTGGGTGTGGTGCTATCAGCC
GTTGTAATCATAACTGGTTGCTTCTCCTACTATCAAGAAGCTAAAAGTTCAAAGATCATGGAATCCTTCAAAAAC
ATGGTCCCTCAGCAAGCCCTTGTGATTGCAAAATGGTGAGAAAATGAGCATAAATGCGGAGGAAGTTGTGGTTGGG
GATCTGGTGGAAGTAAAAGGAGGAGACCGAATTCCTGCTGACCTCAGAATCATATCTGCAAATGGCTGCAAGGTG
GATAACTCCTCGCTCACTGGTGAATCAGAACCCCGAGCTAGGTCTCCAGATTTACAAAATGAAAACCCCTGGAG
ACGAGGAACATTGCCTTCTTTTCAACCAATTGTGTTGAAGGCACCGCACGTGGTATTGTTGTCTACACTGGGGAT
CGCACTGTGATGGGAAGAATTGCCACACTTGCTTCTGGGCTGGAAGGAGGCCAGACCCCATTTGCTGCAGAAATT
GAACATTTTATCCACATCATCACGGGTGTGGCTGTGTTCTGGGTGTGCTTTCTTCTCATCCTTCTCTCATCCTT
GAGTACACCTGGCTTGAGGCTGTCTTCTCCTCATCGGTATCATCGTAGCCAATGTGCCGGAAGGTTGTGCGCC
ACTGTACACGGTCTGTCTGACACTTACTGCCAAACGCATGGCAAGGAAAACTGCTTAGTGAAGAAGTTAGAACT
GTGGAGACCTTGGGGTCCACATCCACCATCTGCTCTGATAAACTGGAACCTCTGACTCAGAACCGGATGACAGTG
GCCCCACATGTGGTTTGACAATCAAATCCATGAAGCTGATACGACAGAGAATCAGAGTGGTGTCTCTTTTGACAAG
ACTTCAGCTACCTGGCTTGTCTGTCCAGAATTGCAGGTCTTTGTAAACAGGGCAGTGTTTCAGGCTAACCCAGGAA
AACCTACCTATTCTTAAGCGGGCAGTTGCAGGAGATGCCTCTGAGTCAGCACTCTTAAAGTGCATAGAGCTGTGC
TGTGGTTCCGTGAAGGAGATGAGAGAAAGATACGCCAAAATCGTCGAGATACCCCTTCAACTCCACCAACAAGTAC
CAGTTGTCTATTTCATAAGAACCCCAACACATCAGAGCCCCAACACCTGTTGGTGATGAAGGGCGCCCCAGAAAGG
ATCCTAGACCGTTGCGAGCTCTATCCTCCTCCACGGCAAGGAGCAGCCCTGGATGAGGAGCTGAAAGACGCCTTT
CAGAACGCCCTATTTGGAGCTGGGGGGCTCGGAGAACGAGTCCCTAGGTTTCTGCCACCTCTTTCTGCCAGATGAA
CAGTTTCTGAAGGGTTCCAGTTTGACACTGACGATGTGAATTTCCCTATCGATAATCTGTGCTTTGTTGGGCTC
ATCTCCATGATTGACCCTCCACGGGCGGCCGTTTCCGTGAGTATGCCGCAAGGTGTGGGCATCATCTCAGAAGGCAAT
ATCATGGTACAGGAGACCATCCAATCAGAGCTAAAGCTATTGCCAAAGGTGTGGGCATCATCTCAGAAGGCAAT
GAGACCGTGGAAGACATTGTGCCCCGCTCAACATCCCAGTCAGCCAGGTGAACCCAGGGATGCCAAGGCCTGC
GTAGTACACGGCAGTGATCTAAAGGACATGACCTCCGAGCAGCTGGATGACATTTTGAAGTACCACACTGAGATA
GTGTTTGCCAGGACCTCCCTCAGCAGAAGCTCATCATTGTGGAAGGCTGCCAAAGACAGGGTGCTATCGTGGCT
GTGACTGGTGACGGTGTGAATGACTCTCCAGCTTTGAAGAAAAGCAGACATTGGGGTTGCTATGGGGATTGCTGGC
TCAGATGTGTCCAAGCAAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTCAATTGTGACTGGAGTAGAG
GAAGGTCGTCTGATCTTTGATAACTGAAGAAATCCATTGCTTATACCTTAACCCAGTAACATTCCCGAGATCACC
CCGTTCCGTGATATTTATTATTGCAAACATTCCACTACCCTGGGGACTGTCAACATCCTCTGCATTGACTTGGGC
ACTGACATGGTTCCCTGCAATCTCCCTGGCTTATGAGCAGGCTGAGAGTGACATCATGAAGAGACAGCCAGAAAT
CCCAAAACAGACAAACTTGTGAATGAGCGGCTGATCAGCATGGCCTATGGGCAGATTGGAATGATCCAGGCCCTG
GGAGGCTTCTTTACTTACTTTGTGATTCTGGCTGAGAACGGCTTCTCCCAATTACCTGTTGGGCCTCCGAGTG
GACTGGGATGACCGCTGGATCAACGATGTGGAAGACAGCTACGGGCAGCAGTGACCTATGAGCAGAGGAAAATC
GTGGAGTTACCTGCCACACAGCCTTCTTCGTCAGTATCGTGGTGGTGCAGTGGGCCGACTTGGTCACTGTGAAG
ACCAGGAGGAATTCGGTCTTCCAGCAGGGGATGAAGAACAAAGATCTTGATATTGGCCTCTTTGAAGAGACAGCC
CTGGCTGCTTTCCCTTCTACTGCCCTGGAATGGGTGTTGCTCTTAGGATGTATCCCTCAAACCTACCTGGTGG
TTCTGTGCCCTTCCCTACTCTCTTCTCATCTTCGTATATGACGAAGTCAGAAAACCTCATCATCAGGCGACGCCCT
GGCGGCTGGGTGGAGAAGGAAACCTACTATTAGCCCCCGTCTGCACGCCGTGGAGCATCAGGCCACACACTCT
GCATCCGACACCCACCCCTCTTTGTGTACTTCAGTCTTGGAGTTTGGAACTCTACCTGGTAGGAAAGCACCCGC
AGCATGTGGGGAAGCAAGACGTCCTGGAATGAAGCATGTAGCTCTATGGGGGAGGGGGGAGGGCTGCCTGAAAA
CCATCCATCTGTGGAATGACAGCGGGGAAGGTTTTTATGTGCCTTTTTGTGTTTTGTAAAAAGGAACACCCCGA

WO 2004/030615

PCT/US2003/028547

334/6881
FIGURE 312B

AAGACTGAAAGAATACATTTTATATCTGGATTTTACAAATAAAGATGGCTATTATAATGGAAAAAAAAAAAAA
AAAAA

WO 2004/030615

PCT/US2003/028547

335/6881
FIGURE 313

MGKGVGRDKYEPAAVSEQGDKKGKKGKKDRDMDELKKEVSMDHKLSDDELHRKYGTDLSRGLTSARAAEILARD
 GPNALTTPPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYSIQAATEEEPQNDNLYLGVVLSAVVIITGCFSYQ
 EAKSSKIMESFKNMVPQQALVIRNGEKMSINAEVVVGDLVEVKGGDRIPADLRISANGCKVDNSSLTGESEPQ
 TRSPDFTNENPLETRNIAFFSTNCVEGTARGIVVYTGDRVTMGRIATLASGLEGGQTPIAAEIEHFIHIITGVAV
 FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICS
 DKTGTLTQNRMTVAHMMWFDNQIHEADTTENQSGVSFDKTSATWLALSRIAGLCNRAVFQANQENLPILKRAVAGD
 ASESALLKCIELCCGSVKEMRERYAKIVEIPFNSTNKYQLSIHKNPNTSEPQHLLVMKGAPERILDRCSSILLHG
 KEQPLDEELKDAFQONAYLELGGLGERVLGFCHLFLPDEQFPEGFQFDTDDVNFPIDNLCFVGLISMIDPPRAAVP
 DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPVSQVNPRDAKACVVHGSDDLKDMTS
 EQLDDILKYHTEIVFARTSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGIAGSDVSKQAADMIL
 LDDNFASIVTGVEEGRILFDNLKKSIAYTLTSTNIPEITPFLIFIIANIPPLPLGTVTILCIDLGTDMVPAISLAYE
 QAESDIMKRQPRNPKTDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPIHLLGLRVDWDDRWINDDVED
 SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFEETALAAFLSYCPGMG
 VALRMYPLKPTWWFCAFPYSLLIFVYDEVKLIIRRRPGGWVEKETYY

WO 2004/030615

PCT/US2003/028547

336/6881
FIGURE 314A

TTCCAAAAC TGTCTCTGGAGCTATAAGTGGATTGCCAGAAATGAGAGATTAGGAGCTGGGAGAAGAGGAAGCGC
CTTGTGTTGTGTCTCCTGGAGGCTGCCGACATGAAGTGCTTTTTCCCGGTGCTGAGCTGTCTGGCTGTGCTGGGT
GTGGTGTGTCAGCACAGCGGCAGGTACCGTTTCAGGAAGGACCCCTGTACCGCACGGAGGGCTCCCACATCACTATC
TGGTGCAATGTGAGTGGCTACCAGGGACCTTCTGAGCAGAATTTCCAGTGGTCCATTTACCTGCCTTCGTGCGCA
GAGCGAGAGGTGCAGATCGTCAGCACCATGGACTCTTCCTTCCCCTATGCCATCTACACCCAGCGCGTCCGCGGA
GGGAAGATCTTCATAGAAAGAGTCCAGGGGAACCAACCTATTGCACATCACAGATCTTCAGGCCCGGGATGCC
GGGGAGTATGAATGCCACACACCCAGCACTGATAAGCAATACTTTGGGAGTTACAGTGCAAAGATGAACCTAGTG
GTGATCCCAGACTCCCTGCAGACCACTGCCATGCCCCAGACTCTGCACAGAGTGGAGCAGGACCCGCTGGAGCTC
ACTTGTGAGGTGGCCTCAGAGACCAATTCAGCACAGCCACCTGTCTGTGGCCTGGCTCCGGCAGAAAGTTGGCGAG
AAGCCCGTGGAGGTATCTCCTGAGCCGAGATTTTCATGCTTCACTCCAGCAGCGAATATGCCAGAGGCAGAGC
CTGGGGGAGGTGCGGCTGGACAAGCTGGGGAGGACCACTTCCGCTCACCATCTTCCACCTGCAGCCTTCTGAC
CAGGGCGAATTTCTACTGCGAGGCCCGGAGTGATCCAGGATCCGGATGGGTGCTGGTATGCTATGACCCGAAAG
CGTTCCGAGGGAGCCGTGGTCAACGTCCAGCCAACTGACAAAGAATTAAGTGTTCGGCTGGAGACAGAGAAGCGG
CTGCACACGGTGGGCGAGCCGTGGAGTTTCAGATGCATCTCTGGAGGCTCAGAATGTTCCCGACCGTTACTTTGCT
GTCTCCTGGGCCTTCAACAGCTCGCTCATCGCCACCATGGGTCTAACGCTGTGCCTGTCTCAACAGCGAATTT
GCTACCGGGGAAGCCAGGGGACAGCTTAAGGTGGCCAAAGAGAGCGACAGTGTCTTTGTGCTGAAGATCTACCAC
CTCCGCCAGGAAGATAGCGGAAATACAACCTGCCGGGTGACTGAGCGAGAGAAAACCGTGACCGGGGAATTCATT
GATAAGGAGAGCAAGCGTCCCAAGAACATCCCCATCATAGTCTCTCCCTCAAGAGCAGCATCTCCGTGGAGGTG
GCCAGCAATGCCAGCGTCATCTTGAGGGCGAGGACCTGCGCTTCTCTGTCAGTGTCCGCACGGCAGGCAGGCCG
CAGGGTTCGCTTCTGTCTATCTGGCAGCTTGTGGACAGGCAGAACCGCCGAGCAATATCATGTGGCTAGACCGG
GATGGCACCGTGCAGCCAGGCTCGTCTACTGGGAGCGCAGCAGCTTTGGGGGCGTCCAGATGGAGCAGGTGCAG
CCCACTCGTTTCAGCCTGGGCATCTTCAACAGCAGGAAGGAGGACGAGGGCCAGTATGAATGCCATGTGACTGAA
TGGGTGCGGGCAGTGGATGGCGAGTGGCAGATTGTTGGGGAGCGCCGGGCCAGCACTCCCATCTCCATCACAGCT
CTTGAAATGGGCTTCGCACTCACAGCCATCTCCCGGACACCGGGGTGACCTACAGCGACTCCTTTGACTTGCAG
TGTATCATCAAACCCCACTACCTTGCTGGGTCCCGGTGTCTGGTGACATGGCGGTTCAGCCGGTGGGCACGGTG
GAGTTCCATGACTTGGTGACCTTACCCGGGACGGAGGGGTCCAGTGGGGGACAGGTCTCCAGCTTCCGAACC
CGAACTGCCATCGAGAAGGCTGAGTCCAGCAACAACGTCCGCCTAAGCATCAGCCGAGCCAGTGACACGGAAGCA
GGCAAGTACCACTGTGTGGCAGAGCTGTGGCGGAAGAACTACAACAACCTGGACGCGACTGGCAGGAGGACC
TCCAACCTGCTGGAGATCAGGGTGTGTCAGCCAGTGACAAAGCTGCAGGTGAGCAAATCGAAGAGGACCTCACC
CTGTTGGAACAAGCCCATTCAGTTGAAGTGTCTAGTCAAGTCTCAGACTAGCCAGAATCCCCTTTGCGGTG
CTCTGGTATGTCCAAAGCCCTCGGATGCCGATGGCAAGCTTATCTGAAGACCACCCACAACCTCCGCTTTGAA
TACGGTACTTACGCCGAGGAGGAGGGCCTGAGAGCCAGGCTCCAGTTTGAAGGCGATGTGTGCGGGGGCCTGTT
AGCCTACCGTCCAGAGAGCCGAGGTGAGCAGCGGAGCTACTACTGCCACGTGGAGGAGTGGCTGCTGAGC
CCCACTACGCTTGGTACAAGCTGGCAGAGGAGGTTTCTGGGCGCACAGAAGTCACTGTGAAACAGCCAGACAGC
CGCTGAGGCTCAGCCAAGCCAGGGGAACCTGTGCGTTCTGGAGACCCGGCAGGTACAGCTGGAGTGTGTGGTT
CTCAACCGCACAGCATAACCTCCCAGCTCATGGTGAATGGTTTGTATGGAAGCCCAACCACCTGAGCGGGAG
ACTGTGGCCCGCTTGAGCCGTGACGCCACCTTCCACTATGGAGAGCAGGCAGCCAAGAACAATCTGAAGGGGCGG
CTGCATTTGGAGAGTCTTCCCCCGGCGTGTACCGTCTCTTCATCCAGAACGTGGCTGTGCAGGACAGCGGGACC
TACAGCTGCCATGTGGAGGAGTGGCTGCCAGCCCCAGTGGCATGTGGTATAAGCGGGCAGAGGACACCGCTGGG
CAGACAGCTCTGACAGTCATGCGACAGATGCTTCCCTGCAGGTGGACACAGTGGTCCCCAATGCCACGGTCTCT
GAGAAGGCAGCTTTCCAGCTGGACTGTAGCATCGTGTCCCGCTCCAGCCAGGACTCCCGCTTCGCTGTGGCCTGG
TATTCCCTGAGGACTAAAGCTGGGGGAAAAGGAGCAGCCCTGGCCTGGAAGAACAGGAAGAGGAAAGGGAGGAG
GAGGAGGAGGAGGACGACGACGACGACGACGACCAACAGAGCGGACGGCCCTGCTGAGCGTGGGCCAGATGCT
GTCTTTGGCCAGAGGGCAGTCTTGGGAGGGCAGGCTTCGCTTCCAGAGGCTCTCCCGGTGCTCTACCGGCTC
ACAGTGCTGCAGGCAAGCCCCAAGATACAGGCAATTACTCTGCCATGTGGAGGAGTGGCTGCCAGCCCTCAG
AAGGAATGGTACCGCTGACGGAGGAGGAGTACGCCCCATCGGCATCCGTGTTCTAGATAAAGTCCCACCTC
CAGTCCATCATCTGCTCCAACGACGCACTCTTCTACTTCGTCTTCTTCTACCCTTTCCCCTCTTTGGCATTCTT
ATCATCACCATCCTTCTGGTGCCTTCAAGAGCCGGAACCTCCAGCAAGAATCTGATGGGAAGAATGGGGTGCCT

WO 2004/030615

PCT/US2003/028547

337/6881
FIGURE 314B

CTGCTGTGGATCAAAGAGCCACACCTCAACTACTCCCCTACTTGCCTGGAGCCCCCTGTTCTCAGTATCCATCCA
GGGGCCATAGACTAAGCGGGTGATGCCCCAGCGGATGTTGGCCACGGAGGAGCTGAGGCTCTCCCTTTTCTCTGTG
ATTGGACAGTTGACAGCACCCAACTCTGGGGTGATGTGTGTGGAAAGTTGTCAGACTTGAAAAGTGTTCCAAG
TTCCCAGTCAGTCACAGAGACAGACTGCCTCTCGGTGGCAGTCTTGGTTGGTTAGCTATTTGCGCGCAAATGTTG
TGATCCTGCCATTATAGATTTCTTGTCTTGTGTTTTAGTAAATGTAGTGAGTAGCTCCAGGTGCCACATCTACTCA
CAGATTTATCTAGTATTCTCAGATAGATGTTACAGGGCTTCTTATTCTTTGTAATGTACTCTTTTTAAATCCCTT
TAGTTTACCCTTTTTGGATTCTTAATGTGGACGAATTTCTCTTACGTACAACGTACAGCAAAGGAAGGGCGAA
CTTTCTAGTGACAAGGAATCTCTTCCAAGACTTTGTTTTTGCACATTTGAAAATGCCACCCATGGATCAAAATAT
ACCCAAACGTTTTTTACTTTCTTAACAAGACTTAAGAATTGTGTGTAGTGTGGGCAAATTTGTATGTTGTCTTT
TCCCTCAGCTGGAGTTATTGGAACCACTTTGTAGTCAAGACGAAAGCACTGAATTTTGCTTCAAAGAACTGTGTA
TGTACAAGAGAAATCCTGCATAACCCCAATTAGGAGTAGATGGTGCCCGGCCTATCTGTCAAGGAGGCAAAAAAGG
CTTCATCCCATCCTTGCCAAAAAATAAGAAAACGTCTTGGAGAATGGGTGAGAAGCCCCAAACGGCACACACTT
TCCAAATTAAAGTGGGCAGGGGCTGCTTTTAGCAGCTGCTGACCTGCAGATTTGTCAAAGCCAGTGACTAGAGAA
GGAAGGGAGAAAGGCTGGCTGTTGGCTTGTCTGTAGCTGCAAGGATGGTCTCTAACTGATTAACTGTGAGCAGGT
GGGCTGTGTCTTCAGGTGCTTTGCCAAACTCTTAAAGAAAGTGTCCAGTGAACCTGGAAGTGGGCCCTGAGC
TGAGCACAGGGCCAAAGCAGCCATGGCAGACACCTGACGGAGGGCACGGGCTGGCTGACACTAAGTTTGGTGGG
ACAGTGAGGGGTGGGAGGGGGGTTTCCAGGGCCTGGTGTGGAGAGTGCAGAGAAATATCTACCTCCCTGGAGGT
GTGAAGACTAGGTTTTCTTCTTCCCTTCCAATTAGATTTTCTTAATTATAGTGATGTCTTCTTATTCATTTT
CTCTCCCTGCCTCTCACTGCCATAAGAATATCAGCCTGGGGGCAGTCCAGACGCAGCCCTTTGTATCCTTTCTG
TTTGCCTAGTCTCAGCAGACTGTGATCACAAAGCATTGTCTGTGGGATTTTCTTCTTCCCTTTCTTGATCTCTCT
TGTGTTCTAGGTTTGTGTTGTTTCTTATGTTGTTGTTTCTTATTTTAAACGCCCTTGAGCCCCATGATGAGC
TGGTGTACCCCTGTTCTTTTACACTGTTGGGCCAGGTGCTGCTTGTCTTCTTAGGGCATCATCAATTGCAAATA
TTTTCTTTTGTCTCCCTTTATGAAGATGTTCTTATACCCTTGCTTTCCCATATTTTCTGGCCAAGCATGCCATCT
CCTTTACTCTGGGAACCTTACATCCTGAATCCCAAGAGGGGTGACAGTTTGGAAAAGTCATCAGGGATTCTGGA
ACTAAGTCTGATAAAAGATTCCAGTGAAGCCCTGTTCTGAGAACGAGCAGACTGCAGGGGAGGCCATGGGATTCC
CCAGGCCAGTGTCTGTGCTGATCCTTCAAGGGTCTGCAGGTATGCAGGTGGCTGGGCTGCTCGGCAGATACTTT
GCTGATTCCCAGCTGAGGGGAGCATGGTGGCGATTGCTCAGCCATTTTCTGACAGACACACAGACCTGCCTTTTT
TCCCCAAGTATACCGTACCCTCCTGTGAGACAGTGTGTGCAGGCACCACCACCTTAATCCTGCTGTTGCCTGAC
ATGCTGATTCTCATTTATTATGCTGCATCAACACATTAGAGGTACAGGAGCGGCTCAGTCATGAAAAAAGAAAGT
CTTTTGCCCCATTTCTTTATTTTCAAGATGTGGGCTTTTCAAGTGGGAATTTGCTGACTCCTACTTTATAGGCTGAG
TCAATGAGGGAAGATGACTGGCGTTTCTCTGTCTAAATGGGAGGTTGCCAGAGCGCTGGCTGGGACTAGGATGT
GTAACTAAGATTTTCAAGTTTGAATCTTAGATTTTCAAGTTCACGGCGATAAAGAAAGTAGGTGCTGCACACAAATATG
TAAAGCAATTGTAGGAAATTTGAAAGGAAAAAAGAAACCGAAGCCAGTATTTTAATAATTGCTTTTTCTGTGTA
TTTTGTATTGGGCTGGGGGATAGCATCAAAGGTTGAACTTTTTGTAGCTTTCTATGAAAAACCCAGGACCTTCTT
TCTTTGGCCATTTCTATGGAATGCGATGTGAGATGGATGGTAATGGTGCCCTCCAGTGGCTGTGAGACCTCATT
GCGCATTGTCTACTGGAGCTTTAGTCTTCTGAGACGGAGGAAAACTGCTGAATACTCTGGATTCTATGTCTA
CAATGTTGCATTTATGAAAACTACACTGTGCTAGGCGCATTCTAGGACATGAATATGACCACACCCCTCTTTTAC
CGGGTGTCTGTAGCAAGTTTTCATATTCTTTTCAAACAATGGTTTCTCTGCGTTAATTATTGAGGAAAAAATA
AGATGGGGTAAGAAAACCTACCCATGCATGATGTAGAGAGCTGTTGATTTGTTTCTGTTTTTTTAAAGGAAAACTA
TTTGTAAGATGTTGCACTAAACATTTTATATACACTTCAGAGACCTGTAGTAAATTATGTTGAAAAT

WO 2004/030615

PCT/US2003/028547

338/6881
FIGURE 315A

GCTCTTTGCCGAGGGCGTGTGGTGAGAGTCCCCACAGCGACCCTGGTTCGAGTGGTGGGCACTGAGCTGGTCATC
CCCTGCAACGTCACTGACTATGATGGCCCCAGCGAGCAAACTTTGACTGGAGCTTCTCATCTTTGGGGAGCAGC
TTTGTGGAGCTTGCAAGCACCTGGGAGGTGGGGTTCCAGCCAGCTGTACCAGGAGCGGCTGCAGAGGGGCGAG
ATCCTGTAAAGGCGGACTGCCAACGACGCCGTGGAGCTCCACATAAAGAACGTCCAGCCTTCAGACCAAGGCCAC
TACAAATGTTCAACCCCCAGCACAGATGCCACTGTCCAGGGAACTATGAGGACACAGTGCAGGTTAAAGTGCTG
GCCGACTCCCTGCACGTGGGCCCCAGCGCGCGGGCCCCGCCGAGCCTGAGCCTGCGGGAGGGGGAGCCCTTCGAG
CTGCGCTGCACCGCCGCTCCGCCCTCGCCGCTGCACACGCACCTGGCGCTGCTGTGGGAGGTGCACCGCGGCCG
GCCAGGCGGAGCGTCTCGCCCTGACCCACGAGGGCAGGTTCCACCCGGGCTGGGGTACGAGCAGCGCTACCAC
AGTGGGGACGTGCGCCTCGACACCGTGGGCAGCGACGCTACCGCCTCTCAGTGTCCCGGGCTCTGTCTGCCGAC
CAGGGCTCCTACAGGTGTATCGTCAGCGAGTGGATCGCCGAGCAGGGCAACTGGCAGGAAATCCAAGAAAAGGCC
GTGGAAGTTGCCACCGTGGTGATCCAGCCATCAGTTCTGCGAGCAGCTGTGCCCAAGAATGTGTCTGTGGCTGAA
GGAAAGGAAGTGGACCTGACCTGTAACATCACACAGACCGAGCCGATGACGTCCGGCCCCAGGTGACGTGGTCC
TTCAGCAGGATGCTGACAGCACCCCTACCTGGCTCCCGCGTGTGGCGCGGCTTGACCGTGATTCCCTGGTGCAC
AGCTCGCCTCATGTTGCTTTGAGTCATGTGGATGCACGCTCCTACCATTACTGGTTCCGGGATGTTAGCAAAGAA
AACTCTGGCTACTATTACTGCCACGTGTCCCTGTGGGCACCCGGACACAACAGGAGCTGGCACAAAGTGGCAGAG
GCCGIGTCTTCCCCAGCTGGTGTGGGTGTGACCTGGCTAGAACCAGACTACCAGGTGTACCTGAATGCTTCCAAG
GTCCCCGGGTTTGCGGATGACCCACAGAGCTGGCATGCCGGGTGGTGGACACGAAGAGTGGGGAGGCGAATGTC
CGATTACGGTTTCGTGGTACTACAGGATGAACCGCGCAGCGACAATGTGGTGACCAGCGAGCTGCTTGCAGTC
ATGGACGGGGACTGGACGCTAAAATATGGAGAGAGGAGCAAGCAGCGGGGCCAGGATGGAGACTTTATTTTTTCT
AAGGAACATACAGACACGTTCAATTTCCGGATCCAAAGGACTACAGAGGAAGACAGAGGCAATTATTACTGTGTT
GTGTCIGCCTGGACCAAACAGCGGAACAACAGCTGGGTGAAAAGCAAGGATGTCTTCTCCAAGCCTGTTAACATA
TTTTGGGCATTAGAAGATTCCGTGCTTGTGGTGAAGGCGAGGCGAGCCAAAGCCTTTCTTTGCTGCCGGAATACA
TTTGAGATGACTTGCAAAGTATCTTCCAAGATATTAAGTCGCCACGCTACTCTGTCTCATCATGGCTGAGAAG
CCTGTCCGGCAGCTCTCCAGTCCCAATGAAACGAAGTACATCATCTCTCTGGACCAGGATTCTGTGGTGAAGCTG
GAGAATTGGACAGATGCATCACGGGTGGATGGCGTTGTTTTAGAAAAAGTGCAGGAGGATGAGTTCCGCTATCGA
ATGTACCAGACTCAGGTCTCAGACGCAGGGCTGTACCGCTGCATGGTGACAGCCTGGTCTCCTGTGAGGGGACG
CTTTGGCGAGAAGCAGCAACCACTCTCTCCAATCCTATTGAGATAGACTTCCAAACCTCAGGTCCTATATTTAAT
GCTTCTGTGCATTACAGACACACCATCAGTAATTCGGGGAGATCTGATCAAATTGTTCTGTATCATCACTGTGAG
GGAGCAGCACTGGATCCAGATGACATGGCCTTTGATGTGTCTGGTTTGCGGTGCACTCTTTTGGCCTGGACAAG
GCTCCTGTGCTCCTGTCTTCCCTGGATCGGAAGGGCATCGTGACCACCTCCCGGAGGGACTGGAAGAGCGACCTC
AGCCTGGAGCGCGTGAGTGTGTGGAATTCTGTGCAAGTGATGGCTCCGAGGACCAGGACTTTGGCAACTAC
TACTGTTCCGTGACTCCATGGGTGAAGTCACCAACAGGTTCTTGCCAGAAGGAGGCAGAGATCCACTCCAAGCCC
GTTTTTATACTGTGAAGATGGATGTGTGAACGCTTCAAGTATCCCTTGCTGATCGGCGTGGTCTGTCCACG
GTCATCGGGCTCCTGTCTGTCTCATCGGGTACTGCAGCTCCCACTGGTGTGTGTAAGAAGGAGGTTTCAAGGACA
CGGCGCAGCGCCGAGGCTCATGTCGATGGAGATGGACTAGGCTGGCCCCGGGAGGGGAGTGACAGAGGGACGTT
CTAGGAGCAATTGGGGCAAGAAGAGGACAGTGATATTTAAAACAAAGTGTGTTACACTAAAAACAGTCCTCTC
TAATCTCAGGTGGGACTTGGCGCTCTCTTTTTCTGCATGTCAAGTCTGAGCGCGGACATGTTTACCAGCACAC
GGCTCTTCTTCCACGGCACTTTCTGATGTAAACAATCGAGTGTGTGTTTTCCCAACTGCAGCTTTTTAATGGTTA
ACCTTCATCTAATTTTTTTTCTCCCACTGGTTTATAGATCCCTCTGACTTGTGTGTGTTTATAGCTTTTTGTTTCG
GGGTTGTGGTGAGGAAGGGGTGATGGCATGCGGAGTCTTTATCTTCAGTGAGAATGTGCCTGCCCGCTGAGA
GCCAGCTTCCGCTTGGAGGCACGTGTTACAGAGAGCTGCTGAGCGCCACCCCTCTACCCGGCTGACAGACAACACA
GACCTGTGCCGAAGGCTAATTTGTGGCTTTTACGACCCCTACCCACCCCTGTTTTTCAGGGGTTTACTACATT
TGAAATCCAACTTGGAGTATATAACTTCTTATTGAGCCCCAACTGCTTTTTTTTTTTTTTTTTTGTCTCTGTC
CCCTTTTCCATTTCTTTTGTATTGTTTTCTGTGAGAGCACTGAAATGGCAGCCCTGGAATCTACAATTTGGCTC
TCCACTGAGCACCTTATCTTGCCACCTTAGCCTTAAGAATGAATATGAAGAAAAATACACAGCCACCTCTGTCCA
GGGCAGTAAGAAGGGCTGCAAGGAAGGGGAGGATGGGGACAAGGAAAGGATCAGATACCTGCTCCAGTAGTTGTG
AGGCCACTGTGTCTCAGGGGACTCCAGGAGGAGCAGAAGAGGGATCCACGAAGTATTCTTACGCAGCTGGGGC
CAGGAGGGTCAGAGTGGTGCCAGGTGCAAGTTAGGCTAAAGAAGCCACCCTATTCTCTCTCTTGGCCATTGTG

WO 2004/030615

PCT/US2003/028547

339/6881
FIGURE 315B

GGGGGCAAAGGCATTGGTCACCAAGAGTCTTGCAGGGGGACCCACAGATATGCCATGTCCTTCACACGTGCTTGG
GCTCCTTAACCTGAAGGCAAATTGCTACTTGCAAGACTGACTGACTTCAAGGAATCAGAAATTACCTAGAAGCAC
CATGTTTTTTCTATGACCTTTTCAGTCCTTCAGGTCATTTTAAGGTCCACTGCAGGGGGTTAGTGAGAAAGGGTA
TACTTTGTGGTATGTTTTGCTTTTCTAATAGGGACATGAAGGAAACCCAGCAATTTGCTGTTATGTGAATGGCCT
GTAGAGCAGAGTCAAGAGCGGTGTGCTTTGCCGACTGCTCCCATCAGGAATAGGAGAGTAGACAGAGATCTTCC
ACATCCCAGGCTTCTGCTGCTGCTTTAAAAGCTCTGTCTTGGAGCCTCCCGCTCCCTGAAGTGTCTCGCCCCCT
GCACAGCACTGGCCTTTTCGGAAGCATCCCAGTAGGGTTTTCTGAGGCTCGCTGGTGACTCATGCCCTAATTGCAA
TCCTCTGCTTTTATCTTGACTTTGAAGGATCTAACACTGCTCTCTCTTCCAAAGGGGAAAAAAGATTCAATTGT
TTTGAGCAATAAATAATAACAAAATGATGGCCATTTCATGTGCAGCTCTTGTACCATGGGCCGGATGAGTTGTG
CTCCTCCTGGCTCACCATTTCCCCCTGCTCCCCACAGCCGGTTCTGCACTTATCACCAGTCGCCCTTGAAGC
AGATTCCCATTGAGTTTTCCCCACCAAGGGGACCATGCACATGGTAGAAACATTAGATTCTGCATTGACAGTAGC
CTTTCTTGGCCCCGGCCTGTGGTGGAAGACGGGCAACAAGTATACCCACCAGGSCCTGAGTGACTAGAGAA
GAGGACGAGGCCTTGTGGCACTAGATTTGGGTATTTCTGCATGTCTATAACATATCCTAACTGCTATTTCAGAA
GAGGCAGCTTGTAGGTGATTGTACAAGTGAGAATTAAAGAGAGAACAGATATTTAAACAGGTGCTGTATTAGTAA
CAGCCAGTGCCCTTTAGCCCTTGCATCTATTAAAAGGAGATTTCAGGATTTTATTGGCACAGGCCCTTCTTAGTA
GGAAGAAAGGGTGCTTAGCTTTGGACCTGACCGGTGTGTGTAAACCATGGACTGAGTCACAGCAGACACTCGA
TGGTGGTAAATGTGATGGGTGCTTACACACTGTACCTTTTCTTTTCATACTGATGCTGCAGTTCAGGGCTGGAGT
TGTTAAGGCATTGACCTCCACCCACCTGCCCATGTCCACTGGGCTGCCAAGCTGCATGTCACCTGAGGGCTGG
CAGGAAGGGGCGAGAAATCCCAGGGCATTGTACCAAGGACCTAGTTCCTTCTAGGGATATAAATTTCCAGGAATG
TGTATTTTAAATGTGGTGAGATGCACTCTTTTGTGTACCAATAGGGCTCCCCACCCACCCCTGCGACAAGTG
CTCTTCTAGAACAGGTTCCTACCAGCAGCACTGGTGTGAATGAAAGAGAGACCCAGCCGCTCTCACACAGGTGG
AATTGCACTTCTTAACAAAAAGGAACCTTTATAAAAGTTTGGGATTTTTTTTCTAATCATAAAAAATAGCCCCAGA
AAGAGCCTAAGCTATGTTTCAGATAGAAGCCTCGAAATTCCTGTAAATTGTTTACTTTATGATGTTTACATACAG
TTTCACTTTGAAAAAAAATGCAAATCGACTTTTTTAACAACCTGTTGAGATGTTTTCATGGGACAGTAGAACTCTGAC
TCACCAACTGGGCTAAATTTTAAATTTAAAAATGATTTTATTGAGTGTCTTTCCCCCCTCACCCTCACCATCTG
AGGGGCTCCCTGAGATCTTGGTAGAGGAGGCCCTCCTGCCAGACCTTCGTTTGTTCGCCGGTGGCCCTTGCT
TCTTGCTTTGCAGACTGCCTGCAGCCATGATTTTGTCACTGACATCTGTGAGCCAAAGACTGAGCCTTTTGGCA
GGAATAATAAGCAATACTACACAACCTTGCTACTTTTCAGAAAACCTTTTTTTTAGCTTCACCGATGACAACAGAGGA
AGAAGGGAACCTGGGATTTGGGTAAGTTCTCCTCCACTGTTTGACCAAATTCCTAGTGATAAATATGTGTGCAGAT
CCCTAGAAGAGAAAACGCTGACTTTCTTTTTTAAGTGTGGCACATAAGGATCTGCAGAATTTCCGTAGACAAAGA
AAGGATCTTGTGATTTTTGTCCATATCCAATGTTATATGAACATAATTGTATTGTTTTTACTGTGACCACAAAT
ATTATGCAATGCACCAATTTGTTTTTTATTTTATTAAAGGAAGTTTAATTT

WO 2004/030615

PCT/US2003/028547

340/6881
FIGURE 316

MPDSTLPGSRVLARLDRDSLHSSPHVALSHVDARSYHLLVRDVSKENSGYYYCHVSLWAPGHNRSWHKVAEAVS
SPAGVGVTWLEPDYQVYLNASKVPGFADDPTELACRVVDTKSGEANVRFTVSWYYRMNRRSDNVVTSELLAVMDG
DWTLKYGERSKQRAQDGDGDFIFSKEHTDTFNFRIQRTTEEDRGNYICVVSATKQRNNSWVKSVDVFSKPVNIFWA
LEDVSVLVVKARQPKPFFAAGNTFEMTCKVSSKNIKSPRYSVLIMAEKPVGDLSSPNETKYIISLDQDSVVKLENW
TDASRVDGVVLEKVQEDEFYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREAATSLSNPIEIDFQTSGPIFNASV
HSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLSSLDKRGIVTTSSRRDWKSDLSLE
RVSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSPGTSWQKEAEIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIG
LLSCLIGYCSSHWCCKKEVQETRERRRLMSMEMD

WO 2004/030615

PCT/US2003/028547

341/6881
FIGURE 317

GTCCATTTTGTCTGGTAGAGGCAGAAGGAGAAGGTCGGATTGTAGAAGCTGGGGTGGCCGGCAGCTCGCTCATCGG
TGTTTCGTGGGCTTTGTCTGGTCCGTGCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCAACGTCGAGAGGGAGCC
GCTGCCGCGTTAGTTCGAGCTTGAAGTCACTAGGACTTCTCTCAAACCTTGAGTGCTGAGGAGACTCAGATGTTG
GCCTCAGCTCCTAGGCTGAACTCAGCAGATCGGCCCATGAAAACCTTCTGTATTGAGACAAAGGAAGGGATCTGTC
AGAAAGCAACACTTGTATCTTGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAG
CAGACTGAAAGGTGACAAAGAAGCTGAAGATGGGTGGTAGAGAGAGGTATAACATTCCAGCCCCCTCAATCTAGAA
ATGTTAGTAAGAACCAACAACAGCTTAACAGACAGAAGACCAAGGAACAGAATTCCCAGATGAAGATTGTTTCATA
AGAAAAAGAAAGAGGACATGGTTATAACTCATCAGCAGGTGCCTGGCAGGCCATGAAAAATGGGGGGAAGAACA
AAAATTTTCAAATAATCAAAGTTGGAATTCTAGCTTATCAGGTCCCAGCTTACTTTTAAATCTCAAGCTAAAC
AGAACTATGCTGGTGCCAAATTTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCAAGCCACTGGGTCC
CTGTTTCCTTTAATCCTTCAGATAAGGAAATAATGACATTTCAACTTAAACCTTACTTAAAGTACAGGTATAAA
ATAAGACAAATGTTTAAAGTTTAGTTATGTTTACAGATAGTTGTCAATTGGTCTGAAACAAATTTGCTAGGGAATC
TATTTGTGTAGAACTAATTAATGTAAAAAAATAGACTTCATCTCGTGTGTGTGCACTGTGATATAATGGTAGT
ATCAGTGCAACTTAACTAATGATTGTAATTGATATTAAGTGTTCTCAACTGAGTAACTTTTAAAGTGGAAACCA
GTTTAGATTTGGGGAGTGGTAAAGGAATCAGCTTTTCTATTGTTAGGGGAAGATAGTAATTTATCATTCATGGA
CCAGTAGATTGTTGAAAGTTGGTGAATCGGATTATAAGCTTCTGGCTAACACAAGGATTCAGAATTAGGTAAACA
TCTGAAGGTTTAGTATATTAGAAACACCCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAAATGTGA
ATTTTTCGTAATAATTGCATTTTAGTGAATTGTACAGTGGGTGGAAAGGGCATTGAGGCTCATTAGAATGAGAC
ATAGTACACCCCAATGGCCCTGTTTATTAAATGTAGTGGATTAAAGTGCTGTCAACAAATACACCAAAACCATTT
TTTATAGAAACAGTATTTAATGGTCACTCAATAGCTTTCAAATACATTTTGTATTACAGCACTGCACAAGCTA
TTCTAATAGTGATCTGGCCTCCTCATTCTGCCAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTTAAAGTA
CCTAGGGGAGAAAGAGCCATGTAAATATCTGTAATAAACTTGTAGCATATGTAAAGTTTCTTGGCCTTTATCTT
ACAAAAATGGAATATTTTAGTATGAATTTGCTGAATGTAAGACCGTGACTGTTTTTATAATATGGCCTAATTT
TAAAGGTCCAAAATAACTTGTTTTTAAAGTTTGCCCTTGCTGCTAAAGTGCCAGTGATGTATGTTATACCTTGATT
TGGTTGTAAACTATATTTCAAAGTAAACCTAGTGTAAAGTTTATAACTAAAAAGGTTTAAAGCTGCTAAAC
TATTTTTAAGAGATGTGAAATGCAGTATGGGACTATCTTTTCTCCTCTAAGCCCAAGATTAACTAGAGTC
CCTCCAACCTTATAGATTTTGGCTTTCACAACTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGT
GATGTTTTGTTTTGTTTGGTCAAGGGTAGGTGCAACCAATGGACCACTTATGCAAAAGATGTAAACTCTTGC
ATAATACATCGATAACATGTTTTGCCAACCTTAAATGCTTAAACATAAGCGAAACCAAGTAGCAAGTATGTGGGTC
AGTTTAAAAATTTTGATTGTTAATGCCCTATTTTCTAATTTGGCACCTCTTTTGATGCCTAAGCAGGTAAGCAGA
TGCCTAAGCTGTATTTCTCAAATAAATCAAGAGGAAGTACTGCCCAAGTTAAATATTGATAGCCTAAAGACAAA
TTCATGTAGTACTTAATGTACATGATATGAATTTGAAGCATAAAATTAAATTTTTCCCCATTG

WO 2004/030615

PCT/US2003/028547

342/6881
FIGURE 318A

TTTCAGCCAAACTTCGGGCGGCGGCTGAGGCGGCGGCCGAGGAGCGGCGGACTCGGGGCGGGGAGTCGAGGCA
TTTGCGCCTGGGCTTCGGAGCGTAGCGCCAGGGCCTGAGCCTTTGAAGCAGGAGGAGGGGAGGAGAGAGTGGGGC
TCCTCTATCGGGACCCCCCTCCCATGTGGATCTGCCAGGCGGCGGCGGCGGCGGAGGAGGAGCGACCGAG
AAGATGCCCCGCCCTGCGCCCCGCTCTGCTGTGGGCGCTGCTGGCGCTCTGGCTGTGCTGCGCGGCCCCCGCGCAT
GCATTGCAGTGTGAGATGGCTATGAACCTGTGTAAATGAAGGAATGTGTGTTACCTACCACAATGGCACAGGA
TACTGCAAATGTCCAGAAGGCTTCTTGGGGGAATATTGTCAACATCGAGACCCCTGTGAGAAGAACCGCTGCCAG
AATGGTGGGACTTGTGTGGCCAGGCCATGCTGGGGAAAGCCACGTGCCGATGTGCCTCAGGGTTTACAGGAGAG
GACTGCCAGTACTCAACATCTCATCCATGCTTTGTGTCTCGACCCTGCCTGAATGGCGGCACATGCCATATGCTC
AGCCGGGATACCTATGAGTGCACCTGTCAAGTCGGGTTTACAGGTAAGGAGTGCCAATGGACGGATGCCTGCCTG
TCTCATCCCTGTGCAAATGGAAGTACCTGTACCCTGTGGCCAACCAAGTTCTCCTGCAAATGCCTCACAGGCTTC
ACAGGGCAGAAATGTGAGACTGATGTCAATGAGTGTGACATTCCAGGACACTGCCAGCATGGTGGCACCTGCCTC
AACCTGCCTGGTTCTTACCAGTGCCAGTGCCCTCAGGGCTTCACAGGCCAGTACTGTGACAGCCTGTATGTGCCC
TGTGCACCTCACCTTGTGTCAATGGAGGCACCTGTGCGCAGACTGGTGACTTCACTTTTGAGTGCAACTGCCTT
CCAGGTTTTGAAGGGAGCACCTGTGAGAGGAATATTGATGACTGCCCTAACCCACAGGTGTGAGAATGGAGGGGTT
TGTGTGGATGGGGTCAACACTTACAAC TGCCGCTGTCCCCACAATGGACAGGACAGTTCTGCACAGAGGATGTG
GATGAATGCCTGCTGCAGCCCAATGCCTGTCAAATGGGGCACCTGTGCCAACCAGCAATGGAGGCTATGGCTGT
GTATGTGTCAACGGCTGGAGTGGAGATGACTGCAGTGAGAACATTGATGATTGTGCCTTCGCCTCCTGTACTCCA
GGCTCCACCTGCATCGACCGTGTGGCCTCCTTCTTGTGATGTGCCAGAGGGGAAGGCAGGTCTCCTGTGTGCTAT
CTGGATGATGCATGCATCAGCAATCCTTGCCACAAGGGGGCACTGTGTGACACCAACCCCTAAATGGGCAATAT
ATTTGCACCTGCCCACAAGGCTACAAAGGGGCTGACTGCACAGAAGATGTGGATGAATGTGCCATGGCCAATAGC
AATCCTTGTGAGCATGCAGGAAAATGTGTGAACACGGATGGCGCCTTCCACTGTGAGTGTCTGAAGGGTTATGCA
GGACCTCGTTGTGAGATGGACATCAATGAGTGCCATTACAGACCCCTGCCAGAATGATGCTACCTGTCTGGATAAG
ATTGGAGGCTTCACATGTCTGTGCATGCCAGGTTTCAAAGGTGTGCATTGTGAATTAGAAATAAATGAATGTGAG
AGCAACCCCTTGTGTGAACAATGGGCAGTGTGTGGATAAAGTCAATCGTTTCCAGTGCCTGTGTCTCCTCGGTTTC
ACTGGGCCAGTTTGCCAGATTGATATTGATGACTGTTCCAGTACTCCGTGTCTGAATGGGGCAAAGTGATATCGAT
CACCCGAATGGCTATGAATGCCAGTGTGCCACAGGTTTCACTGGTGTGTTGTGTGAGGAGAACATTGACAACGT
GACCCCGATCCTTGCCACCATGGTCAGTGTGAGGATGGTATTGATTCTTACACCTGCATCTGCAATCCCGGGTAC
ATGGGCGCCATCTGCAGTGACCAGATTGATGAATGTTACAGCAGCCCTTGCTGAACGATGGTCCGCTGCATTGAC
CTGGTCAATGGCTACCAAGTGCAACTGCCAGCCAGGCACGTGAGGGGTTAATTGTGAAATTAATTTGATGACTGT
GCAAGTAACCCCTTGTATCCATGGAATCTGTATGGATGGCATTAAATCGCTACAGTTGTGTCTGCTCACCAGGATTC
ACAGGGCAGAGATGTAACATTGACATTGATGAGTGTGCCCTCCAATCCCTGTGCGAAGGGTGCAACATGTATCAAC
GGTGTGAATGGTTTCCGCTGTATATGCCCCGAGGGACCCATCACCCAGCTGCTACTCACAGGTGAACGAATGC
CTGAGCAATCCCTGCATCCATGGAACCTGTACTGGAGGTCTCAGTGGATATAAGTGTCTCTGTGATGCAGGCTGG
GTTGGCATCAACTGTGAAGTGGACAAAAATGAATGCCCTTTCAAATCCATGCCAGAATGGAGGAACTTGTGACAA
CTGGTGAATGGATACAGGTGTACTTGCAAGAAGGGCTTTAAAGGCTATAACTGCCAGGTGAATATTGATGAATGT
GCCTCAAATCCATGCCTGAACCAAGGAACCTGCTTTGATGACATAAGTGGCTACACTTGCCACTGTGTGCTGCCA
TACACAGGCAAGAATTGTGAGACAGTATTGGCTCCCTGTTCCCCAAACCCCTTGTGAGAATGCTGCTGTTTGCAAA
GAGTCACCAAATTTTGAGAGTTATACTTGCTTGTGTGCTCCTGGCTGGCAAGGTCAGCGGTGTACCATTGACATT
GACGAGTGTATCTCCAAGCCCTGCATGAACCATGGTCTCTGCCATAACACCCAGGGCAGCTACATGTGTGAATGT
CCACAGGCTTCAGTGGTATGGAAGTGTGAGGAGGACATTGATGACTGCCTTGCCAATCCTTGCCAGAATGGAGGT
TCCTGTATGGATGGAGTGAATACTTTCTCCTGCCTCTGCCTTCCGGGTTTCACTGGGGATAAGTGCCAGACAGAC
ATGAATGAGTGTCTGAGTGAACCTGTGAAGATGGAGGGACCTGCTGACTACGTCAACAGTTACACTTGCAAG
TGCCAGGCAGGATTTGATGGAGTCCATTGTGAGAACAACATCAATGAGTGCAGTGCAGCTCCTGTTTCAATGGT
GGCACATGTGTTGATGGGATTAACCTCCTTCTTGTGCTTGTGCCCTGTGGGTTTCACTGGATCCTTCTGCCTCCAT
GAGATCAATGAATGCAGCTCTCATCCATGCCTGAATGAGGGAACGTGTGTTGATGGCTGGGTACCTACCGCTGC
AGCTGCCCCCTGGGCTACACTGGGAAAACTGTGAGCCCTGGTGAATCTCTGCAGTCGGTCTCCATGTAAAAAC
AAAGGTACTTGCCTTCAGAAAAAGCAGAGTCCAGTGCCTATGTCCATCTGGATGGGCTGGTGCCTATTGTGAC
GTGCCCAATGTCTTGTGACATAGCAGCCTCCAGGAGAGGTGTGCTTGTGTAACACTTGTGCCAGCACTCAGGT

WO 2004/030615

PCT/US2003/028547

343/6881
FIGURE 318B

GTCTGCATCAATGCTGGCAACACGCATTACTGTCTAGTGCCCCCTGGGCTATACTGGGAGCTACTGTGAGGAGCAA
CTCGATGAGTGTGCGTCCAACCCCTGCCAGCACGGGGCAACATGCAGTGACTTCATTGGTGGATACAGATGCGAG
TGTGTCCCAGGCTATCAGGGTGTCAACTGTGAGTATGAAGTGGATGAGTGCCAGAATCAGCCCTGCCAGAATGGA
GGCACCTGTATTGACCTTGTGAACATTTCAAGTGCTCTTGCCACCAGGCACTCGGGGCTACTCTGTGAAGAG
AACATTGATGACTGTGCCCGGGGTCCCCATTGCCTTAATGGTGGTCAGTGCAATGATAGGATTGGAGGCTACAGT
TGTGCTGCTTGCCTGGCTTTGCTGGGGAGCGTTGTGAGGGAGACATCAACGAGTGCCCTCTCCAACCCCTGCAGC
TCTGAGGGCAGCCTGGACTGTATACAGCTCACCAATGACTACCTGTGTGTTTGCCGTAGTGCCCTTACTTGGCCGG
CACTGTGAAACCTTCGTCGATGTGTGTCCCCAGATGCCCTGCCCTGAATGGAGGGACTTGTGTGTGGCCAGTAAC
ATGCCTGATGGTTTCATTTGCCGTTGTCCCCGGGATTTTCCGGGGCAAGGTGCCAGAGCAGCTGTGGACAAGTG
AAATGTAGGAAGGGGGAGCAGTGTGTGCACACCGCCTCTGGACCCCGTGCTTCTGCCCAGTCCCCGGGACTGC
GAGTCAGGCTGTGCCAGTAGCCCTGCCAGCACGGGGCAGCTGCCACCTCAGCGCCAGCCTCCTTATTACTCC
TGCCAGTGTGCCCCACCATTCTCGGGTAGCCGCTGTGAACCTACACGGCACCCCCCAGCACCCCTCCTGCCACC
TGTCTGAGCCAGTATTGTGCCGACAAAGCTCGGGATGGCGTCTGTGATGAGGCCGTGCAACAGCCATGCCCTGCCAG
TGGGATGGGGGTGACTGTTCTCTCACCATGGAGAACCCCTGGGCCAACTGCTCCTCCCCACTTCCCTGCTGGGAT
TATATCAACAACCAAGTGTGATGAGCTGTGCAACACGGTCGAGTGCCCTGTTTGACAACCTTGAATGCCAGGGGAAC
AGCAAGACATGCAAGTATGACAAATACTGTGCAGACCACTTCAAAGACAACCACTGTGACCAAGGGTGCAACAGT
GAGGAGTGTGGTTGGGATGGGCTGGACTGTGCTGCTGACCAACCTGAGAACCCTGGCAGAAAGTACCCTGGTTATT
GTGGTATTGATGCCACCTGAACAACCTGCTCCAGGATGCTCGCAGCTTCTTGCGGGCACTGGGTACCCTGCTCCAC
ACCAACCTGCGCATTAAGCGGGACTCCCAGGGGAACCTGAGGTGTACCCCTATTATGGTGAGAAAGTCAGCTGCT
ATGAAGAAACAGAGGATGACACGCAGATCCCTTCTGGTGAACAAGAACAGGAGGTGGCTGCTAAAGTCTTT
CTGGAAATTGACAACCGCCAGTGTGTTCAAGACTCAGACCACTGCTTCAAGAACACGGATGCAGCAGCAGCTCTC
CTGGCCTCTCAGCCATACAGGGGACCCTGTATACCCTCTTGTGTCTGCTCAGTGAATCCCTGACTCCAGAA
CGCACTCAGCTCCTCTATCTCCTTGCTGTTGCTGTTGTCATCATTCTGTTTATTATTCTGCTGGGGGTAAATCATG
GCAAAACGAAAGCGTAAGCATGGCTCTCTCTGGCTGCCTGAAGGTTTCACTCTTCGCCGAGATGCAAGCAATCAC
AAGCGTCGTGAGCCAGTGGGACAGGATGCTGTGGGGCTGAAAAATCTCTCAGTGCAAGTCTCAGAAGCTAACCTA
ATTGGTACTGGAACAAGTGAACACTGGGTCGATGATGAAGGGCCCCAGCCAAAGAAAGTAAAGGCTGAAGATGAG
GCCTTACTCTCAGAAGAAGATGACCCCATTTGATCGACGGCCATGGACACAGCAGCACCTTGAAGCTGCAGACATC
CGTAGGACACCATCGCTGGCTCTCACCCCTCCTCAGGCAGAGCAGGAGGTGGATGTGTTAGATGTGAATGTCCTG
GGCCAGATGGCTGCACCCCATTTGATGTTGGCTTCTCTCCGAGGAGGCAGCTCAGATTGAGTGATGAAGATGAA
GATGCAGAGGACTCTTCTGCTAACATCATCACAGACTTGGTCTACCAGGGTGCCAGCCTCCAGGCCAGACAGAC
CGGACTGGTGAGATGGCCCTGCACCTTGCAGCCCGCTACTCACGGGCTGATGCTGCCAAGCGTCTCCTGGATGCA
GGTGCAGATGCCAATGCCCAGGACAACATGGGCCGCTGTCCACTCCATGCTGCAGTGGCAGCTGATGCCCAAGGT
GTCTTCCAGATTCTGATTGCGAACCGAGTAACCTGATCTAGATGCCAGGATGAATGATGGTACTACACCCCTGATC
CTGGCTGCCCCGCTGGCTGTGGAGGGAATGGTGGCAGAATGATCAACTGCCAAGCGGATGTGAATGCAGTGGAT
GACCATGGAAAATCTGCTCTTCACTGGGCAGCTGCTGTCAATAATGTGGAGGCAACTCTTTTGTGTGAAAAAT
GGGGCCAACCGAGACATGCAGGACAACAAGGAAGAGACACCTCTGTTTCTTGCTGCCCGGGAGGGGAGCTATGAA
GCAGCCAAGATCCTGTTAGACCATTTTGCCAATCGAGACATCACAGACCATATGGATCGTCTTCCCCGGGATGTG
GCTCGGGATCGCATGCACCATGACATTGTGCGCCTTCTGGATGAATACAATGTGACCCCAAGCCCTCCAGGCACC
GTGTTGACTTCTGCTCTCTCACCTGTCTCTGTGGGCCCAACAGATCTTCTCAGCCTGAAGCACACCCCAATG
GGCAAGAAGTCTAGACGGCCCAAGTGCCAAGAGTACCATGCCTACTAGCCTCCCTAACCTTGCCAAGGAGGCAAG
GATGCCAAGGGTAGTAGGAGGAAGAAGTCTCTGAGTGAGAAGGTCCAACCTGTCTGAGAGTTCAGTAACCTTATCC
CCTGTTGATTCCCTAGAATCTCCTCACACGTATGTTTCCGACACCACATCCTCTCCAATGATTACATCCCCTG
ATCTTACAGGCCTCACCCAACCTATGTTGGCCACTGCCGCCCTCCTGCCCCAGTCCATGCCCAGCATGCACTA
TCTTTTTCTAACCTTCATGAAATGCAGCCTTTGGCACATGGGGCCAGCACTGTGCTTCCCTCAGTGAGCCAGTTG
CTATCCCACCACCACTTGTGTCTCCAGGCAGTGGCAGTGTGGAAGCTTGAGTAGGCTCCATCCAGTCCCAGTC
CCAGCAGATTGGATGAACCGCATGGAGGTGAATGAGACCCAGTACAATGAGATGTTTGGTATGGTCTGGCTCCA
GCTGAGGGCACCCATCCTGGCATAGCTCCCCAGAGCAGGCCACCTGAAGGGAAGCACATAACCACCCCTCGGGAG
CCCTTGCCCCCATTTGTGACTTTCCAGCTCATCCCTAAAGGCAGTATTGCCCAACCAGCGGGGGCTCCCCAGCCT

WO 2004/030615

PCT/US2003/028547

344/6881
FIGURE 318C

CAGTCCACCTGCCCTCCAGCTGTTGCGGGCCCCCTGCCACCATGTACCAGATTCCAGAAATGGCCCGTTTGCCC
AGTGTGGCTTTCCCCACTGCCATGATGCCCCAGCAGGACGGGCAGGTAGCTCAGACCATTCTCCCAGCCTATCAT
CCTTTCCCAGCCTCTGTGGGCAAGTACCCACACCCCCCTTCACAGCACAGTTATGCTTCTCAAATGCTGCTGAG
CGAACACCCAGTCACAGTGGTCACCTCCAGGGTGAGCATCCCTACCTGACACCATCCCCAGAGTCTCCTGACCAG
TGGTCAAGTTCATCACCCCACTCTGCTTCTGACTGGTCAGATGTGACCACCAGCCCTACCCCTGGGGGTGCTGGA
GGAGGTCAGCGGGGACCTGGGACACACATGTCTGAGCCACCACACAACAACATGCAGGTTTATGCGTGAGAGAGT
CCACCTCCAGTGTAGAGACATAACTGACTTTTGTAAATGCTGCTGAGGAACAAATGAAGGTTCATCCGGGAGAGAA
ATGAAGAAATCTCTGGAGCCAGCTTCTAGAGGTAGGAAAGAGAAGATGTTCTTATTTCAGATAATGCAAGAGAAGC
AATTCGTCAAGTTTCACTGGGTATCTGCAAGGCTTATTGATTATTCTAATCTAATAAGACAAGTTTGTGGAAATGC
AAGATGAATACAAGCCTTGGGTCCATGTTTACTCTCTTCTATTTGGAGAATAAGATGGATGCTTATTGAAGCCCA
GACATTCTTGACGCTTGGACTGCATTTTAAGCCCTGCAGGCTTCTGCCATATCCATGAGAAGATTCTACACTAGC
GTCCTGTGGGAATTATGCCCTGGAATTCTGCCTGAATTGACCTACGCATCTCCTCCTCTTGACATTCTTTTG
TCTTCATTTGGTGCTTTTGGTTTTGCACCTCTCCGTGATTGTAGCCCTACCAGCATGTTATAGGGCAAGACCTTT
GTGCTTTTGATCATTCTGGCCCATGAAAGCAACTTTGGTCTCCTTTCCCTCCTGTCTTCCCGGTATCCCTTGGA
GTCTCAAAAGGTTTACTTTGGTATGGTTCTCAGCACAAACCTTTCAAGTATGTTGTTTTCTTTGGAAAATGGACAT
ACTGTATTGTGTTCTCCTGCATATATCATTCCTGGAGAGAGAAGGGGAGAAGAATACTTTTCTTCAACAAATTTT
GGGGGCAGGAGATCCCTTCAAGAGGCTGCACCTTAATTTTTCTTGCTGTGTGTCAGGTCTTCATATAAACTTTAC
CAGGAAGAAAGGTTGTAGTGTGTTGTTTTCTGTGTATGGGCCTGGTCAGTGTAAGTTTTATCCTTGATAGTCT
AGTTACTATGACCCCTCCCCACTTTTTTAAAACAGAAAAAGGTTTGGAAATGTTGGAATGACCAAGAGACAAGTTA
ACTCGTGCAAGAGCCAGTTACCCACCCACAGGTCCCCCTACTTCTGCCAAGCATTCCATTGACTGCCTGTATGG
AACACATTTGTCCCAGATCTGAGCATTCTAGGCCTGTTTCACTCACTCACCCAGCATATGAACTAGTCTTAACT
GTTGAGCCTTTCTTTCATATCCACAGAAGACACTGTCTCAAATGTTGTACCCTTGCCATTTAGGACTGAACCTT
CCTTAGCCCAAGGGACCCAGTGACAGTTGTCTTCCGTTTGTGATGATCAGTCTCTACTGATTATCTTGCTGCT
TAAAGGCCTGCTCACCAATCTTTCTTTCACACCGTGTGGTCCGTGTTACTGGTATACCCAGTATGTTCTCACTGA
AGACATGGACTTTATATGTTCAAGTGCAGGAATTGGAAAGTTGGACTTGTTTTCTATGATCCAAAACAGCCCTAT
AAGAAGGTTGGAAAAGGAGGAACATATAGCAGCCTTGTCTATTTCTGCTACCATTCTTTTCTCTGAAGCGG
CCATGACATTTCCCTTTGGCAACTAACGTAGAACTCAACAGAACATTTTCTTCTTAGAGTCACCTTTTAGATG
ATAATGGACAACATATAGACTTGTCTCATTGTTTCAGACTGATTGGCCCTCACCTGAATCCACTCTCTGTATTATGC
TCTTGGEAATTTCTTTGACTTTCTTTTAAGGGCAGAAGCATTTTATGTTAATTGTAGATAAAGAATAGTTTTCTTC
CTCTTCTCCTTGGGCCAGTTAATAAATTGGTCCATGGCTACACTGCAACTTCCGTCCAGTGCTGTGATGCCCATGA
CACCTGCAAAAATAAGTTCTGCCTGGGCATTTTGTAGATATTAACAGGTGAATTCCCGACTCTTTTGGTTTGAATG
ACAGTTCTCATTCTCTATGGCTGCAAGTATGCATCAGTGCTTCCCACTTACCTGATTTGTCTGTGCGGTGGCCC
CATATGGAAACCCTGCGTGTCTGTTGGCATAATAGTTTTACAAATGGTTTTTTCAGTCCCTATCCAAATTTATTGAA
CCAACAAAATAAATTACTTCTGCCCTGAGATAAGCAGATTAAGTTTTGTTTCTCTGCTTTATTCTCTCCATGT
GGCAACATTTCTGTGAGCCTCTTTTCATAGTGTGCAACATTTTATCATTCTAAATGGTGACTCTCTGCCCTTGAC
CCATTTTATTATTACAGATGGGGAGAACCTATCTGCATGGACCTCTGTGGACCACAGCGTACCTGCCCTTTCTG
CCCTCCTGCTCCAGCCCCACTTCTGAAAGTATCAGCTACTGATCCAGCCACTGGATATTTTATATCCTCCCTTTT
CCTTAAGCACAAATGTGAGACCAATTGCTTGTTTTCTTTTCTTGACTACTTTAATTTGGATCCTTTGGGTTTGG
AGAAAGGGAATGTGAAAGCTGTCAATTACAGACAACAGGTTTCAAGTATGAGGAGGACAACACTGCCTTTCAAAC
TTTTACTGATCTCTTAGATTTTAAAGACTCTTGAATTGTGTGGTATCTAATAAAAGGGAAGGTAAGATGGATAAT
CACTTTCTCATTGTTGTTCTGAATTGGAGACTCAGTTTTTATGAGACACATCTTTATGCCATGTATAGATCCTC
CCCTGCTATTTTTGGTTTTATTTTTATGTTATAAATGCTTTCTTTGACTCCTCTTCTGCCTGCCTTTGGGG
ATAGGTTTTTTTTGTTTGTATTTGCTTCTCTGTTTTGTTTTAAGCATCATTTTCTTATGTGAGGTGGGGAAGG
GAAAGGTATGAGGGAAGAGAGTCTGAGAATTAATAATTTTAGTATAAGCAATTGGCTGTGATGCTCAAAATCCA
TTGCATCCTCTTATTGAATTTGCCAATTTGTAATTTTGCATAATAAAGAACCAAGGTGAATGTTTTGTTGAG
AGGTGGTTTTAGGGATTTTGGCCCTAACCAATACATTGAATGTATGATGACTATTTGGGAGGACACATTTATGTAC
CCAGAGGCCCCCACTAATAAGTGGTACTATGGTTACTTCTTGTGTACATTTCTCTTAAAGGTGATATTATATCT
GTTTGTATGAGAAACCCAGTAACCAATAAAATGACCGCATATTCCTGACTAAACGTAGTAAGGAAAATGCACACT

WO 2004/030615

PCT/US2003/028547

345/6881

FIGURE 318D

TTGTTTTTACTTTTCCGTTTCATTCTAAAGGTAGTTAAGATGAAATTTATATGAAAGCATTTTTATCACAAAATA
AAAAAGGTTTGCCAAGCTCAGTGGTGTGTATTTTTTATTTTCCAATACTGCATCCATGGCCTGGCAGTGTTACC
TCATGATGTCATAATTTGCTGAGAGAGCAAATTTTCTTTTCTTTCTGAATCCCACAAAGCCTAGCACCAAAC TTC
TTTTTTTCTTCCTTTAATTAGATCATAAAATAAATGATCCTGGGGAAAAAGCATCTGTCAAATAGGAAACATCACA
AAACTGAGCACTCTTCTGTGCACTAGCCATAGCTGGTGACAAACAGATGGTTGCTCAGGGACAAGGTGCCTTCCA
ATGGAAATGCGAAGTAGTTGCTATAGCAAGAATTGGGAACTGGGATATAAGTCATAATATTAATTATGCTGTTAT
GTAAATGATTGGTTTGTAAACATTCCTTAAGTGAAATTTGTGTAGAACTTAATATACAGGATTATAAAATAATATT
TTGTGTATAAATTTGTTATAAGTTCACATTCATACATTTATTTATAAAGTCAGTGAGATATTTGAACATG

WO 2004/030615

PCT/US2003/028547

346/6881
FIGURE 319

GAGGAGGAGGAGGAGATGACTGGGGAGCGGGAGCTGGAGAATACTGCCAGTTACTCTAGCGCGCCAGGCCGAAC
CGCAGCTTCTTGGCTTAGGTACTTCTACTCACAGCGGCCGATTCGAGGCCAACTCCAGCAATGGCTTTTGCAAA
TCTGCGGAAAGTGCTCATCAGTGACAGCCTGGACCCTTGCTGCCGGAAGATCTTGCAAGATGGAGGGCTGCAGGT
GGTGGAAAAGCAGAACCTTAGCAAAGAGGAGCTGATAGCGGAGCTGCAGGACTGTGAAGGCCCTATTGTTTCGCTC
TGCCACCAAGGTGACCGCTGATGTCATCAACGCAGCTGAGAACTCCAGGTGGTGGGCAGGGCTGGCACAGGTGT
GGACAATGTGGATCTGGAGGCCGCAACAAGGAAGGGCATCTTGTTATGAACACCCCCAATGGGAACAGCCTCAG
TGCCGCAGAACTCACTTGTGGAATGATCATGTGCCTGGCCAGGCAGATTCCCCAGGCGACGGCTTCGATGAAGGA
CGGCAAATGGGAGCGGAAGAAGTTTCATGGGAACAGAGCTGAATGGAAAGACCCTGGGAATTCTTGGCCTGGGCAG
GATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCCTTGGGATGAAGACTATAGGGTATGACCCCATCATTTCCCC
AGAGGTCTCGGCCCTCCTTTGGTGTTCAGCAGCTGCCCTGGAGGAGATCTGGCCTCTCTGTGATTTCACTACTGT
GCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCCAGTGCAAGAAGGGGGTGCG
TGTGGTGAACGTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGCAGTCTGGCCAGTGTGC
CGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGACCATGAGAATGTATCAG
CTGTCCCCACCTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAATTGCTGTTCAGTTTCGTGGA
CATGGTGAAGGGGAAATCTCTCACGGGGGTTGTGAATGCCAGGCCCTTACCAGTGCCCTCTCTCCACACACCAA
GCCTTGGATTGGTCTGGCAGAAGCTCTGGGGACACTGATGCGAGCCTGGGCTGGGTCCCCCAAAGGGACCATCCA
GGTGATAACACAGGGAACATCCCTGAAGAATGCTGGGAACGCCAAGCCCCGCAGTCATTGTGGCCTCCTGAA
AGAGGCTTCCAAGCAGGCGGATGTGAACCTGGTGAACGCTAAGCTGCTGGTGAAGAGGCTGGCCTCAATGTAC
CACCTCCCACAGCCCTGCTGCACCAGGGGAGCAAGGCTTCGGGGAATGCCTCCTGGCCGTGGCCCTGGCAGGCGC
CCCTTACCAGGCTGTGGGCTTGGTCCAAGGCACTACGCCCTGTACTGCAGGGGCTCAATGGAGCTGTCTCAGGCC
AGAAGTGCCCTCTCCGAGGGACCTGCCCCTGCTCCTATTCCGGACTCAGACCTCTGACCCTGCAATGCTGCCTAC
CATGATTGGCCTCCTGGCAGAGGCAGGCGTGCGGCTGCTGTCTTACCAGACTTCACTGGTGTGAGATGGGGAGAC
CTGGCACGTATGGGCATCTCCTCCTTGCTGCCCAGCCTGGAAGCGTGGAAGCAGCATGTGACTGAAGCCTTCCA
GTTCCACTTCTAACCTTGGAGCTCACTGGTCCCTGCCCTTGCGGGCTTTTCTGAAGAAACCCACCCACTGTGATCA
ATAGGGAGAGAAAATCCACATTCTTGGGCTGAACGCGGGCCTCTGACACTGCTTACACTGCACTCTGACCCTGTA
GTACAGCAATAACCGTCTAATAAAGAGCCTACCCCC

WO 2004/030615

PCT/US2003/028547

347/6881
FIGURE 320

MAFANLRKVLISDSLDPCCRKILQDGGQLQVVEKQNLKSKEELIAELQDCEGLIVRSATKVTADVINA AEKLQVVGR
AGTGVDNVDLEAATRKGILVMNTPNGNSLSAAELTCGMIMCLARQIPQATASMKGKWERKKFMGTELNKTLGI
LGLGRIGREVATRMQSFGMKTIGYDPIISPEVSASFGVQQLPLEEIWPLCDFITVHTPLLPSTTGLLNDNTFAQC
KKGVRVVNCARGGIVDEGALLRALQSGQCAGAALDVFTTEPPRDALVDHENVISCPHLGASTKEAQSRCGEEIA
VQFVDMVKGKSLTGVVNAQALTSAFSPHTKPWIGLAEALGTLRAWAGSPKGTIQVITQGTSLKNAGNCLSPAVI
VGLLKEASKQADVNLVNAKLLVKEAGLNVTTSHSPAAPGEQGFGECLLAVALAGAPYQAVGLVQGTPVLQGLNG
AVFRPEVPLRRDLPLLLFRITQSDPAMLPTMIGLLAEAGVRLLSYQTSLSVSDGETWHVMGISSLLPSLEAWKQHV
TEAFQFHF

WO 2004/030615

PCT/US2003/028547

348/6881
FIGURE 321

GGGCAGGGGTGCGGAGGGACCGACGGACGCACGGGCGGGCGGCCGGGAGCCATGGAGCGCGGCCCTGGGGCCCGG
GGGCGCGGGCCGGGGTGGGCTTCCACGGCACGACATGGAGACCTGTGGTTGCGAGGCTCCCTGGGGCTCGGCTT
GGACCGCGATGGGGCTGGGCCCTGGCCTCCTAACGGGGCTGTGTCTGGGGCGGTAGCTGGGGGGGCGCTCTCCC
CCCTGCCCCGCGACTCGGAGCACCCACCCCTCCCCCTGCCGGGGCCAGGCCGGGCGGCGTTGTTGGCGGGGGCCCCG
GTGGAGGCCCCGGCCGGGCGGCGCCCGCCATGAACGGGGCTGTGCTGAGTGAGCTCTGCTGCCTCTTCTGCTGCC
CTCCCTGCCCCGGCCGCATCGCTGCCAAGCTCGCCTTCCTGCCGCCGGAGGCCACCTACTCCCTGGTGCCTGAGC
CCGAGCTGGGGCCTGGTGGGGCCGGGGCCGCCCCCTTGGGGACCCCTGAGAGCCTCCTCGGGCGCACCCGGGCGCT
GGAAGCTGCACCTGACGGAGCGTGCCGACTTCCAGTACAGCCAGCGCGAGCTGGACACCATCGAGGTCTTCCCCA
CCAAGAGCGCCCCGCGGCAACCGTGTCTCCTGCATGTATGTTTCGCTGCGTGCTGCTGGTGCCAGGTACACGGTCTCT
TCTCGCACGGCAATGCCGTGGACCTGGGCCAGATGAGCAGCTTCTACATTGGCCTGGGCTCCCGCCTCCACTGCA
ACATCTTACCTACGACTCCTCCGGCTACGGTGCCAGCTCGGGCAGGCCTTCCGAGAGGAACCTCTATGCCGACA
TCGACGCCACCTGGCAGGCCCTGCGCACCCAGGTACGGCATCAGCCCGGACAGCATCATCCTGTACGGGCAGAGCA
TCGGCACGGTGCCCCACCATGGACCTGGCCTCGCGCTACGAGTGTGCCGCGGTGGTGCTGCACTCGCCGCTCACCT
CGGGCATGCGCGTCGCCTTCCGCGACACCAAGAAGACCTACTGCTTCGACGCCTTCCCTAACATCGAGAAGGTGT
CCAAGATCACGTCTCCCGTGCTCATCATCCACGGCAGGGAGGACGAGGTGATCGACTTCTCGCACGGGCTGGCGC
TCTACGAGCGCTGCCCCAAGGCGGTGGAGCCGCTGTGGGTGGAGGGCGCCGGGCACAACGACATCGAGCTCTACA
GCCAGTACCTGGAGCGCCTGCGTCGCTTCATCTCCCAGGAGCTGCCAGCCAGCGCGCCTAGCGGCGGGCCCCAAC
CAGCCGGACCTCAGCAATAAGGCGGCCCCCGGACCTCACCCCGCGCCGGCCCCCAGGGGGCTGCATGTGGAC
CCCCCGGGCGGGCCAGGGGACCCCGCCCCGACCCAGGGGCTGTGGACGATGTACAGGCAACAGAGCTACGCACT
CCTTTCCTTTTGGAAGCAAGAAGAAAATACGTGAAAACGGAAATTAAAGATTTAAAATT

WO 2004/030615

PCT/US2003/028547

349/6881
FIGURE 322

MNGLSLSELCCCLFCCPPCPGRIAAKLAFLPPEATYSLVPEPELGPGGAGAAPLGTLRASSGAPGRWKLHLTERAD
FQYSQRELDTIEVFPTKSARGNRVSCMYVRCVPGARYTVLF SHGNAVDLGQMSSFYIGLGSRLHCNIFTYDSSGY
GASSGRPSEPNLYADIDATWQALRTRYGISPDSIIILYGQSIGTVPTMDLASRYECAAVVLHSPLTSGMRVAFRDT
KKTYCFDAFPNIEKVSKITSPVLIHGREDEVDFSHGLALYERCPKAVEPLWVEGAGHNDIELYSQYLERLRRF
ISQELPSQRA

WO 2004/030615

PCT/US2003/028547

350/6881
FIGURE 323A

AGCGTGAACCTGGGAGGCAGAGCTTGCACTGAGCCTAGATCGCGTCACTGCACTCCAGCCTGGGAGACAGAGTGA
GACTCTGTCTCAAAAAAAAAAAAAAGTCAAAAACAAGAGAACATACTAAATGATTCCATTTTTTTTATTTATGACTT
CATGACTACCATTAAAGAAAATATAACCTGTTGGGAAACTGTTTCTGCCTTGATGATGTTGTACAGACAAGAGATA
AACAGTGAGGAATGTGCTTAGATGTATTGGGAAAGACACGGGTCTGTGGCATTGTACAAAGGGTACACGAATACT
GAGAGTGAATGCTGAAGGAATGATCCCCATTGGTGGTGACCTCAGGTGAGACTAGGGTGCCTGTGTTTCAGCAA
AGCCTGGGCAATTGGAATGCAGGGCTCCTAAGATTCCATGACACCCCCACCTTCTAATTCTGTTATTGCAACTGC
AGACCGTTACCTGGCACGCTGGCCACAATCTACCTCACTCTTATCAGAGTCTGAGCTACTGGCAGTGCTTTCAGC
TCTGAGTTGAGGCACCTCGAACCTTGTTTTTGTGGTGAAGGATCCTAAAGTGCTGTGGGAGTGATCACATTTTTTC
ACAACAGTAACTCCCTGACTCCACCTCTTCTGCCACAAACGTCAGCATGGTGGTATCAGCCGGCCCTTGGTCCAG
CGAGAAGGCAGAGATGAACATTCTAGAAATCAACGAGAAATTGCGCCCCCAGTTGGCAGAGAACAACAGCAGTT
CGTAAACCTCAAAGAGATGTTTTCTAACTCAACTGGCCGGCTTCTGGCCAACCGACAGAAGAAATACAGCAATA
TAAAGTCTCGTTCACTCTCAGGAACGAGAGCTGACGCAGTTAAAGGAGAAGTTACAGGAAGGGAGAGATGCCTC
CCGCTCATTGAATGAGCATCTCCAGGCCCTCCTCACTCTGGATGAGCCGGACAAGTCCCAGGGGCAGGACCTCCA
AGAACAGCTGGCTGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACGAAGATGA
GGATGAAGATGTTCAAGTTGAGGAGGATGAGAAAGTGCAAGAAATCATCTGCCCCAGGGAGGTGCAGAAGGCTGA
AGTGAGCAAAGTCCCTGAGGACTCACTGGAGGAATGTGCCATCACTTGTTCAAATAGCCACGGCCCTTGTGACTC
CAACCAGCCTCACAAGAACATCAAAATCACATTGAGGAAGACGAAGTCAACTCAACTCTGGTTGTAGACAGAGA
ATCCTCTCATGATGAATGTGAGGATGCTCTAAACATTCTCCAGTCCCTGGCCCCACCTCTTCTGCCACAAACGT
CAGCATGGTGGTATCAGCCGGCCCTTGTGCCAGCGAGAAGGCAGAGATGAACATTCTAGAAATCAATGAGAAATT
GCACCCCCAGCTGGCAGAGAAGAAACAGCAGTTGAGAAACCTCAAAGAGAAATGTTTTCTAACTCAACTGGCCGG
CTTCTTGGCCAACAGCAGAGAACAATAACAAGTATGAAGAGTGTAAAGACCTCATAAAATTTATGCTGAGGAATGA
GCGACAGTTCAAGGAGGAGAAGCTTGACAGAGCTGAAGCAAGCTGAGGAGCTCAGGCAATATAAAGTCTCGGT
TCACGCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTGCGGGAAGGGAGAGATGCCTCCCGCTCATTGAA
TGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCAGGGGCAGGACCTCCAAGAACAGCTGGC
TGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACAACGATGACAAATGAAGATGT
TCAAGTTGAGGTGGCTGAGAAAGTGCAAGAAATCGTCTGCCCCAGGGAGATGCAGAAGGCTGAAGAAAAGGAAGT
CCCTGAGGACTCACTGGAGGAATGTGCCATCACTTATTCAAATAGCCATGGCCCTTATGACTCCAACAGCCACA
TAGGAAAACCAAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCTCATTGGCTCATCTCTCATGTTGAACG
GGAAGATGCTGTACACATTATTCCAGAAAATGAAAGTGATGATGAGGAAGAGGAAGAAAAGGGCCAGTGCTCTCC
CAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCAGGAGTCTGGGATGAAGGTTATTTCGACTCCCTCAAT
TCCTCTGAAATGTTGGCCTCGTACAAGTCTTACAGCAGCACATTTCACTCATTAGAGGAACAGCAAGTCTGCAT
GGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAAGGAGGACCAAGAGGCAACAGGTCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGGGCCTGAAGTCTTGACAGGACTCACTGTATAGATGTTATTCAACTCCTTCAGG
TTGTCTTGAACGACTGACTCATGCCAGCCCTACAGAAGTGCCCTTTTACGTATTGGAGCAACAGCGTGTGGCTT
GGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCAAGACCCATCATGCCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGAGCCTGAAGTCTTGACAGGACTCACTGGGTAGATGGTATTTCGACTCCTTCAGG
TTATCTTGAACGCTGACTTAGGCCAGCCCTACAGCAGTGCTGTTTACTCATTGGAGGAACAGTACCTTGGCTT
GGCTCTTGACTTGGACAGAATTAAGAAAGGACCAAGAAGAGGAAGAAGACCAAGGCCCACCATGCCCCAGGCTCAG
CAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGACAGGACTCACTGGATAGATGTTATTCAACTCCTTCAG
TTGTCTTGAACAGCCTGACTCCTGCCAGCCCTATGGAAGTTCCTTTTATGCATTGGAGGAAAAACATGTTGGCTT
TTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAGAAGGAAAG
AAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCCCAGGCTCAACGGCGTGCTGATGGAAGT
GGAAGAGCCTGAAGTCTTGACAGGACTCACTGGATGGATGTTATTCTACTCCGTCAATGTACTTTGAACTACCTGA
CTCATTCCAGCACTACAGAAGTGTTTACTCATTGAGGAACAGCACATCAGCTTCGCCCTTTACGTGGACAA
TAGGTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTGTCCAGATGGAAGTCATATTCCACAATAAGCAGC
CCTTACTAAGCCGAGAGATGTCATTCTGCAGGCAGGACCTATAGGCACGTGAAGATTTGAATGAACTACAGTT
CCATTTGGAAGCCGAGACATAGGATGGGTGAGTGGGCATGGCTCTATTCTATTCTCAAACCATGCCAGTGGCAA
CCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACAGTTACATAACTGTGCAGCACATGCCGGGA

WO 2004/030615

PCT/US2003/028547

351/6881
FIGURE 323B

GTGATCAGTCAGACATTTTAATTTGAACCACGTATCTCTGGGTAGCTACAAAATTCCTCAGGGATTTTCATTTTGC
AGACATGTCTCTGAGCTTCTATACCTGCTCAAGGTCATTGTTCATCTTTGTGTTTAGCTCATCCAAAGGTGTTACC
CTGGTTTCAATGAACCTAACCTCATTCTTCGTGCTTTCAGTGTTGGCTTGTTTTAGCTGATCCATCTGTAACACA
GGAGGGATCCTTGGCTGAGGATTGTATTTGAGAACCACCAACTGCTCTTGACAATTGTTAACCCGCTAGGCTCCT
TTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCAGTACTTAGGAAGACCACAGCTAGATGGACAAA
CAGCATTGGGAGGCCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGAGAACAGGAGTCAGGAGCCGCTGGCAGG
AGACAGCATGTCAACCAGGACTCTGCCGGTGCAGAAATATGAACAATGCCATGTTCTTGCAGAAAACGCTTAGCCT
GAGTTTCATAGGAGGTAATCACCAGACAACCTGCAGAAATGTAGAACAACCTGAGCAGGACAACCTGACCTGTCTCCTTC
ACATAGTCCTTATCACCACAAATCACACAACAAAAAGGAGAAGAGATATTTTGGGTTCAAAAAAGTAAAAAGAT
AATGTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCTCATCTTTTTGTTGTTGTTCATGGATGGTGG
TGACATGGACTTGTTTATAGAGGACAGGTCAGCTGTCTGGCTCAATGATCTACATTCTGAAGTTGTCTGAAAATG
TCTTCATGATTAAATTCAGCCTAAACGTTTTGCCGGGAACACTGCAGAGACAATGCTGTGAGTTTCCAACCTCAG
CCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATATCAGGACTGGTTACTTGGTTAAGGAGG
GGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTACTTGGGAAAGCGGTTTTCAAGAGTAT
AAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTTATTAATCCTCCCTGCCTGTGTCTATTATT
ATATTATATCTCTACGCTGCAAAATTTGGGTCTCAATTTTACTGTGCCTTTGTTTTTACTAGTGTCTGCTGTT
GCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTGTCCAAAGTTAATTTAATCTATACAATTAAAC
CTTTTGCCATCACTCTGGACTTTTGATTGTTTTTACATTCAAGTGTATAATTTGATTATGCTGATTGGTT
TTGGTGGGTACTGATGCGAATTAATAAAAACATTTTCATTTCC

WO 2004/030615

PCT/US2003/028547

352/6881
FIGURE 324A

GTTTTGTAACCTCAACTGGCCGGCTTCCTGGCCAAGCAGCAGAACAAATACAAATATGAAGAGTGCAAAGACCTCA
TAAATCTATGCTGAGGAATGAGCTACAGTTCAAGGAGGAGAAGCTTGAGAGCAGCTGAAGCAAGCTGAGGAGC
TCAGGTGAGGGGACCCCATGGGGGCAGGCAGGGGGCAGGTGTGTAATCTCTGAAGTACAACAGCTCGGTGGGG
AGACTTAAGAGCTAAGCTGGGCCAGGGGAAGGGCAGGAATTGCCATGGCAGGCTCGCTACACACAAATATTTATC
AAACAGAGAAGAAGGATAATAAAAAATTTATGGGTTGCAGTGTCTCAGAGCCTGTTTTCTTTTTTCAAACAAGT
AATGTTGATGTGAAATTTACATAACACAAAATTAACCAAAGGAGTGTGAACCACACAGCAGCATTAGTATACTC
AAAATGGTGTGCCATCACCACCCCACTTACCCTAGTGAGAATCACCTCCTGACTGACTGCGGCTTCTCATTCTTT
CACTCAATCAATGTTGCCTTCTCGACCCTGTCATTCTTTCTTCTTTCGTCTTTTCAATTGCGCCTATCTGCATC
TGGCCTCATTCTGTACATGGCTTTGTATCTAATGGCCGCAAGATGCACTATGTGTATTTTACATGGAAATGTC
CATGGCCAGAGTGAGGAAGTGAAGGATGTCTTTTTGAAACGGAATTAGGAAGACACCTACTTTTGTTTACAGAG
GGGAAAGATGAATGGAACATCATCGAGGATCTTGACAGGAGCCCTCTCTGATACAGAGGAAGCCTGTAAACCATTT
TCTATTCTTTCTCTTGGCCACAGACATTCCTTTCAACATGTGCTGACCTTCTGCTTGGAGGTCTCCTTGAGGACA
TTGCTCTAGAAATCTCTGTTGCAATATTTGAACGGATCACTCAACCCCTTCCACTCTTAAATTTCTCTACCGTC
TCACCTTAGGCAATATAAAGTCTCGGTTCACTCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTACGGGA
AGGGAGAGATGCCTCCCGCTCATTGAATGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCA
GGGGCAGGACCTCCAAGAACAGCTGGCTGAGGGGTGTAGACTGGCACAACACCTTGTCAAAAGCTCAGCCCAGA
AAATGATAACGATGACGATGAAGATGTTCAAGTTGAGGTGGCTGAGAAAGTGAGAAATCGTCTTCCCCCAGGGA
GATGCAGAAGGCTGAAGAAAAGGAAGTCCCTGAGGACTCACTGGAGGAGTGTGCCATCACTTGTTCAAATAGCCA
TGGCCCTTATGACTCCAACCAGCCACATAGGAAAACCAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCT
CATTGGCTCATCTCTCATGTTGAATGGGAGGATGCTGTACACATTATCCAGAAAATGAAAGTGATGATGAGGA
AGAGGAAGAAAAGGGCCAGTGCTCTCCAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCCAGGAGTCCCTG
GGATGAAGGTTATTGACTCTCTCAATTCCCTCCTGAAAGGTTGGCCTCATACCAGTCTTACAGCAGCACATTTCA
CTCATTAGAGGAACAGCAAGTCTGCATGGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAGGAGGA
CCAAGAGGCAACAGGTCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGACAGGACTCACT
GGATAGATGTTATTCAACTCCTTCAGTTTATCTTGGACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTA
CGTATTGGAGCAACAGCGTGTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGA
CCAAGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGACAGGACTCACT
GGATAGATGTTATTGACTCCTTCAGGTTATCTTGAATGCTGACTTAGGCCAGCCCTACAGAAGTGCTGTTTA
CTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGA
CCAAGGCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGACAGGACTCACT
GGATAGATGTTATTCAACTCCTTCCAGTTGTCTGAACAGCCTGACTCCTGCCAGCCCTACAGAAGTTCCTTTTTA
TGCATTGGAGGAAAACATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAG
AAGGGGAAGAAGATCAAAGAAGAAAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCC
CAGGCTCAACAGCGTGTGATGGAAGTGGAAGAGCCTGAAGTCTTGACAGGACTCACTGGATAGATGTTATTTCGAC
TCCATCAATGTACTTTGAACACTACCTGACTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTGTAGGAACAGCA
CATCACCTTTGCCCTTGACATGGACAATAGCTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTCTTCCAGAT
GGGAGTCATATTCCACAAATAAGCAGCCCTTACTAAGCCGAGAGGTGTCATTCTGACGGCAGGACCTATAGGCA
CCTGAAGATTTGAATGAACTATAGTTCCATTGGAAGCCCAGACATAGGATGGGTGAGTGGGCATGGCTCTATT
CCTATTCTCAGAGCATGCCAGTGGCAACCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTT
CACATAACTGTGCAGCACATGCCGGGAGTGATCAGCCGGACATTTTAATTTGAACCATGTATCTCTGGGTAGCTA
CAAAATTCCTCAGGGATTTTCAATTTGACAGGCATGTCTCTGAGCTTCTATACCTACTCAAGGTCAGTGTCTCTT
GTGTTTAGTTTATCCAAAGGTGTTACCCTGGTTTCAATGAACCTAACCTCATTATTTGTGTCTTCAGTGTGGCT
TGTTTTAGCTGATCCATCTGTAACACAGGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCT
TGACAATTGTTAACCCGCTAGGCTCCTTTGGTTAGAGAAGCCACAGTCTTCAGCCTCCAATTGGTGTGAGTACT
TAGGAAGACCACAGCTAGATGGACAAACAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCATCCTGTAGA
GAACAGGAGTCAGGAGCCGCTGGCAGGAGACAGCATGTCACCCAGGACTCTGCCGGTGCAGAATATGAGCAATGC
CATGTTCTTGACAGAAAACGCTTAGCCTGAGTTTCATAGGAGGTAATCACCAGACAAGTGCAGAAATGTAGAACACT
GAGCAGGACAACCTGACCTGTCTCCTTACATAGTCCATATCACCACAAATCACACAACAAAAGGAGAAGAGATA

WO 2004/030615

PCT/US2003/028547

353/6881
FIGURE 324B

TTTTGGGTTGAAAAAAGTAAAAAGATAATTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCTCAT
CTTTTTGTTGTTGTCATTGATGGTGGTGACATGGACTTGTTTATAGAGGACAGGTCAGCTCTCTGGCTCAATGAT
CTACATTCTGAAGTTGTCTGAAAAATGTCTTCATGATTAAATTCAGCCTAAACTTTTTGCTGGGAACACTGCAGAG
ACAATGCTGTGAGTTTCCAACCTCAGCCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATAT
CAGGACTGGTTACTTGGTTAAGGAGGGGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTA
CTTGGGAAAGCGGTTTTCAAGAGTATAAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTAT
AATCCTCCCTGCCTGTGTCTATTATTATATACATATCTCTACGCTGCAAATTTTGGGTCTCAATTTTACTGTGC
CTTTGTTTTTACTAGTGTCTGCTGTTGCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTGTCCAAAG
TTAATTTTAATCTATACAATTAAAACCTTTTGCCTATC

WO 2004/030615

PCT/US2003/028547

354/6881
FIGURE 325

MLRNELQFKEEKLAELKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSINEHLQALLTPDEPDKSQGQDL
QEQLAEGCRLAQHLVQKLSPENDNDDDEDVQVEVAEKVQKSSSPREMQAEEKEVPEDSLEECAITCSNSHGPYD
SNQPHRKTITFEEDKVDSTLIGSSSHVEWEDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEVEVPQESWDEGY
STLSIPPERTSVGSSEKGGPRGNRSQAQQAAG

WO 2004/030615

PCT/US2003/028547

355/6881
FIGURE 326

CTCCGCGGTCTTCTGAGCGGTCACGTGAACGGCTTCCTGCAGGCTGGCCATGGCGCTTCAAGTTCCCAAGGCTCC
GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAATGGTTATCAACTA
CTTGAGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAAGAAAGCTCATGAGATTCTTCCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAAAAATCTGGG
CTGTGGTATCACTTCCTCTTCAGTATTGCATGGCATGGTTTTTAAGAAGGAAACAGAAGGTGATGTACATCTGTC
AAAGATGCAAAAATAGCAGTGTACTCTTGTCCTTTTGATGGCATGATAACAGAACTAAGGGAAACAGTGTGATA
AAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAAATCTCATGGATGCATAAGTCAAAGCTATTGCT
GATACTGGTGCAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGCAAAACAAATATAAT
ATGATGTTAGTGAAGCTAAACTCAAAATGGGATGTCTGAAGACTCTGTAAAAACAGTTGGTGCTACAGCTCTTCCT
AGATTGACACCTCCTGTCTTGAAGAAATGGGACACTGAGACAGTGTTCCTCTCAGAAGTTGGAGATACTCAG
GTGGTGGTTTTTAAGCATGAAAAGGAAGATGGCATCATTCTACCATAGTACTTCAGGGCTCTACAGACAATCTG
ATGGATGACATAGAAAGGGCAGTAGATGATGGTGTAAATACTTTCAAAGTTCTTACAAGGGATAAACGTCTTGTA
CCCGGAGGTGGAGCAACAGAAATTGAATTAGCCAAACAGATCACATCATATGGAGAGACATGTCTGGACTTGAA
CAGTACGCTATTAAGAAGTTTGCTGAGGCGTTTGAAGCTATTCCCCGTGCACTGGCAGAAATACTCTGGAGAAAA
CTCTGGAGTTAAGGCCAATGAAGTAATCTCTAAACTTTATGCAGTACCTCAAGAAGGAAATAAAAAATGTTGGATT
AGATACTGAGGCTGTAGTCCCTGCTGTAACGGACATGTTGGAAGCTGGTGTCTAGATACTTACCTGGGAAAACA
CTGGTCTATCAAACCTCGCTGCTAATGCTGCAGTCACTGTACTTAGAGTGGGTCAGGTAATCATGGCAAAACCAGA
TGGTGGGCCCAAGCCTCCAAGTGGGAAGAAAGACTGGGATGATGACCAAAATGATTGAAATTGGCTTAATTTTA
CTGTAGGTGAAGGCTGTATTTGTAGTAGTATTCTAAGAATCGCGTGATGTTTTCTTATTCTCCTTACATTAAGAG
GTATTTTGTGTTTGTATTCTTGGCTGGATGTTATAATAAACATATTGTTACTGTC

WO 2004/030615

PCT/US2003/028547

356/6881
FIGURE 327

GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAATGGTTATCAACTA
CTTGGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAAGAAAGCTCATGAGATTCTTCCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAAAATTCTGGG
AACAGTGTGATAAAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAATCTCATGGATGCATAAGT
CAAAGCTATTGCTGATACTGGTGCAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGC
AAACAAATATAATATGATGTTAGTGAAGCTAAACTCAAATGGGATGTCTGAAGACTCTGTAAAACAGTTGGTGC
TACAGCTCTTCCTAGATTGACACCTCCTGTCCTTG

WO 2004/030615

PCT/US2003/028547

357/6881
FIGURE 328

GTGGGTAGGAGCTTGCTTATAGAAAAGTGGAATCGAGTAGTCCTTGCTGGTGGAGCCGCTGCCGCCAGGGAACTC
AGGGCCGGCTCCTGTTTCCTTCAAGAGTGCTGGAGGCCAAACTTGAAATACAAGTTTAATGTTCTCGTCGGGCAA
AAGATAAGGATCCGATCTCCCCGGCCCGGTGTGCAGCAGGAGCGACCAACCCCGACCCGGGTAAAACTCCAG
GGACTCTTCGCTGCTGCCACCTCTTGTTCTCTCCCCGTTCCTACTCGGGGTCTCCCTCAGGGCCGGGAGGCACA
GCGGTCCCTGCTTGCTGAGGGGCTGGATGTACGCATCCGCAGGTTCCTCGCGGACTTGGGGGCGCCCGCTGAGCCC
CGGCGCCCGCAGAAGACTTGTGTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATC
ACTGGTGTGTTTCAGCATGCGCTTGTTGGACCCAGTGGGCGTCTTGACCTCGCTGGCGTACTGCCTGCACCAGCGG
CGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCTGAAGTTGAAAAATG
GTGCAGGTGCTGTTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCCGCTGGAGGAGCAGGTAGAGTGGAAC
CCCCAGCTATTAGAGGTCCACCCCAAACCTCAGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCA
TATTCTCCTTACGACTCTCAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTG
GGCATGCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTACCA
ACCTTCAACCCACAGGAGGTCTTTATTCTGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCGTGTTTGCTG
GCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCATCCACACTGATGAAGCAGATTGAGAACTCTTGAT
CCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGA
ATCTCAGAGGATTTGAAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTC
CTGGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATC
GAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGGGAAAGTCTTCAGATGGCAGTAGGC
CCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGCCCCGACAAGATCAGAAAG
CTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGGACCACAAATGG
CCACCGTTTGCTGTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTAT
TACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCTGGACATGTTCTTGAATGCCATG
TCAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAATGAA
GAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTAAAAATAAAGTGCCTTTATACAATGCCAAAAAAAAAAAA
AAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

358/6881
FIGURE 329

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMOVVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRTASLQ
PGISEDLLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPDLMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

WO 2004/030615

PCT/US2003/028547

359/6881
FIGURE 330

CTTAAAGTGAAATAATTTTTTGCAAAGGGGTTTCCTCGATTGGAGCTTTTTTTTTCTTCCACCGTCATTTCTAA
CTCTTAAAACCAACTCAGTTCCATCATGGTGATGTTCAAGAAGATCAAGTCTTTTGAGGTGGTCTTTAACGACCC
TGAAAAGGTGTACGGCAGTGGCGAGAAGGTGGCTGGCCGGGTGATAGTGGAGGTGTGTGAAGTTACTCGTGTCAA
AGCCGTTAGGATCCTGGCTTGCGGAGTGGCTAAAGTGCATCCTCAACAACAATGTGCAGTGAGCATGTGGAAGAA
AAGAAGCAGCTTTACCTACTTGTCTTTTTGTCTCTCTTCTGGACACTCACTTTTTTCAGAGACTCAACAGTCT
CTGCAATGGAGTGTGGGTCCACCTTAGCCTCTGACTTCCTAATGTAGGAGGTGGTCAGCAGGCAATCTCCTGGGC
CTTAAAGGATGCGGACTCATCCTCAGCCAGCGCCCATGTTGTGATACAGGGGTGTTTGTGGATGGGTTAAAAA
TAACTAGAAAACTCAGGCCCATCCATTTTCTCAGATCTCCTTGAAAATTGAGGCCTTTTCGATAGTTTCGGGTC
AGGTAAAAATGGCCTCCTGGCGTAAGCTTTTCAAGGTTTTTGGAGGCTTTTGTAAATTGTGATAGGAACTTTG
GACCTTGAACTTATGTATCATGTGGAGAAGAGCCAATTTAACAACTAGGAAGATGAAAAGGGAATTGTGGCCA
AACTTTGGGAAAA

WO 2004/030615

PCT/US2003/028547

360/6881
FIGURE 331

TGACTTGCTCACTATCATGAACTCAAAAGAACTAGCAATTTTTTAGACTTCCTTTGGGATCCTTGTAACGCATC
CTATACTGCTTTTATGTTTCATGTGTGCATTTGTGTACATGTATACACATATTACTCCATAACGAAGCACAGTCTT
CTTTTATACCTTTCCCTGGTTGGGGTAGTAGAGGAATTTTACAGCCTACAATCAGACACATCCAGAAGAAGAGTGG
AATATGTATGATACCTTAAAAATCAGCACATTTAACAAAGTATAACTTACTCATGGTTACAACCTAAGTTAATGTT
TTTTCCCTTTATTTTTCAAAAGGCTCATTTTTCTCCATTTCTCTACTATCAAAGTCAAGAACTGCCAATGGCTC
TGTC AAGGAGGCTCCAGCTCCTACTCCCACTTCTCTGGAAGTCTCAAGTCCACCAGATACTACAGAGGAAGAAGA
TCATAAGCCTAAACTCTGCAGGCTGGCTAAAGGTGAAAATGGCTATGGCTTTCACTTAAATGCGATTTCGGGGTCT
GCCAGGCTCATTCATCAAGAGGTACAGAAGGGCGGTCTGCTGACTTGGCTGGGCTAGAGGATGAGGATGTCAT
CATTGAAGTGAATGGGGTGAATGTGCTAGATGAACCCATGAGAAGGTGGTGGATAGAATCCAGAGCAGTGGGAA
GAATGTCACACTTCTAGTCTGTGGAAAGAAGGCCTATGATTATTTCCAAGCTAAGAAAATCCCTATTGTTTCCTC
CCTGGCTGATCCACTTGACACCCCTCCAGATTCTAAAGAAGGAATAGTGGTGGAGTCAAAGCATGACTCGCACAT
GGCAAAAGAACGGGCCACAGTACAGCCTCACATTTCTTCCAATTCTGAAGATACAGAGATGTGATGAAAACA
AGCGGCTATTGCAGACGGCTAATTTATGCTTAACCTAGGAAGAGATAAGGTTTCCTTGAGCACCAAAGATGATTCA
TAACTCTGTATAGGTGACAGCTGCTTATAAAAGCATCTTAGCAGATAAGCCTATTAAAATTGTGCTTTTGTAACA
ATGTTGTGGTTGCTAGAATAAATACCATTAAACAAA

WO 2004/030615

PCT/US2003/028547

361/6881
FIGURE 332

GTCCCAACTCTTGGA CTCCATTTGCTATTCTCTTTCTCCCCACACCTATCTGGTGGTGGTAGTGGGCGTTT
ATATTTGCGTTCCTTTTCATTCAATTTCTAAATCTCTTAAAAATTTGGGTGGGGGTATTGGGGAAGGCAGGAAA
GGGAAAAGGAGAGTAGTAGCTGAAGAGCAAGAGGAGGACATGGAGATGAAGAAGAAGATTAACTGGAGTTAAGG
AACAGATCCCCGGAGGAGGTGACAGAGTTAGTCCTTGATAATTGCCTGTGTGTCAATGGGGAAATTGAAGGCCTG
AATGATACTTTCAAAGAACTAGAATTTCTGAGTATGGCTAATGTGGA ACTAAGTTCGCTGGCCCGGCTTCCCAGC
TTAAATAAACTTCGAAAATTGGAGCTTAGTGATAATATAATTTCTGGAGGCTTGGAAGTCCTGGCAGAGAAATGT
CCAAATCTTACCTACCTCAATCTGAGTGGAAACAAAATAAAAGATCTCAGTACAGTAGAAGCTCTGCAAAATCTT
AAAAATTTGAAAAGTCTTGACCTGTTTAACTGTGAGATCACAAACCTGGAAGATTATAGAGAAAGTATTTTTGAA
CTACTGCAGCAAATCACATACTTAGATGGATTTGATCAGGAGGATAATGAAGCGCCGGACTCTGAAGAGGAGGAT
GATGAGGATGGAGATGAAGATGATGAAGAGGAAGAGGAAAATGAAGCTGGTCCACCGGAAGGATATGAGGAAGAG
GAGGAGGAAGAGGAAGAGGAGGATGAGGATGAGGATGAAGATGAAGATGAAGCAGGTTGAGAGTTGGGAGAGGGA
GAAGAGGAAGTGGGCCTCTCATACTTAATGAAAGAAGAAATTCAGGATGAAGAAGATGATGATGACTATGTTGAA
GAAGGGGAAGAAGAGGAAGAAGAGGAAGAAGGAGGTCTTCGAGGGGAGAAGAGGAAACGAGATGCTGAAGACGAT
GGAGAGGAAGAAGATGACTAGATCATTCTAAGACCAGATTCTCTAATGTTTCTGGGTGTGCAATAGAGTGATCAC
ATCTTTGTTTCTTCATGTACGATAGCTATCCCTACAGAAGATAATGTGTAACTTTTATAGGAAAAGTGTGGTTT
TACTATTTTGCCTTATCATTCCAAATAAGAACTAGTCTGTTAATGATCATATTGTATGTAGAGAAAAATTTTCA
TTGACTCCCATTGTGGAATTCCCTAGCAATTTATTTAGACTTAATTTTTTAAATTCAAGCTTACTGTATTAGTCA
TTTTTAGCCCATAAATTAACATGATCACTTTTAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

362/6881
FIGURE 333

MEMKKKINLELRNRSPEEVTELVLNCLCVNGEIEGLNDTFKELEFLSMANVELSSLARLP SLNKL RKLELS DNI
ISGGLEVLA EKCPNLTYLNLSGNKIKDLSTVEALQNLK NLKSLDLFNCEITNLEDYRESIFELLQQITYLDGFDQ
EDNEAPDSEEEDEDEDGEDDEEEENEAGPPEGYEEEEEEEEDEDEDEDEDEAGSELGEGEEVGLSYLMKEE
IQDEEDDDDYVEEGEEEEEEEEEGGLRGEKRKRDAEDDGEEEDD

WO 2004/030615

PCT/US2003/028547

363/6881
FIGURE 334

GTGGGGTCGCGTTGCCACCCACGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTCAGGCC
CCACCCCCCTTCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTCCGCCCCG
CCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCATTTTTCT
GGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGACCGACCGGTCAGATGCCCCG
TCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACA
AGCTGCTTAAGAAGGCAGATGAGGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGA
TGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCAC
TTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCCTGACTTCAGCCTTTCTGACAGCAGCCA
TTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCGTGTGAGAGGAGACGGTACTGGGCTTTGGGCC
TGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCA
TCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCA
GCTCTTGTGTAAGGACTGACTACCTGGACTGATCGCCTGCAGATCCCACCTGCCTGTCCACTGCCCATGACTGA
GCCCAGCCCCAGCCCGGGTCCATTGCCACATTCTCTGTCTCCTTCTCGTCGGTCTACCCCACTACCTCCAGGG
TTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTTTACCAGGAGCAGCCTGGGTTTCAGCCAGTCAGTGACT
GGTGGGTTTGAATCTGCACTTATCCCCACCACCTGGGGACCCCTTGTTGTGTCCAGGACTCCCCCTGTGTCACT
GCTCTGCTCTCACCTTGCCCAAGACTCACCTCCCTTCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT
GGTGTATTCTGCCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGCCTGGGGTGCCCTC
CTGATGTCTCTGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCCAGGTTGCCAAGAAAAGGGACCTAGTTTA
GCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAAGGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGA
CTGGACATCTTGGTCTTTTTCTCAGGCCTGAGGGGGAACCATTTTTTGGTGTGATAAATACCCTAACTGCCTTTT
TTTCTTTTTTGAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTCTAACCTCCTTGGGCTATATTTCTCTCC
TCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCCAGACCTTGGGGGAAAGGAAGGAA
GTGCATGTTTGGGAACGGCATTACTGGAACATAATGGTTTTAACCTCCTTAACCACCAGCATCCCTCCTCTCCCC
AAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGCCACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCAT
GACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTAT
AAACTGTATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTAATCAAGGTGATTGTGATTTTACTAATAAA
AAAGAATTTGTAAAAAA

WO 2004/030615

PCT/US2003/028547

364/6881
FIGURE 335

MGA AVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVWFILVHVTD RSDARLQYGLLIFG
AAVSVLLQE VFRFAYYKLLKKADEGLASLSE DGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVG I H
GDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSSCVRTDYLD

WO 2004/030615

PCT/US2003/028547

365/6881
FIGURE 336

TTCCGGTGGGCTAGGTACTGAGCGCGCGAGGCTCTACAGAGTGAAGGTTTAAATCCAAGGTCAATGGCAAAACATC
TGAAGTTCATCGCCAGGACTGTGATGGTACAGGAAGGGAACGTGGAAAGCGCATACAGGACCCTAAACAGAATCC
TCACTATGGATGGGCTCATTGAGGACATTAAGCATCGGCGGTATTATGAGAAGCCATGCCGCCGGCGACAGAGGG
AAAGCTATGAAAGGTGCCGGCGGATCTACAACATGGAAATGGCTCGCAAGATCAACTTCTTGATGCGAAAGAATC
GGGCAGATCCGTGGCAGGGCTGCTAGAGGCCTGTGGGTGGGACACCCAGTGCGAAACCCTCATCCAGTTTTCTCTC
CATCTCTTTTCTTTGTACAATCCCATTTCTATTACCATTTCTCTGCAATAAACTCAAATCACATGTCTGCAAAAA

WO 2004/030615

PCT/US2003/028547

366/6881
FIGURE 337

MAKHLKFIARTVMVQEGNVESAYRTLNRILTMDGLIEDIKHRRYYEKPCRRRQRESYERCRRIYNMEMARKINFL
MRKNRADPWQGC

WO 2004/030615

PCT/US2003/028547

367/6881
FIGURE 338A

ATGTCCTCCACTTCTGAGAAGCATCTGTGACATCACTGAAATTTTCAATCAGTATGTCTCTCATGATTGTGATGGA
GCAGCATTAACTAAGAAAGACCTGAAGAACCCTCCTTGAAAGGAATTTGGAGCTGTGCTTCGGAGACCACATGAC
CCTAAGACGGTAGATCTGATCCTGGAACCTTCTGGATCTTGACAGTAATGGCGTGTCGATTTCAACGAATTCCTC
CTATTTATTTTCAAAGTGGCTCAAGCTTGTTACTATGCTCTCGGCCAGGCCACGGGACTGGATGAGGAGAAGCGA
GCCCGGTGTGACGGAAGGAGAGCCTGTTACAAGATCGCAGGCAAGAAGAAGACCAAAGGAGATTTCGAGCCCCGG
GACAGACAACCTGGAAGAAGAACCTGGGCAACGACGCAGGCAGGAAGAGGACAGGAGAGGGAGCTAGCTGAG
GGAGAGGAGCAAAGTGAGAAACAAGAGCGACTTGAAACAGCGCGACAGGCAGCGCCGCGACGAGGAGCTGTGGCGG
CAAAGGCAAGAATGGCAAGAACGGGAAGAGCGCCGTGCAGAGGAAGAGCAGCTGCAGAGTTGCAAAGGTCACGAA
ACTGAGGAGTTTCCAGACGAAGAGCAACTGCGAAGGCGGGAGCTGCTGGAGCTGAGGAGGAAGGGCCGCGAGGAG
AAACAGCAGCAAAGGCGAGAGCGGCAAGACAGAGTGTTCAGGAGGAAGAAGAGAAAGAGTGGAGGAAGCGCGAG
ACAGTGCTCCGGAAGGAAGAAGAGAAGCGCGAACGTTGGCTGAAGCTCGAGGAGGAGGAGAGGCGCGAGCAGCAG
GAGAGGCGCGAGCAGCAACTAAGGCGGGAGCAAGAGGAGAGGCGCGAGCAGCGGCTGAAGCGCCAGGAGGAGGAA
GAGAGGCTCCAGCAGCGTTGAGGAGCGAGCAACAATAAGACGCGAGCAGGAGGAGAGGCGCGAGCAGCTGCTG
AAGCGCGAGGAGGAGAAGAGGCTCGAGCAGGAGAGGCGAGAGCAGCGGCTGAAGCGCGAGCAGGAGGAGAGGCGC
GATCAGCTGCTGAAGCGCGAGGAGGAGAGGCGCCAGCAGCGGCTGAAGCGCGAGCAGGAAGAGAGGCTCGAGCAG
CGACTGAAGCGCGAGGAGGTGGAGAGACTCGAGCAGGAGGAGAGGCGCGAGCAGCGGCTGAAGCGCGAGGAGGCCG
GAGGAAGAGAGGCGCCAGCAGCTGCTGAAGAGCGAGGAGCAGGAGGAGAGGCGCCAGCAGCAACTAAGGCGCGAG
CAGCAGGAAAGGCGCGAGCAGCGGCTGAAGCGCGAGGAGGAGGAAGAGAGGCTCGAGCAGCGGCTGAAGCGCGAG
CATGAGGAAGAGAGGCGCGAGCAGGAGCTAGCTGAGGAGGAGCAGGAACAGGCCGGGAGCGGATTAAGAGCCGC
ATCCCGAAGTGGCAGTGGCAGCTAGAAAGCGAGGCCGACGCACGGCAAAGCAAAGTCTACTCGAGGCCCGCAAG
CAGGAAGGGCAGAGGCGCCGCAAGAGCAGGAGGAAAAGAGGCGGCGCCGGGAGAGTGAGCTGCAATGGCAGGAG
GAGGAACGGGCTCACCGGCAGCAGCAGGAAGAGGAGCAGCGCCGGGACTTCACATGGCAGTGGCAGGCGGAGGAA
AAGAGCGAAGAGGGGCCGTGAGAGGCTGTCGGCCAGGCCCCATTGCGGGAGCAGCGGGAGAGGCAGCTGAGGGCC
GAGGAGCGCCAGCAGCGGGAACAACGGTTTCTCCGGAGGAGGAGGAGAAGGAGCAGCGGCGCCGCCAGCGACGC
GAGAGGGAGAAAGAGCTGCAGTTCTTGGAGGAAGAGGAGCAGCTCCAGCGGCGGGAGCGTGCCCAACAGCTCCAG
GAGGAGGAGGACGGCCTCCAGGAGGATCAGGAGAGGAGGCGAAGCCAGGAGCAGCGCCGCGACCAAAAATGGAGG
TGGCAACTAGAAGAAGAAAGGAAGAGACGCCGCCACACGCTGTACGCCAAGCCAGCCCTACAAGAGCAGCTGAGG
AAGGAACAGCAGCTGCTGCAGGAGGAGGAGGAGGAGCTACAGAGAGAGGAGCGCGAGAAGAGAAGGCGCCAAAGAA
CAGGAGAGACAATACCGCGAGGAAGAGCAGCTGCAGCAGGAGGAAGAGCAGCTGCTGAGAGAGGAACGGGAGAAA
AGAAGACGCCAGGAGCGGGAAAGGCAATATCGGAAGGATAAGAAGCTGCAGCAGAAGGAAGAGCAGCTGCTGGGA
GAGGAACCGGAGAAGAGAAGGCGCCAGGAGCGGGAGAAAATAACCGGAGGAAGAGGAGTTGCAGCAGGAGGAA
GAGCAGCTGCTGAGAGAGGAACGGGAGAAAGAGAAGGCGCCAGGAGTGGGAGAGGCACTACCGCAAAAAGAGCAG
CTGCAGCAGGAAGAAGAGCAGCTGCTGAGAGAGGAACGGGAGAAAAGAAGACTCCAGGAGCGGGAGAGGCAATAT
CGGGAGGAAGAGGAGCTGCAGCAGGAGGAAGAGCAGCTGCTGGGAGAGGAACGGGAGACGAGAAGGCGCCAGGAG
CTGGAGAGGCAATATCGGAAGGAAGAGGAGCTGCAGCAGGAGGAAGAGCAGCTGCTGAGAGAGGAACCGGAGAA
AGAAGGCGCCAGGAGCGGGAGAGGCAATGCAGAGAGAAATGAACAGTTCCGGCAGTTGGAAGATTCCAGCTGCGC
GACAGACAATCCCAGCAAGATCTGCAGCACCTGCTGGGTGAACAGTAAGAGCGAGATCGTGAGCAAGAGAGGAGG
CGCTGGCAGCAGCGCGACAGGCATTTCCAGAGGAAGAAGAGAGTGGAGCGAGAAGAGCAAAAGGAAGCCAAAAGG
CGCGACAGGAAGTCCCAAGAGGAAAAGCAGTTGCTGAGAGAGGAAGAAGAGAAGAGACGCCGTCAAGAGACA
GACAGAAAATTCGCGAGGAGGAACAGCTGCTCAGGAAAGGGAGGAACAGCCGCTGCGCCGCCAAGAGCGTGAC
AGAAAATTCGCGAAGAGGAACCTGCGCCATCAGGAACAAGGGAGAAAATTCCTCGAGGAGGAACAGCGGCTGCGC
CGCCAGGAACGGGAGAGAAAATTCCTTAAGGAGGAACAGCAGCTGCGCTGCCAGGAGCGCGAGCAACAGCTGCGT
CAGGACCGCGACAGTAAATTCGCGAGGAGGAACAGCAGCTGAGCCGCCAAGAGCGTGACAGAAAATTCGCTGAA
GAGGAACAGGAGTGCAGCGCCAGGAACGAGAGAGAAAATTCCTGGAGGAGGAACAGCAGCTGCGCCAGGAGCGT
CACAGAAAATTCGCGAAGAGGAACAGCTGCTCAGGAAAGGGAGGAACAGCAGCTGCACCGCCAAGAGCGTGAC
AGAAAATTCCTGGAGGAGGAACAACAGCTGCGCCGCCAAGAGCGTGACAGAAAATTCGCGAACAGGAACCTGCGC
AGTCAGGAACAGAGAGAAAATTCCTCGAGGAGGAACAGCAGCTGCACCGCCAGCAACGGCAGAGAAAATTCCTC
CAGGAGGAACAGCAGCTGCGCCGCCAGGAGCGCGGGCAACAGCGGCGTCAGGACCGTGACAGAAAATTCGCGGAG

WO 2004/030615

PCT/US2003/028547

368/6881

FIGURE 338B

GAGGAACAGCTGCGCCAGGAGAGGGAGGAACAGCAGCTGAGCCGCCAAGAGCGTGACAGAAAATTCCGTTTAGAG
GAACAGAAAGTGCGCCGCCAGGAACAAGAGAGAAAATTCATGGAGGACGAACAGCAGCTGCGCCGCCAGGAGGGC
CAACAACAGCTGCGCCAGGAGCGCGACAGAAAATTCGCGAAGACGAACAGCTGCTCCAGGAAAGGGAAGAACAG
CAGCTGCACCGCCAAGAGCGTGACAGAAAATTCCTCGAGGAGGAACCGCAGCTGCGCCGCCAGGAGCGCGAACA
CAGCTGCGTCACGACCGCGACAGAAAATTCCTGTAAGAGGAACAGCTGCTCCAGGAAGGGGAGGAACAGCAGCTG
CGCCGCCAAGAGCGTGACAGAAAATTCGCGAAGAGGAACAGCAGCTCCGCCGTCAGGAACGAGAGAGAAAATTC
CTCCAGGAGGAACAGCAGCTGCGCCGCCAGGAACCTGGAGAGAAAATTCCTGAGGAGGAACAGCTGCGCCAAGAA
ACGGAGCAAGAGCAGCTGCGCCGCCAAGAACGCTACAGAAAATCCTAGAGGAAGAGCAGCTCCGTCCGGAAGG
GAAGAACAGCAGCTGCGCCGCCAGGAGCGCGACAGAAAATTCGCGAGGAGGAACAGCTCCGCCAGGAGAGGGAG
GAACAGCAGCTGCGCAGCCAAGAGTCTGACAGAAAATTCGCGAGGAGGAACAGCTACGCCAGGAGAGGGAAGAA
CAGCAGCTGCGCCCCAACAGCGTGACGGAAGTATCGCTGGGAAGAAGAGCAGCTCCAACCTTGAGGAACAAGAG
CAGAGGCTGCGGCAGGAGCGGAGACCGGCAGTACCGGGCGGAGGAGCAGTTTGCCACGCAGGAGAAGAGTCGTCTGT
GAGGAACAAGAACTATGGCAAGAAGAGGAGCAGAAACGTCGCCAGGAACGGGAAGGAAATTACGGGAAGAACAC
ATCCGCCGCCAGCAGAAGGAGGAACAGAGGCACCGCCAAGTCGGGGAGATAAAATCCCAAGAAGGGAAGGGCCAT
GGGCGGCTTCTGGAGCCCGGCACTCATCAGTTTGCCAGTGTCCAGTGCGCTCCAGCCCTCTCTATGAGTACATC
CAAGAGCAGAGATCTCAATACCGCCCTTAA

WO 2004/030615

PCT/US2003/028547

369/6881
FIGURE 339

MSPLLRSIDITEIFNQYVSHDCDGAALTKKDLKNLLEREFGAVLRRPHDPKTVDLILELLDLDSDNGRVDFNEFL
LFIFKVAQACYALGQATGLDEEKRARCDGKESLLQDRRQEEDQRRFEPDRDQLEEEPGQRRRQKRQEERELAE
GEEQSEKQERLEQDRDRRDEELWRQRQEWQEREERRAEELQSCKGHETEEFPDEEQLLRRRELLELRRKGREE
KQQRRRERQDRVFQEEEEKEWRKRETVLRKEEEKRERWLKLEEEERREQQERREQQLRREQEERREQRLKQEEE
ERLQQLRSEQQLRREQEERREQLLKREEEKRLQEERREQRLKREQEERRDQLLKREEERRQQLKREQEERLEQ
RLKREEVERLEQEERREQRLKREEPEEERRQQLLKSEEQEERRQQLRREQEERREQRLKREEEEEERLEQRLKRE
HEERREQELAEELQEQARERIKSRIPKWQWQLESEADARQSKVYSRPRKQEGQRRRQEQEERRRRRESELQWQE
EERAHQQQEEEQRRDFTWQWQAEKSERGRQLSARPPLEQRERQLRAEERQQREQRFLEPEEEKEQRRRQRR
EREKELQFLEEEQLQRRERAQQLQEEEDGLQEDQERRRSQEQRRDQKWRWQLEEEERKRRRHTLYAKPALQEQLR
KEQQLLQEEEEEELQREEREKRRRQEERQYREELQLEEEQLLREEREKRRRQERERQYRKDKKLQKKEEQLLG
EEPEKRRRQEREKKYREELQLEEEQLLREEREKRRRQEWERQYRKDELQLEEEQLLREEREKRRRQERERQY
REELQLEEEQLLGEERETRRRQELERQYRKEELQLEEEQLLREEPKRRRQERERQCRENEQFRQLEDSQLR
DRQSQQDLQHLLGEQQERDREQERRWQQRDRHFPEEEQLEREQKEAKRRDRKSQEEKQLLREEREKRRRQET
DRKFREELQLEEEQLLQERERDRKFREELRHQEQGRKFLEEEQLLRRQERERKFLKEEQQLRCQEREQQLR
QDRDRKFREELQLSRQERDRKFREELQVRRQERERKFLKEEQQLRQERHRKFREELQLEEREQQQLHRQERD
RKFLKEEQQLRRQERDRKFREELRSQEPERKFLEEEQLLHRQQRQKFLQEEQQLRRQERGGQQQLRQERDRKFREDEQLLQEREQQ
EEQLRQEREQQLSRQERDRKFRLEEQVRRQEERKFMEDQQLRRQEGQQQLRQERDRKFREDEQLLQEREQQ
QLHRQERDRKFLEELPQLRRQEREQQLRHDDRDRKFREELQLEEGEEQQLRRQERDRKFREELQQLRRQERERKF
LQEEQQLRRQELERKFREELQLEETEQQQLRRQERYRKILEEQQLRPEREEQQLRRQERDRKFREELQLEERE
EQQLRSQESDRKFREELQLEEREQQLRPQQRDGKYRWEEELQLEEQQLRQERDRQYRAEEQFATQEKSRR
EEQELWQEEQKRRQERERKLREEHIRRQQKEEQRRHQVGEIKSQEGKGHGRLLLEPGTHQFASVPVRSSPLYEYI
QEQRSQYRP

WO 2004/030615

PCT/US2003/028547

370/6881
FIGURE 340

GGGCAAGGCTGGGCCGGAAGGGCGTGGGTTGAGGAGAGGCTCCAGACCCGCACGCCGCGCGCACAGAGCTCTCA
GCGCCGCTCCCAGCCACAGCCTCCCGCGCCTCGCTCAGCTCCAACAATGGCAAAAATCTCCAGCCCTACAGAGACT
GAGCGGTGCATCGAGTCCCTGATTGCTGTCTCCAGAAGTATGCTGGAAAGGATGGTTATAACTACACTCTCTCC
AAGACAGAGTTCCTAAGCTTCATGAATACAGAACTAGCTGCCTTCACAAAGAACCAGAAGGACCCTGGTGTCTT
GACCGCATGATGAAGAACTGGACACCAACAGTGATGGTCAGCTAGATTCTCAGAATTTCTTAATCTGATTGGT
GGCCTAGCTATGGCTTGCCATGACTCCTTCCTCAAGGCTGTCCCTTCCCAGAAGCGGACCTGAGGACCCCTTGGC
CCTGGCCTTCAAACCCACCCCTTTCTTCCAGCCTTTCTGTCATCATCTCCACAGCCCACCCATCCCCTGAGCA
CACTAACCACCTCATGCAGGCCCCACCTGCCAATAGTAATAAAGCAATGTCACCTTTTTTAAACATGAAA

WO 2004/030615

PCT/US2003/028547

371/6881
FIGURE 341

MAKISSPTETERCIESLIAVFQKYAGKDGNYTLSKTEFLSFMNTELAFTKNQKDPGVLDMMKKLDTNSDGQL
DFSEFLNLIGGLAMACHDSFLKAVPSQKRT

WO 2004/030615

PCT/US2003/028547

372/6881
FIGURE 342

CCGGTGGGGCGGGAAGCCCGGCTTCTGGGGAGGTGCCGCCCCCTCCACTGGCGCAGGCCGCCGAGACCCCCAGACG
GACCTCCTAGGGCTAATCTGATAGTGCCTCTGAGGTCGATAGGACTCCACGTGCCACTCCCTGCAGGGTCATCCA
GCAAGTAATTCCTAGACCCGTAGGTGGCCGCAGAGCCGGTTACCTCTGGTTCTGCGCCAGCGTGCCCCACCCGCA
GGACGGCCGGGTTCTTTGATTTGTACACTTTCTAAAACCAAACCCGAGAGGAAGGGCAGGCTCAGGGTGGGGATG
CCCTGAAATATTCGAGAGCAGGACCGTTTCTACTGAAGAGAAGTTTACAAGAACGCTCTGTCTGGGGCGGGCGAG
GCCTCTGCGAGGCGGGTCCGGGAGCGAGGGCAGGGCGTGGGCCGCGCGCCCGGGGTCGGGGGAGTCGGGGGCAGG
AAGAGGGGGAGGAGACAGGGCTGGGGGAGCGCCCTGCCGAGCGCCCGCCAGGCTCCTCCCGCTCCCGCGCCGCT
CCCTCTACCCACCCGCCGCACGTACTAAGGAAGGCGCACAGCCCGCCGCGCTCGCCTCTCCGCCCCGCGTCCAGC
TCGCCCAGCTCGCCAGCGTCCGCCGCGCCTCGGCCAAGGCTTCAACGGACCACACCAAAATGCCATCTCAAATG
GAACACGCCATGGAAACCATGATGTTTACATTTACAAATTCGCTGGGGATAAAGGCTACTTAACAAAGGAGGAC
CTGAGAGTACTCATGGAAAAGGAGTTCCCTGGATTTTTGGAAAATCAAAAAGACCCCTCTGGCTGTGGACAAAATA
ATGAAGGACCTGGACCAAGTGTAGAGATGGCAAAGTGGGCTTCCAGAGCTTCTTTTCCCTAATTGCGGGCCTCACC
ATTGCATGCAATGACTATTTTGTAGTACACATGAAGCAGAAGGGAAAGAAGTAGGCAGAAATGAGCAGTTCGCTC
CTCCCTGATAAGAGTTGTCCCAAAGGGTCGCTTAAGGAATCTGCCCCACAGCTTCCCCCATAGAAGGATTCATG
AGCAGATCAGGACACTTAGCAAATGTAAAAATAAAATCTAACTCTCATTTGACAAGCAGAGAAAGAAAAGTTAAA
TACCAGATAAGCTTTTGATTTTTGTATTGTTTGCATCCCCTTGCCCTCAATAAATAAAGTTCTTTTTTAGTTCC

WO 2004/030615

PCT/US2003/028547

373/6881
FIGURE 343

MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDGKVGFSFFSL
IAGLTIACNDYFVVHMKQKGKK

WO 2004/030615

PCT/US2003/028547

374/6881
FIGURE 344

CGGCTGAAGCGCCGCCGGCGGGGCTCACTGTGGTGGTGTGAGTGGGAGGCGGCGGCGCTGGTGGCTGCAGCTGGG
GTGAGGCGCGAGGCGGCGCACTCGACGGCTGACTGGAGCAGCGGTAAAGGCGAGGATGGAGACCGAAGGATATAA
GTCAAAGAGTACAGCAGAAAATGTCTACTGAACGGACTTCTTGGACAAGCCTGTCCACCATTTCAGAAAATAGCCC
TGGGCCTTGGGATCCCAGCCAGTGCAACAGTTGCCTATATCCTATACCGCAGGTATAGGGAAAGCAGAGAAGAGC
GGCTGACATTTGTTGGGGAAGATGACATTGAGATAGAGATGCGGGTTCCCCAGGAGGCTGTGAAACTCATCATTG
GCCGGCAAGGAGCCAAATATTAAACAGCTGCGGAAACAGACAGGTGCTCGGATTGATGTGGACACAGAGGATGTAG
GCGATGAGCGAGTGCTGCTTATCAGTGGTTTTCTGTTCAGGTGTGCAAGGCCAAAGCAGCAATCCATCAGATCC
TGACAGAGAATACCCAGTGCTGAGCAGCTTTCAGTTCCCCAGAGATCTGTGGGCAGAATCATAGGGAGAGGCG
GCGAGACAATTCGTTCTATCTGTAAGGCATCTGGAGCCAAAATTACCTGTGACAAAGAATCAGAAGGGACATTAC
TACTATCAAGACTTATAAAAATCTCAGGAACACAGAAGGAAGTGGCAGCAGCCAAGCATTGATACTGGAGAAAG
TTTCAGAAGATGAAGAACCTCGGAAGAGAAATTGCTCATTCTGCAGAAACCAGGGTCCCACGCAAACAGCCAATCA
GTGTGAGAAGAGAAGACATGACAGAGCCAGGTGGAGCTGGAGAGCCAGCATTATGGAAAAACACCAGTTCTAGCA
TGGAGCCGACTGCACCCCTGGTGACTCCTCCACCCAAAGGAGGAGGCGACATGGCTGTGGTAGTGTCAAAGGAAG
GTTCTTGGGAGAAACCTAGTGATGACAGCTTTCAGAAAGTCTGAAGCCCAGGCCATCCCAGAGATGCCCATGTTTG
AAATCCCCAGTCCCTGACTTCAGTTTTCATGCTGATGAGTACCTAGAAGTCTACGTTTCTGCTTCTGAGCACCTTA
ACCACTTCTGGATCCAGATCGTTGGCTCCCGCAGCCTGCAATTGGATAAGCTTGTCAATGAGATGACCCAGCACT
ATGAGAATAGTGTGCCTGAAGACTTGACTGTGCATGTAGGAGACATTGTAGCAGCACCTTTACCTACAAATGGTT
CCTGGTATCGAGCCCGGGTCCTCGGCACCTTGGAGAATGGGAACCTGGACCTCTATTTTGTGTGACTTTGGAGATA
ATGGAGATTGCCCACTGAAGGACCTCAGGGCTCTCAGGAGTGACTTCCTAAGCCTTCCATTTCAAGCAATAGAAT
GTAGTCTGGCACGGATTGCTCCCTCAGGTGACCAGTGGGAAGAGGAAGCTTTGGATGAGTTTGATAGACTCACTC
ATTGTGCTGACTGGAAGCCTCTGGTAGCCAAGATCTCTAGCTATGTCCAGACTGGGATCTCAACTTGGCCAAAGA
TCTACTTATATGATACTAGCAATGGGAAGAACTTGATATGGGCTAGAATTAGTACACAAAGGATACGCAATTG
AGCTTCCTGAAGACATAGAAGAAAACAGAGCTGTCCCAGACATGTTGAAGGACATGGCCACAGAAACAGATGCCT
CTCTCAGCACGTTGCTCACTGAGACCAAAAAGAGCTCTGGAGAGATAACACATACCCTGTCTGCTCAGCTTAT
CAGAAGCTGCTTCCATGCTGGTGATGATAACCTTGAAGATGACTACTTACTCGGAAGTCTGGGCTTCAGTTTGC
TCAGCCATCTGCTTTGCTGTATGTTGCCGTGAATGAACTCGCTGAAGCATGCTCAGCCCTGGAAGTGGTGCTACC
AGAGTTCCGTAGGGAACCTTTACTCTTTAGAGGTTCCCTTGATATAAAATCATTTCATAAGACTTCCTACCCTGGAAA
ATGAGTAATGCTCATTTCTTACCTGCAGTTTGTACTATGTATAAAAGTCTTTTCTTTAATATGCCTTTAAGTC
TTACCTGTTTACAGCCATTCTGATGGGTTCTTTGTCATTCTGTAGTATAACCCAGTACTTTTCTGCTGCCTG
GAATGCCCTCTTCTATGTTACCTATTCTGTCCGTTGAGATGCCCCAACTTGGGCCAAAGCCAAGAGATCTATGTG
CCTTCTCTGGTTTTCTCCACATCTATAGCACCTCAACTGAAATATATGGATAAAAACAGCCTAACAAAAA
AAAAA

WO 2004/030615

PCT/US2003/028547

375/6881
FIGURE 345

MSTERTSWTSLSTIQKIALGLGIPASATVAYILYRRYRESREERLTFVGEDDIEIEMRVPQEAVKLIIGRQGANI
KQLRKQTGARIDVDTEDVGDERVLLISGFPVQVCKAKAAIHQILTENTPVSEQLSVPQRSVGRIGRGETIRSI
CKASGAKITCDKESEGTLILLSRLIKISGTQKEVAAAKHLILEKVSEDEELRKRIAHSAETRVPRKQPISVRREDM
TEPGGAGEPALWKNTSSSMEPTAPLVTPPPKGGDMAVVVSKEGSWEKPSDDSFQKSEAQAIPEMPMFEIPSPDF
SFHADEYLEVYVSASEHPNHFQIIVGSRSLQDKLVNEMTQHYENSVPEDLTVHVGDIVAAPLPTNGSWYRARV
LGTLENGNLDLYFVDFGDNGDCPLKDLRALRSDFLSLPFQAIECSLARIAPSGDQWEEELDEFDRLTHCADWKP
LVAKISSYVQTGISTWPKIYLYDTSNGKKLDIGLELVHKGYAIELPEDIEENRAVPDMLKDMATETDASLSTLLT
ETKKSSGEITHLTLCLSLSEAASMSGDDNLEDDYLLGSLGFSLLSHLLCCMLPAMNSLKHAQPWNWCYQSSVGNL
YSLEVP

WO 2004/030615

PCT/US2003/028547

376/6881
FIGURE 346

TTTTTCTGCTACCGTGAAGATGAAGCGTTTTTGGGGTCGCGGTCCGGACTTTGGGCGGGGGTCCGGCCC
CAGGACAGTTTTACCGCATTCCGTCCACTCCCGATTCTTCATGGATCCGGCGTCTGCACTTTACAGAGGTCCAA
TCACGCGGACCCAGAACCCCATGGTGACCGGGACCTCAGTCCTCGGCGTTAAGTTCGAGGGCGGAGTGGTGATTG
CCGCAGACATGCTGGGATCCTACGGCTCCTTGGCTCGTTTCCGCAACATCTCTCGCATTATGCGAGTCAACAACA
GTACCATGCTGGGTGCCCTCTGGCGACTACGCTGATTCCAGTATTTGAAGCAAGTTCTCGGCCAGATGGTGATTG
ATGAGGAGCTTCTGGGAGATGGACACAGCTATAGTCTAGAGCTATTCATTTCATGGCTGACCAGGGCCATGTACA
GCCGGCGCTCGAAGATGAACCCCTTGTGGAACACCATGGTCATCGGAGGCTATGCTGATGGAGAGAGCTTCCTCG
GTTATGTGGACATGCTTGGTGTAGCCTATGAAGCCCTTCGCTGGCCACTGGTTATGGTGCATACCTGGCTCAGC
CTCTGCTGCGAGAAGTTCTGGAGAAGCAGCCAGTGCTAAGCCAGACCGAGGCCCGCGACTTAGTAGAACGCTGCA
TGCGAGTGCTGTACTACCGAGATGCCCGTTCTTACAACCGGTTTCAAACCGCCACTGTACCGAAAAAGGTGTTG
AAATAGAGGGACCATTGTCTACAGAGACCAACTGGGATATTGCCACATGATCAGTGGCTTTGAATGAATAACAG
ATGCATTATCCAGAACTGAAGTTGCCCTACTTTTAACCTTGAACCTGGCTAGTTCAAAGATAGACTCTTCTTTTG
TAAAGTAAATAAATTCCTCAAATG

WO 2004/030615

PCT/US2003/028547

377/6881
FIGURE 347

MEAF LGS R SGLWAGGPAPGQFYRI PSTPDSFMDPASALYRGPI TRTQNPMVTGTSVLGVKFEGGVVIAADMLGSY
GSLARFRNISRIMRVNNSTMLGASGDYADFQYLKQVLGQMVIDEELLGDGHSYSPRAIHSWLTRAMYSRRSKMNP
LWNTMVI GGYADGESFLGYVDM LGVAYEAPSLATGYGAYLAQP LLREVLEKQPVL SQTEARDLVERCMRVLYYRD
ARSYNRFQTATVTEKGVEIEGPLSTETNWDIAHMISGFE

WO 2004/030615

PCT/US2003/028547

378/6881
FIGURE 348

AATTGGAGGAGTTGTTGTTAGGCCGTCCCGGAGACCCGGTCGGGAGGGAGGAAGGTGGCAAGATGGTGTGGAAA
GCACTATGGTGTGTGTGGACAACAGTGAGTATATGCGGAATGGAGACTTCTTACCCACCAGGCTGCAGGCCCAGC
AGGATGCTGTCAACATAGTTTGTTCATTCAAAGACCCGAGCAACCCTGAGAACAACGTGGGCCTTATCACACTGG
CTAATGACTGTGAAGTGCTGACCACACTCACCCAGACACTGGCCGTATCCTGTCCAAGCTACATACTGTCCAAC
CCAAGGGCAAGATCACCTTCTGCACGGGCATCCGCGTGGCCCATCTGGCTCTGAAGCACCGACAAGGCAAGAATC
ACAAGATGCGCATCATTGCCTTTGTGGGAAGCCAGTGGAGGACAATGAGAAGGATCTGGTGAAACTGGCTAAAC
GCCTCAAGAAGGAGAAAGTAAATGTTGACATTATCAATTTTGGGGAAGAGGAGGTGAACACAGAAAAGCTGACAG
CCTTTGTAAACACGTTGAATGGCAAAGATGGAACCGGTTCTCATCTGGTGACAGTGCCCTCCTGGGCCCAGTTTGG
CTGATGCTCTCATCAGTTCTCCGATTTTGGCTGGTGAAGGTGGTGCCATGCTGGGTCTTGGTGCCAGTGACTTTG
AATTTGGAGTAGATCCCAGTGCTGATCCTGAGCTGGCCTTGGCCCTTCGTGTATCTATGGAAGAGCAGCGGCAGC
GGCAGGAGGAGGAGGCCCGGCGGGCAGCTGCAGCTTCTGCTGCTGAGGCCGGGATTGCTACGACTGGGACTGAAG
ACTCAGACGATGCCCTGCTGAAGATGACCATCAGCCAGCAAGAGTTTGGCCGCACTGGGCTTCTTGACCTAAGCA
GTATGACTGAGGAAGAGCAGATTGCTTATGCCATGCAGATGTCCCTGCAGGGAGCAGAGTTTGGCCAGGCGGAAT
CAGCAGACATTGATGCCAGCTCAGCTATGGACACATCTGAGCCAGCCAAGGAGGAGGATGATTACGACGTGATGC
AGGACCCCGAGTTCCTTCAGAGTGTCCTAGAGAACCTCCAGGTGTGGATCCCAACAATGAAGCCATTTCGAAATG
CTATGGGCTCCCTGGCCTCCCAGGCCACCAAGGACGGCAAGAAGGACAAGAAGGAGGAAGACAAGAAGTGAGACT
GGAGGGAAAGGGTAGCTGAGTCTGCTTAGGGGACTGCATGGGAAGCACGGAATATAGGGTTAGATGTGTGTTATC
TGTAACCATTACAGCCTAAATAAAGCTTGCAACTTTT

WO 2004/030615

PCT/US2003/028547

379/6881
FIGURE 349

MVLESTMVCVDNSEYMRNGDFLPTRLQAQQDAVNIVCHSKTRSNPENNVGLITLANDCEVLTTLTPTDTGRILSKL
HTVQPKGKITFCTGIRVAHLALKHRQGKNHKMRIIAFVGSPVEDNEKDLVKLAKRLKKEKVNVDIINFGEDEVNT
EKLTAFFVNTLNGKDGTGSHLVTVPPGPSLADALISSPILAGEGGAMLGLGASDFEFGVDPSADPELALALRVSM
EQRQRQEEEEARRAAAASAAEAGIATTGTEDSDDALLKMTISQQEFGRGTGLPDLSSMTEEEQIAYAMQMSLQGAEF
GQAESADIDASSAMDTSEPAKEEDDYDVMQDPEFLQSVLENLPGVDPNNEAIRNAMGSLASQATKDGKKDKKEED
KK

WO 2004/030615

PCT/US2003/028547

380/6881
FIGURE 350

CTGGTGAGGGGCTGCAGGTGGCGGCGCAGTCTCGGTAGGCGGTATGAGTTTGGCTGGGGGCCGGGCACCCCGGAA
GACCGCTGGGAACCGGCTTTCTGGGCTTTTGGAGGCAGAGGAGGAAGATGAGTTCTACAGACGACTTATGGGGG
TTTCACAGAGGAATCCGGAGATGATGAGTATCAAGGGGACCAGTCAGACACAGAGGACGAAGTGGACTCTGACTT
TGACATTGATGAAGGGGATGAACCATCCAGTGATGGAGAAGCAGAAGAGCCAAGAAGGAAGCGCCGAGTAGTCAC
CAAGGCCTATAAGGAACCTCTCAAGAGCTTAAGGCCTCGAAAGGTCAACACCCCGGCTGGTAGCTCTCAGAAGGC
GCGAGAAGAGAAGGCACTACTGCCATTAGAACTACAAGATGACGGCTCTGACAGTCGGAAGTCTATGCGTCAGTC
TACAGCTGAGCATACACGACAAACGTTCCCTTCGGGTACAGGAGAGGCAGGGCCAGTCAAGACGGCGAAAGGGGCC
CCACTGTGAGCGGCCACTAACCCAGGAGGAAGTCTCCGGGAGGCCAAGATCACAGAAGAGCTTAATTTACGGTC
ACTGGAGACATATGAGCGGCTCGAGGCTGATAAAAAGAAGCAGGTTTCATAAGAAGCGGAAGTGCCCCGGGGCCAT
AATCACCTATCATTGAGTACAGTGCCACTTGTTGGGGAGCCAGGCCCCAAGGAAGAGAACGTTGACATAGAAGG
ACTTGATCCTGCTCCCTCGGTGTCTGCATTGACTCCTCATGCTGGGACTGGACCCGTCAACCCCCCTGCTCGCTG
CTCAGTACCTTCATCACTTTTAGTGATGATGCAACTTTTCAGGAATGGTTCCCCCAAGGGCGGGCCCCAAAAGT
CCCTGTTTCGTGAGGTCTGTCCAGTGACCCATCGTCCAGCCCTATACCGGGACCCTGTTACAGACATACCCTATGC
CACTGCTCGAGCCTTCAAGATCATTTCGTGAGGCTTACAAGAAGTACATTACTGCCCATGGACTGCCGCCCCACTGC
CTCAGCCCTGGGCCCCGGCCCCGCCACCTCCTGAGCCCTCCCTGGCTCTGGGCCCCGAGCCTTGCGCCAGAAAAT
TGTCATTAAATGAAGAGATGTCTAGTCTCAGAACTTCTTTTCTGCCCTGATTGGGGCTCTTGCTGTTCCGTTT
CTTCTCCCTGCTTCTCCCCCTTTGTCTCTCTGATCTTTGCCTAATCTGTTTCTTTTCTTTTCCCCTAGTTCTT
ACAGGTTTCGTTGTGTTTTTTAATCTAATAAAATAGAAAGATCCCTTTT

WO 2004/030615

PCT/US2003/028547

381/6881
FIGURE 351

MSLAGGRAPRKTAGNRLSGLLEAEEEEDEFYQTTYGGFTEESGDDEYQGDQSDTEDEVDSDFDIDEGDEPSSDGEA
EEPRRKRRVVTKAYKEPLKSLRPRKVNTAGSSQKAREEKALLPLELQDDGSDSRKSMRQSTAEHTRQTFLRVQE
RQGQSRRRKGPHCERPLTQEELLREAKITEELNLSLETYERLEADKKKQVHKRKCPCGPIITYHSVTVPPLVGEP
GPKEENVLDIEGLDPAPSVSALTPHAGTGPNPPARCSRTFITFSDDATFEWFPPQGRPPKVPVREVCVTHRPAL
YRDPVTDIPYATARAFAKIREAYKKYITAHGLPPTASALGPGPPPEPLPGSGPRALRQKIVIK

WO 2004/030615

PCT/US2003/028547

382/6881
FIGURE 352

CCTGGCTTTGTGCATTGGGTTCTGGTGCCTGATGGACACATTTTCCAGTTACAGGCCGAATGGTCTCAATGTAG
CTGAAGAACTGTGCCCCTGATCAGTATTACGTATTGCAAATGCAGGAGGTGGCTGTATCTGACAGACCCAGGCC
TTCCAGCTCCGACAGATCCAGTTCTGGGATGGGCATCCTCCAGAAAAGAAAGGAAGTGTACTGGCTACTCACAGG
GTCCCTCATAGCTTCCTAGAAAAGAAACCACTTGTGAGTCTTCATGCTACAGCAACTTCTTTGTGGCCCATGGCCT
TTCCTTGCTTAGATACTCCACATACTGTTCTCCCCGAGGGGCGGCGGCCTTGAGGGGCTGCAGAGGCACCCCTCC
CACGTCCCGCGCAGTGCAGTGCCTCCGAGTCCAGAGGGGAGCAGTGCGCCGGGCTCCGAGCCGGACGGGTTTCG
TAATCGCGTCGCGCGCGCTTCCGCCCCAGCCGGCCCCACCTCTGCCGGCTCGTACTCGGCTCCCCACCTCGCC
GCAGAGCTAGCCCGGGAAGCCACACTGGCGGCCACGGAGCAGAGTCCCTACCCCCACAGCTGTAGCTGAACG
TCTGGATGGTGGAGAAGAGCAGGTGAGGCCGTGAGTTGGTCCCTTGCCCGCCTGCCGCGCCGGCCGGCCAGG
CGGAGACACACCGGATGCGGGGTGTGGGGGAGGCGGGTGTCTGGGCTGCAGAGATGCTGGGGTGGTGGGAAGG
GGTGCGCGCCCGGGGTGGCCGTAGTCATCCACGCTCCTGGGGTGCGCAGGCTGAGGCCGCTGAAGAGTAGAAGGA
AAAGAAGGAAGTGAATGTTGGGGGAGGTGGGAGGGAGAGGGTCCGAAAGATTCCCAGAGAGTCCCAGTCCGGT
TAAGGGTTGAGAACAGCAGAGAACTTCTAGGTAGAGTTGTGTAGTGGGGGAGACAGATACAGGAATCTGTGTGAT
TGAATATATTTGGGGAGGGGAGGCTTAGGGCCTAGCCCTCTTTCCTCTTAAGCCCCAGAAGACCTTTCTGGGG
AAGGGAAGGTTGGTGTGGGCTGTCACTTGGCTGAAATATGGAGTCCACACCGCTTCTAGCCAGAATTGCCATGCCAT
GCCCTCCATGTCTCGGGTCTCCACACAGGACCAGCTGTGCCCCGGGCTTCTAGCCAGAATTGCCATGCCAT
TCTCTCGATTCTTTCTTCTCTCCAGCTGCTTCATGTGAGGGCTTGTGAGGCCGCGGGTTGGAGGCCTTAGGGCC
AGAGGCGGTGGGACCGGGAGAACCGGTTTGGGGCCCGAACAGGACCAGAGAACTAGCCTGTACATCCTTCCCTCC
TGGCACCTCTTTCCCATCCCTTCTGCTCACCTCCCAACAGCTCTGAGACCCCTCAAGTCCTAGTATGATCTTGGTG
GGGGCGGGGGGTGGCTTTCCCGGTTCCATATTTCACTCTTGCCATTGGAAGTCTGAGAGAGGTCGAGTTCTGAGCA
CCACTTGGCTCTCAGGACGTGGCCTTATGAGGTCTAATCCTCATCCCTCCTGTTGTTTTCTCAGCCCCCTTCCCTA
TTCAGTGTGGGGTTGGATTTCGGGTGGCTCTTCCGGCTGGGCTGACCAGCTCAGGACTTCATTTTTCTCAACCCA
CTCTCTTCTGGCTGCTTTAAAGAAGAGTGGCCGCCAGTGGCTCTTACTTCCCTTTCTGGCTTTGTTCCCATCCCC
CACTGCCCTGCGCTACCATCACATTACCCCTGACCTGTCTTCTTCCACTCTGACCCACCCCTCAAGTTTCAGAG
ACCCTAATGTCTTAGGGAATGGAATTTCCCTGGTCACTTCTCGTCATCATTGGTCAATTCATGCCAAGTCCCACAC
ACACGCTTTCCCTCCACCCAGCTCTGGTCAAGTCCCTGGAAAAGAAACAGAAATGGCCTTGTCTCTCCACTGCC
CCTTTCCCTCTCTCTTCTCTCTCCCCCTCTCTTCTCTTCCCTCCCAGCACTATCCACCTCTGTCCCTCAGCTTG
AGCAGAGTGGGGGATGTTGAGGGAGAGTCCAGTACAGTACAGCCTGCCTGCTGGTGTGGGGGTTTCTCTAAT
TCTTCATTTTTTCCCCAACCTTACCACCTGCCACCACCACCATCAGGACAAACCTATGACTGACTCACTGACGT
CCCAGTACCACAGCTCCCTCTCTGGACAGCGTGTTTAGCTTCCGCTCCTTCTGGTTACTCCTCCCTTCCAGT
GGTGAGAAGAGAAGAGAAAGCCAGCCTCCTGGGTTCTCCCTCCCTAGAAAGCTACATTTGAGTGTGTTGTGTGA
TCTCATCTCAAGGCTGTT

WO 2004/030615

PCT/US2003/028547

383/6881
FIGURE 353

AGTCAGCACGGGGGTGCTGGAAGAGATCGGGGAATAATAGCGCAGACCAATGAGCCTAGGGAGATGCTTTTCATCGT
CTCTCCTTCCCTCAAGTGTTCTGGAACCTATCATTTGAATTAGCCGAGTCAGGCAGGAGGGGGCGGGGAATCCTT
CCGCCCTTCTTAGGAGGGGCTGCATTGCAGGGGGAGAGTGAACTGACAGACTCAGTCACTGAAGAGGGGAAAAGGA
GTGAGAAGACAAAGCCGTCAAAGCCCCAACAGCTTTGTATTTCTCCAGCCCGGCGCAGACCCCGGAGCTCCCGAG
GCACTCCCTCCATCTTTGGAACACGCCAGTAATTGATTGATAACAGGAAGCTATGAGGGACCCTGTGAGTAGCCA
GTACAGTTCCTTTCTTTCTGGAGGATGCCCCATCCCAAGCTGGATCTGTCTGGAGCTGGAAGGCCTGGGTCTGTC
AGATACAGCCACCTACAAGGTCAAAGACAGCAGCGTTGGCAAATGATCGGGCAAGCAACTGCAGCAGACCAGGA
GAAAAACCCTGAAGGTGATGGCCTCCTTGAGTACAGCACCTTCAACTTCTGGAGAGCTCCCATTGCCAGCATCCA
CTCCTTCGAACTGGACTTGCTCTAAGGCCAAGACTTCTCTCTCCCATCACCTTGCCCTCATTGTCTTCCCTCTCA
AGCCCCCTCCTTTCCACTCCTTTCCCATTTTAATCTTGTTCTCTCCCTACTGTGTTGGTGGTGCTGATGAATCTG
CCAGAGTTGAGTTCATGTATTTATTTATCTATCTGTCTACTCCATTTCTCTCAAAAGCCCTCAAGTCACAAAGT
AAATGGTTCAGCAATGGAGTACTGGGTACAGGGATTCTCTCTTCCCCCCCCAAATATTAATCCAGAACTAG
GCCTGACTGGGGACACCTGAGAGTAGTATAGTAGTGCAAAATGGAAGACTGATTTTTGACTCTATTATAATCAGC
TTCAGAGATTCCTTAAACCTTCCTAATTTCTGCTCCAGGGCAGTAAACACAAATATTTCTTCAAGGGGTGATGA
AAACCTCGGAAGTTTTAATTTGAGGTTATCTGCTACGAAACAGTATTTCTAAAAGGCTAAAGTGATAAGTCTCTT
GCTTTTTTTTGATCCTGCTCTTATATTCTTTTTTTTCTCAGAGAAATCAGGAGGGTAGTTAGAGGTATAAAACA
GGAGGAAATATTATGGAATGAAAATAGGGAAAATAATTGAATCATTTTAGAAGTAGCTAATTTCTTTTCTCAA
AAGAGTGTCCTTCTTACACCTACTCACTTTACAACCTTTGCTCCTAACTGTGGGTGAAAACCTCTAGCTAAAGA
AAGTTATCAAATCTTAACATGCATTCCTACTATTATGATAGTTTTTAAGGTTTCAATTCAATCTTCTGAACGGCA
TAAGTCCTATTTTAGCCTTACCTCCTGCATTTGCAATACGTAATACTGATCAGTGGGCACAGTTCTTCAGCTACA
TTGAGACCCTGAAATGAACAATTATATTCTGACTCGACATCTTGTCCCCAATCCTTCCAAAAATATTGATGGTGA
TTTGTGCTACCATTACTCGTTTATTTAATAAAGACATTCAATCCC

WO 2004/030615

PCT/US2003/028547

384/6881
FIGURE 354

GGGGGCGGGGCGACGCCGGACTCCGGAGCGCCCGCTTACGCAGTTCCCTCCCGGGGTCCGGAGGCCGATTCCGCCGTG
TGGCGGGTTCGAGTCCCGCCTCCTGACTCTGGCCTCTAGTCCCTGAGTCCCGGGGCGGGCTGCATTTCGTCCGGGAA
ACCTCTCCTCGACCAGGGGACCTCTACTCGACCAGGGGCGACGGCGTACTTTGGGCTTCATCATCGGAGGACTAC
CTGCAGGGTTGTCGAGCTGCTCTGCAGGAGTCCCGACCTCTACATGTTGTGCTGGGAAATGAAGCCTGTGATTTG
GACTCCACAGTGTCTGCTCTTGCCCTGGCTTTTTACCTAGCAAAGACAACCTGAGGCTGAGGAAGTCTTTGTGCCA
GTTTTAAATATAAAACGTTCCTGAACCTCTGCGAGGTGACATTGTCTTTCTTTCTTCAGAAGGTTTCATATTCCA
GAGAGTATCTTGATTTTTTCGGGATGAGATTGACCTCCATGCATTATACCAGGCTGGCCAACTCACCCTCATCCTT
GTCGACCATCATATCTTATCCAAAAGTGACACAGCCCTAGAGGAGGCAGTAGCAGAGGTGCTAGACCATCGACCC
ATCGAGCCGAAACACTGCCCTCCCTGCCATGTTTCAGTTGAGCTGGTGGGGTCCCTGTGCTACCCTGGTGACCGAG
AGAATCCTGCAGGGGGCACCAGAGATCTTGGACAGGCCAACTGCAGCCCTTCTGCATGGAACCATCATCCTGGAC
TGTTGCAACATGGACCTTAAATTTGGAAAGGCAACCCCAAAGGACAGCAAATATGTGGAGAACTAGAGGCCCTT
TTCCAGACCTACCCAAGAGAAATGATATATTTGATTCCCTACAAAAGGCAAAGTTTGATGTATCAGGACTGACC
ACTGAGCAGATGCTGAGAAAAGACCAGAAGACTATCTATAGACAAGGCGTCAAGGTGGCCATTAGTGCAATATAT
ATGGATTTGGAGGCCCTTCTGTCAGAGGTCTAACCTCCTTGAGATCTCCATGCTTTCTGCCAGGCTCACAGCTAT
GATGTCTGTTGCCATGACTATCTTTTTCAACACTCACAATGAGCCAGTGCGGCAGTTGGCTATTTTCTGTCCC
CATGTGGCACTCCAAACAACGATCTGTGAAGTCTTGAACGCTCCCACTCTCCACCCCTGAAGCTGACCCCTGCC
TCAAGTACCCACCTAACCTCCATGCCTATCTTCAAGGCAACACCCAGGTCTCTCGAAAGAACTTCTGCCCTG
CTCCAGGAAGCCCTGTGACATATTTTACTCCATGAAGATCCCTTCAGGACAGCCTGAGACAGCAGATGTGTCC
AGGGAGCAAGTGGAACAAGGAATTGGACAGGGCAAGTAACTCCCTGATTTCTGGCCTGAGTCAAGATGAGGAGGAC
CCTCCGCTGCCCCCGACGCCCATGAACAGCTTGGTGGATGAGTGCCCTCTAGATCAGGGGCTGCCTAAACTCTCT
GCTGAGGCCGTCTTCGAGAAGTGAGTCAGATCTCACTGTACAGTCTACCACAGCCTCCCTGTCCAAGAAGTGA

CTGTTGAGAGGCGAGGAGGTAGTGGGTGAGGCTACCTGACTCACTTCAAATGCATGTTTTGAGATGTTTGAGAT
TCAGCAATTCTGTCTTCATTGCTCCAGGATCTGGTATACTGTTCTCATAAACTGAGAGGAGAAAAAAGTGAA
GAAAGCAGCTGCTTTAAGAATGGTTTTCCACCTTTTCCCCCTAATCTCTACCAATCAGACACATTTTATTATTTA
AATCTGCACCTCTCTCTATTTTATTGCCAGGGGACGATGTGACATATCTGCAGTCCCAGCACAGTGGGACAAA
AAGAATTTAGACCCCAAAAGTGCTCTCGGCATGGATCTTGAACAGAACCAGTATCTGTCTGGAACCTGAACATTC
ATCGATGGTCTCCATGTATTCAATTTACTTGTTCATTCAAGTATTTATTGAATACCTGCCTCAAGCTAGAGA
GAAAAGAGAGTGCGCTTTGGAAATTTATCCAGTTTTACGCTACAGCAGATTATCAGCTCGGTGACTTTTCTTT
CTGCCACATTTAGGTGATGGTGGTTGATTTCAGAGATGGCTGAATTTCTATTCTTAGCTTATTGTGACTGTTTCA
GATCTAGTTTGGGAACAGATTAGAGGCCATTGTCTTCTGCTGATCAGGTGGCCTGGCTGTTTCTTTGGATCCC
TCTGTCCCAGAGCCACCCAGAACCCTGACTCTTGAGAATCAAGAAAACACCCAGAAAGGCCTTAATGACCTCATA
GGCACTCTTCCAAAAGACAACAGAACTGGAATGAGAGGCCTGGGTCTGTCTCCTGCCTTAGCAGGCCTATCAAT
TTCTTGCAATCTCTTTTTTCTCTGCTCACATTAAGGAAGCATGGAGTTCTAATGCTCCCATAACTATGTA
TTTTGGCAAGACACTTCACTACTCCAGGTCTCACTTTCCCCATCTGTAAAACAGGGTTTGGACTAGGTGTTCCCT
GGTATTCTGTGATCTGCCTCTTGCTGCCATTCTTTCTCTCCTCTGCTTCTCTGTATTTTCTTCTGTTATCCCTG
GGGTGCTCAGGTTCACTTGATTGTCTGTATTTCTGTGTGGTTGTAGCAAGGACTCAGCCTCATGTAGCACGAAT
AGGGGTGTGGTTCATGGCGTGTGACCCAGCAGAGCACTCCCTCCCACTAACTTGTTCTGCATGTGTAGAGTCTC
CCCATTTTTTTTAAACGCAACCCCTTTCCCTTTTTCTACCCACAGCTCTGTTCCATGTAAGTTGCCAACAGTTT
CACTGAACAGTGGGGTATGTGATGGTTTTGGCATGACATCTTCAGTATGAGGGGGACAGTTTGACTTCACTTTGA
GGGTGTGATGTCTGTAGCTATGTGGAAGGTAAAAATAGTGGTGTGATCATGAACCAAGGAATTTATGTTTTGTA
ACTTGGGTACTTTATTTTGCATTTTGTATATACTATTAAATAATTTTTCTCTGT

WO 2004/030615

PCT/US2003/028547

385/6881
FIGURE 355

MEDYLQGCRAALQESRPLHVVLGNEACDLSTVSALALAFYLAKTTEAEVFPVVLNKRSELPLRGDIVFFLQK
VHIPESILIFRDEIDLHALYQAGQLTLILVDHHILSKSDTALEEAVAELDHRPIEPKHCPPCHVSVELVGSCAT
LVTERILQGAPEILDRQTAALLHGTIILDCVNMDLKIGKATPKDSKYVEKLEALFPDLPKRNDIFDSLQAKFDV
SGLTTEQMLRKDQKTIYRQGVKVAISAIYMDLEAFLQRSNLLADLHAFCAHSYDVLVAMTIFFNTHNEPVRQLA
IFCPHVALQTTICEVRLERSHSPPLKLTTPASSTHNLHAYLQGNTQVSRKKLLPLLQEALSAYFDSMKIPSGQPET
ADVSREQVDKELDRASNSLISGLSQDEEDPPLPPTPMNSLVDECPLDQGLPKLSAEAVFEKCSQISLSQSTTASL
SKK

WO 2004/030615

PCT/US2003/028547

386/6881
FIGURE 356

GAAACAAGCACTGGATTCCATATCCCACTGCCAAAACCGCATGGTTTCAGATTATCGCTATTGCAGCTTTCATCAT
AATACACACCTTTGCTGCCGAAACGAAGCCAGACAACAGATTTCCATCAGCAGGATGTGGGGGCTCAAGGTTCTG
CTGCTACCTGTGGTGAGCTTTGCTCTGTACCCTGAGGAGATACTGGACACCCACTGGGAGCTATGGAAGAAGACC
CACAGGAAGCAATATAACAACAAGGTGGATGAAATCTCTCGGCGTTTTAATTTGGGAAAAAACCTGAAGTATATT
TCCATCCATAACCTTGAGGCTTCTCTTGGTGTCCATACATATGAACTGGCTATGAACCACCTGGGGGACATGACC
AGTGAAGAGGTGGTTCAGAAGATGACTGGACTCAAAGTACCCCTGTCTCATTCCCGCAGTAATGACACCCTTTAT
ATCCCAGAATGGGAAGGTAGAGCCCCAGACTCTGTGCGACTATCGAAAGAAAGGATATGTTACTCCTGTCAAAAAT
CAGGGTCAGTGTGGTTCCTGTGTGGGCTTTTAGCTCTGTGGGTGCCCTGGAGGGCCAACTCAAGAAGAAAACCTGGC
AAACTCTTAAATCTGAGTCCCAGAACCTAGTGGATTGTGTGTCTGAGAATGATGGCTGTGGAGGGGGCTACATG
ACCAATGCCTTCCAATATGTGCAGAAGAACCGGGGTATTGACTCTGAAGATGCCTACCCATATGTGGGACAGGAA
GAGAGTTGTATGTACAACCCAACAGGCAAGGCAGCTAAATGCAGAGGGTACAGAGAGATCCCCGAGGGGAATGAG
AAAGCCCTGAAGAGGGCAGTGGCCCGAGTGGGACCTGTCTCTGTGGCCATTGATGCAAGCCTGACCTCCTTCCAG
TTTTACAGCAAAGGTGTGTATTATGATGAAAGCTGCAATAGCGATAATCTGAACCATGCGGTTTTGGCAGTGGGA
TATGGAATCCAGAAGGGAAACAAGCACTGGATAATTA AAAACAGCTGGGGAGAAAACCTGGGGAAACAAGGATAT
ATCCTCATGGCTCGAAATAAGAACAACGCCTGTGGCATTGCCAACCTGGCCAGCTTCCCCAAGATGTGACTCCAG
CCAGCCAAATCCATCCTGCTCTTCCATTCTTCCACGATGGTGCAGTGTAACGATGCACCTTGAAGGGAGTTGG
TGTGCTATTTTTGAAGCAGATGTGGTGATACTGAGATTGTCTGTTTCAAGTTTCCCCATTTGTTTGTGCTTCAAATG
ATCCTTCCTACTTTGCTTCTCTCCACCCATGACCTTTTTCACTGTGGCCATCAGGACTTTCCTGACAGCTGTGT
ACTCTTAGGCTAAGAGATGTGACTACAGCCTGCCCTGACTGTGTTGTCCCAGGGCTGATGCTGTACAGGTACAG
GCTGGAGATTTTACATAGGTTAGATTCTCATTACGGGACTAGTTAGCTTTAAGCACCCCTAGAGGACTAGGGTA
ATCTGACTTCTCACTTCCCTAAGTTCCCTTCTATATCCTCAAGGTAGAAATGTCTATGTTTTCTACTCCAATTCAT
AAATCTATTCTAAGTCTTTGGTACAAGTTTACATGATAAAAAGAAATGTGATTGTCTTCCCTTCTTTGCACTT
TTGAAATAAAGTATTTATC

WO 2004/030615

PCT/US2003/028547

387/6881
FIGURE 357

MWGLKVLLLPVVSFALYPEEILDTHWELWKKTHRQYNNKVDEISRRLIWEKNLKYISIHNLASLGVHTYELAM
NHLGDMTSEEVVQKMTGLKVPLSHSRSDTLYIPEWEGRAPDSVDYRKKGYVTPVKNQGQCGSCWAFSSVGALEG
QLKKKTGKLLNLSQNLVDCVSENDGCGGGYMTNAFYVQKNRGIDSEDAYPYVGQEESECMYNPTGKAAKCRGYR
EIPGNEKALKRAVARVGPVSVDAIDSLTSFQFYSGVYYDESCNSDNLNHAVLAVGYGIQGNKHWI IKNSWGE
NWGNKGYILMARNKNNACGIANLASFPKM

WO 2004/030615

PCT/US2003/028547

388/6881
FIGURE 358

GGCACGAGGAAGGAACATGCCCCCTGTATCAGAGGTGGCGGTGTCTCCGGCTCCAAGGTTTACAGGCTTGACGGCT
ACACACGGCAGTTGTGTGCGACCCCTCCACGCTGGTTGGCAGAGCGGCTTGGCCTTTTTGAGGAGCTGTGGGCTGC
TCAGGTAAAGAGATTAGCAAGCATGGCACAGAAGGAACCCCGGACTATTAAGATATCACTTCTTGGAGGCCAGAA
AATTGATGCTGTGGCATGGAACACAACCCCTACCAACTAGCCCCGGCAGATCAGTTCAACACTGGCAGATACTGC
AGTGGCTGCTCAAGTGAATGGAGAACCCTTATGATCTGGAGCGGCCCTTGGAGACAGATTCTGACCTCAGATTTCT
GACATTGATTCCCCAGAGGGGAAAGCAGTGTTCTGGCACTCCAGCACCCATGTCTGGGGGCAGCAGCTGAACA
ATTCTTAGGTGCTGTTCTCTGCAGAGGTCCAAGTACAGAAATATGGCTTTTACCATGATTTCTTCTGGGAAAGGA
GAGGACAATCCGGGGCTCAGAGCTGCCTGTTTTGGAGCGGATTTGCCAGGAACCTTACAGCTGCTGCTCGACCCCT
CCGGAGGCTAGAGGCTTCACGGGATCAGCTTCGCCAGTTGTTCAAGGATAACCCCTTTAAGCTTCACTTGATTGA
GGAGAAAGTGACAGGTCCAACAGCAACAGTATATGGGTGTGGCACATTGGTTGACCTTTGCCAGGGCCCCACCT
TCGGCATACTGGACAGATTGGAGGACTGAAGCTGCTATCGAACTCATCATCTTATGGAGGTCTTCAGGGGCCCC
AGAGACACTGCAGAGAGTGTGACGGGATTTCTTCCCCACAACAGAATTGCTGAGGGTCTGGGAAGCATGGAGGGA
GGAAGCAGAATTGCGGGACCACCGGCGCATTGGGAAGGAACAGGAGCTCTTCTTCTTCCATGAACCTGAGCCCTGG
GAGCTGCTTCTTCTGCCACGAGGGACAAGGGTGTATAATGCACTAGTGGCGTTTATCAGGGCTGAGTATGCCCA
TCGTGGTTTTCTCCGAGGTGAAACTCCCCACTGTTTTCTACGAAGCTCTGGGAACAGTCAGGGCACTGGGAGCA
TTATCAGGAAGACATGTTTGCCGTGCAGCCCCAGGCTCTGACAGGCCTCCCAGCTCCCAGAGTGACGATTCTAC
CAGGCATATCACAGATACACTCGCCCTCAAGCCTATGAAC TGCCCTGCACACTGCCTGATGTTGCCCCACCGGCC
CAGATCCTGGCGGGAAC TGCCCTGCGACTAGCTGACTTTGGGGCTCTACACCGGGCCGAAGCCTCTGGTGGTCT
GGGGGGACTGACCCGACTGCGGTGCTTCCAGCAGGATGACGCTCACATCTTCTGTACAACAGATCAGCTGGAAGC
AGAGATCCAAAGCTGTCTTGATTTCCCTCCGTTCGGTCTATGCCGTTCTTGGCTTCTCCTTCCGCTGGCACTGTC
CACCCGGCCATCTGGCTTCCCTGGGGGACCCCTTGCCCTTTGGGACCAGGCCGAACAGGTCCTTAAACAGGCCCTGAA
GGAATTTGGAGAACCCTGGGACCTCAACTCTGGAGATGGTGCCCTTCTATGGACCTAAGATTGACGTGCACCTCCA
CGATGCCCTGGGCGGGCCACATCAGTGTGGGACAATTCAGCTTGACTTCCAACCTGCCCCCTGAGATTTGACCTCCA
GTATAAGGGGCAGGCGGGTGCCCTGGAGCGTCCAGTCCCTCATTACCGAGCAGTGCTCGGTTCTGTGGAAAGACT
GTTGGGAGTGCTGGCAGAAAGCTGCGGGGGGAAATGGCCACTGTGGCTGTCCCCGTTCAGGTGGTGGTCATCCC
TGTGGGGAGTGAGCAAGAGGAATACGCCAAAGAGGCACAGCAGAGCCTGCGGGCTGCAGGACTGGTCAGTGACCT
GGATGCAGACTCTGGACTGACCCCTCAGCCGGAGAATCCGCGGGGCCAGCTTGCCCCACTACAATTTTCAGTTTGT
GGTTGGCCAGAAAGAGCAAAGTAAGAGAACAGTGAACATTTCGGACTCGAGATAATCGTCGCCCTTGGGGAGTGGGA
CTTGCCCTGAGGCTGTGCAGCGACTGGTGGAGCTACAGAACACGAGGTCCCAAATGCCGAAGAAATTTCTGAGC
CTTTGTACATAGATGAGGCAAAAACCTGCGAGTGCCATCAGCCTCCCTCACATGGGAGACCCCAACCCAGCTGAC
AATGTGGAGCCCCAGAACTTCAGAACTGTGTGGAGGCACATGTCTGCTCTCCTGAAAAGAGACTTGGTTTGGGG
ACCCACAAAAGGAGGGAAGCTGTAGCTGTTTGGATGTGAGGAGAATGAACTACAAAAA

WO 2004/030615

PCT/US2003/028547

389/6881
FIGURE 359

MALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEELWAAQVKRLASMAQKEPRTIKISLPGGQKIDAVA
WNTTPYQLARQISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAVFWHSSTHVLGAAAEQFLGAV
LCRGPSTEYGFYHDFFLGKERTIRGSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHLIEEKVTG
PTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSSLWRSSGAPETLQRVSGISFPTTELLRVWEAWREEAELR
DHRRIGKEQELFFFHELSPGSCFFLPRGTRVYNALVAFIRAEYAHRGFSEVKPTLFTSTKLWEQSGHWEHYQEDM
FAVQPPGSDRPPSSQSDSTRHITDTLALKPMNCPAHCLMFHRPRSWRELPLRLADFGALHRAEASGGLGGLTR
LRCFQQDDAHIFCTTDQLEAEIQSCLDFLRSVYAVLGFSEFRLALSTRPSGFLGDPCLWDQAEQVLKQALKEFGEP
WDLNSGDGAFYGPKIDVHLHDALGRPHQCGTIQLDFQLPLRFDLQYKGQAGALERPVLIHRAVLGSVERLLGVLA
ESCGGKWPLWLSPPQVVVIPVGSEQEEYAKEAQQSLRAAGLVSDLDADSGLTLSRRIRRAQLAHYNFQFVVGQKE
QSKRTVNIRTRDNRRRLGEWDLPEAVQRLVELQNTRVPNAEEIF

WO 2004/030615

PCT/US2003/028547

390/6881
FIGURE 360

ACCAGATCCCAGAGGCTGAACACCTCGACCTTCTCTGCACAGCAGGTCCAGCATCCTTTGAAGCATGAGTTCTTA
CCAGCAGAAGCAGACCTTTACCCCAACACCTCAGCTTCAACAGCAGCAGGTGAAACAACCCAGCCAGCCTCCACC
TCAGGAAATATTTGTTCCCAACAACCAAGGAGCCATGCCACTCAAAGGTTCCACAACCTGGAAACACAAAGATTCC
AGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGA
GCCAGGTTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGTTGTACCAAGGTCCCTGAGCC
AGGCTACACCAAGGTCCCTGAACCAGGCAGCATCAAGGTCCCTGACCAAGGCTTCATCAAGTTTCTGAGCCAGG
TGCCATCAAAGTTCTGAGCAAGGATACACCAAAGTTCTGTGCCAGGCTACACAAAGCTACCAGAGCCATGTCC
TTCAACGGTCACTCCAGGCCCAGCTCAGCAGAAGACCAAGCAGAAGTAATTTGGTGCACAGACAAGCCCTTGAGA
AGCCAACCACCAGATGCTGGACACCCCTCTTCCCATCTGTTTCTGTGTCTTAATTGTCTGTAGACCTTGTAATCAG
CACATTGTCACCCCAAGCCATAGTCTCTCTCTTATTTGTATCCTAAAAATACGTACTATAAAGCTTTTGTTCACA
CACACTCTGAAGAATCCTGTAAGCCCCCTGAATTAAGCAGAAAGTCTTCATGGCTTTTCTGGTCTTCGGCTGCTCA
GGTTTCATCTGAAGATTGCAATGAAAAGAAATGCATGTTTCTGCTCTTCCCTCATTAAATTGCTTTTAATTCCA

WO 2004/030615

PCT/US2003/028547

391/6881
FIGURE 361

CAGTTCTAAGGGACCATAACAGAGTATTCCTCTCTTCACACCAGGACCAGTCACTGTTGCAGCATGAGTTCCCAGC
AGCAGAAGCAGCCTTGCACCCACCCCCCTCAGCTTCAGCAGCAGCAGGTGAAACAGCCTTGCCAGCCTCCACCTC
AGGAACCATGCATCCCCAAAACCAAGGAGCCCTGCCACCCCAAGGTGCCTGAGCCCTGCCACCCCAAGTGCCCG
AGCCCTGCCAGCCCAAGGTTCCAGAGCCATGCCACCCCAAGGTGCCTGAGCCCTGCCCTTCAATAGTCACTCCAG
CACCAGCCCAGCAGAAGACCAAGCAGAAGTAATGTGGTCCACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGC
TGAATCCCTATCCCATTCGCGTATGAGTCCCATTGCTTGCAATTAGCATTCTGTCTCCCCAAAAAAGAAT
GTGCTATGAAGCTTCTTTCCTACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTT
TCAGCTGCTCAGAATTCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATACCCCATTA
ATTCACTTTCAATTCCA

WO 2004/030615

PCT/US2003/028547

392/6881
FIGURE 362

MSSQQQKQPCTPPPQLQQQVVKQPCQPPPOEPCIPKTKEPCHPKVPEPCHPKVPEPCQPKVPEPCHPKVPEPCPS
IVTPAPAQQKTKQK

WO 2004/030615

PCT/US2003/028547

393/6881
FIGURE 363

ATGACAATTGCAAAGGTGGTAGAAGCTCATGACCAGGTGACAGACAGACACAGAACACATCAACAGAATTGTCTG
ATGGTTCCCAAGGAGAGAGCTGCTGCTCTTTCTTCCGAAGCTCTGGGAGCTGGCACAGCTGAGGACTTCCTTTTC
TTAGCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAGAAAGGGAATCTTTTGCTGTCACAGATCATCACAGGCA
GGCCACAGGTTAAGGAGAAAGAAGCTCCCTGTGCATCCATGGAAGGCTTTGGTGAGAAGATGCAAGTGGAGCTGT
GGAACGAGGGGAGAGAGCTGCTGCTCTTTCTTCCGAAGCTCTGGGAGCTGGCACAGCCCAGGACTTCCTTTGCTCA
GTCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAGAAAAGAACTTTTGCTGTCAGGGATCATCATGGGCAGA
TTACTGGCTAAGGAGAAAGAAGCTCCCTGTGTATCCATGGTAGGCTTTGATGAGAAGATGAAGGTGGAGCTGTGG
AACGAGATACTTTATTTCAGGGAGTGAAAGAAAAGTGACAATTGCACAGGTGGTAGAAGCTCATGCCCAGGTGAAA
GACAGACACAGAACACATCAACAGAATTCTCTGATGGTTCCCAGGCACACAGCTGCAGCTCTTTCTGCTGAAGCT
CTGGGAAGTGACAAAGCCAAGGTTCCCTTTGCTCAGTCTCCACCTGGACAGTGGCATCTCCACCTGGACAGTGGCA
ATATGGCAGCCTCAGAAAGGAAACCTTTTGCTATCAGGGATCATCATGGGCAGATCACTGGCTAAGAGGAAAGAA
GCTAACTGTGTATCCATGGTAGGCTTTGATGAGAAGATGCAGGTGAAGCTGTGGAACAAGTGCAGGCACCAGAGC
AGCAGCAGCCCTAGTGCCCCCAGCATCTCAGACAGGCTCACTTTACAAGTTGAGGTGATGAACTTGAAGCTAAGA
GTTCCCTCACAGTCCAGGGAGTGAAAGGAAAGTGACAAGTGCACAGGTGGTGAAGCTCATGCCCAGGGGACAGAC
AGACACAGAAAACATCAACAGAATTCTCTAATGGTTCCCAGGGAGAGAGCTGCTCTTTCTTCTGAAGCTCTGGGA
GCTGGCACAGCCCAGGACTTCCTTTGCTCAGTCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAAAAAGAAAAC
CTTTTGCTATCAGAGATCATCACAGGCCGATCACAGGCTAAGAGGAAAGAAGCTCCCTGTGTATCCCTGGATGGC
TTTGATGAGAAGATGCAGGTGGAGCTGTGGAACGAGCATCAAATCAACATTCATAGGATTGGATCAACCAAATTC
GCTGTATTCAGATTAAATTCAACATTTTCAGGGCACAAAGAACAGAGGAAGTCCAGGAAGCCGACTCACCAGGTTTC
TCCAAGGCAGATCGGTGCTTAGGAGACTATAATCCGTGTGGACAGCCACCTAGAAGCAAACCTTCTGGCCATGGTA
GCACAGACTGTGTCATCATTCAGGTTCTGTGGCCAAGCCCCCAAACAGGAATCACGTAGTGAAGTTCAAAGAA
ACTTCCAAAAGGTGCAGCAAAAGAAAGAAAAGAAAAACATAA

WO 2004/030615

PCT/US2003/028547

394/6881
FIGURE 364

AAACACTCTGTGTGGCTCCTCGGCTTTGGGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGC
AACATAGAGACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGG
GAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATGAAAAGGTCATAGAA
CACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGG
CTAACCTGGGCCTCCACGAGAAGATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGG
GAGGGCACCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCATGGCCACAGTCATGGTGGCCACGGC
CACAGGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCTGTTATGTCAAAC
GTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTCCTCCAA

WO 2004/030615

PCT/US2003/028547

395/6881
FIGURE 365

MTCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHIMEDLDTNADKQLS
FEEFIMLMARLTWASHEKMHEGDEGPGHHHKPGLGEGTP

WO 2004/030615

PCT/US2003/028547

396/6881
FIGURE 366

GAGCAGCCTTCCTGAGAGAGGAGAGAGAAAAGCTCAGGGAGGTCTGGAGCAAAGATACTCCTGGAGGTGGGGAGTG
AGGCAGGGGATAAGGAAGGAGAGTATCCTCCAGCACCTTCCAGTGGGTGGGGCAAGTCCGTGGGCATCATGTTGAC
CGAGCTGGAGAAAGCCTTGAACCTCTATCATCGACGTCTACCACAAGTACTCCCTGATAAAGGGGAATTTCCATGC
CGTCTACAGGGATGACCTGAAGAAATTGCTAGAGACCGAGTGTCCTCAGTATATCAGGAAAAAGGGTGCAGACGT
CTGGTTCAAAGAGTTGGATATCAACACTGATGGTGACAGTTAACTTCCAGGAGTTCCTCATTCTGGTGATAAAGAT
GGGCGTGGCAGCCCACAAAAAAGCCATGAAGAAAGCCACAAAGAGTAGCTGAGTTACTGGGCCCAGAGGCTGGG
CCCCCTGGACATGTACCTGCAGAATAATAAAGTCATCAATACCTC

WO 2004/030615

PCT/US2003/028547

397/6881
FIGURE 367

GGGACCGCTATAAGGCCAGTCGGACTGCGACATAGCCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCC
CTACCGCTCCAAGCCCAGCCCTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTC
CACAAGTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGATCCAGAAGGAG
CTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGAAGACTTGGACCGGAACAAGGACCAG
GAGGTGAACCTCCAGGAGTATGTCACCTTCCTGGGGGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGA

AAATAAATAGGGAAGATGGAGACACCTCTGGGGGTCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATA
AATTTTTTTTTGGTCAAATTT

WO 2004/030615

PCT/US2003/028547

398/6881
FIGURE 368

MACPLDQAIGLLVAIFHKYSGREGDKHTLSKKELKELIQKELTIGSKLQDAEIARLMEDLDRNKDQEVNFQEYVT
FLGALALIYNEALKG

WO 2004/030615

PCT/US2003/028547

399/6881
FIGURE 369

ATTCTTCCCCCTCTCTACAACCCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCTATGGCG
TGCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAGAGGGTGACAAGTTC
AAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGCCAGCTTCTTGGGGAAAAGGACAGATGAA
GCTGCTTTCCAGAAGCTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTC
TTCCTGTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGA

AAACTCCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTGCGCCAGTGGGCACTTTTTTTTTTTCCA
CCCTGGCTCCTTCAGACACGTGCTTGATGCTGAGCAAGTTCAATAAAGATTCTTGGAAGTTT

WO 2004/030615

PCT/US2003/028547

400/6881
FIGURE 370

MACPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSFLGKRTDEAAFQKLMSNLDSNRDNEVDFQEY
CVFLSCIAMMCNEFFEGFPDKQPRKK

WO 2004/030615

PCT/US2003/028547

401/6881

FIGURE 371

GGTGCTTCTGAGATGTGGGCTTGACACGCTGTTGCTATAGTACGTGTGATCCTGACTGCTGTCAATGGCGTGCCC
TCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAGAGGGTGACAAGTTCAAGCT
CAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGCCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGC
TTTCCAGAAAGCTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCT
GTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGAAAACT
CCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTGCGCCAGTGGGCACTTTTTTTTTTCCACCCTG
GCTCCTTCAGACACGTGCTTGATGCTGAGCAAGTTCAATAAAGATTCTTGGAAGTTT

WO 2004/030615

PCT/US2003/028547

402/6881
FIGURE 372

MACPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSTFLGKRTDEAAFAQKLMSNLDSNRDNEVDFQEY
CVFLSCIAMMCNEFFEGFPDKQPRKK

WO 2004/030615

PCT/US2003/028547

403/6881
FIGURE 373

ACACATTCCCCACCCTCTGGGAGCTCCTAGTCTGAGAGAGGAAACACTCCTGCCCAAGGGAGCTTCCAGTTAGAT
GGCAGAGAGAGATGCCTCTGGCTTCAGGAGTCCCCGAGTCTAAGGAGGGAAACGACTCCTTCAGGGAGCTTCCTGC
TCCTAGGCTGTAGCCATGGCTCCTGCCAGACTGCACAGGAGCCCCCATCTGCCAGCCGGTGCATGTGGCCCTGCT
CCCCAGAGCCTGCGCAGATGCCATCAAAATGGGACTCTGGTCAACCCTGTCAATTTCCCTTCTGGCAGACACTAAAA
TGGGGAGCCCTGCCCTCAGGGGGGTGTCCCAAGTGCCATCAGAGGAGGCTTGGTGACTCCCAGACACAAGGAAG
CTTTAGCGTCTGCCCTCAGGGTGAGATGGAGGTATCGCCTCCGGCCTCAGGGAACACAGTCTGAGGGGGAGATG
CAGCCCCTGCCTTCCCATTCAGAGAGGGGTTTTGTGAGGTGGCTTGGGGGCATAGGGCAGAAGTGGATCCTACAG
GCTGAGCTAAGGCCCCAAGAGCCTCAGCAGTGTAACCATCACCTGGCACCTCTGCAGCCACAGATCCATGATGTG
CAGTTCTCTGGAGCAGGCGCTGGCTGTGCTGGTCACTACCTTCCACAAGTACTCCTGCCAAGAGGGCGACAAGTT
CAAGCTGAGTAAGGGGGAAATGAAGGAACCTTCTGCACAAGGAGCTGCCCAGCTTTGTGGGGGAGAAAGTGGATGA
GGAGGGGCTGAAGAAGCTGATGGGCAGCCTGGATGAGAACAGTGACCAGCAGGTGGACTTCCAGGAGTATGCTGT
TTTCTGGCACTCATCACTGTGTCATGTGCAATGACTTCTTCCAGGGCTGCCAGACCGACCCTGAAGCAGAACTCT
TGACTTCTGCCATGGATCTCTTGGGGCCAGGACTGTTGATGCCTTTGAGTTTTGTATTCAATAAACTTTTTTTG
TCTGTTGATAATATTTTAATTGCTCAGTGATGTTCCATAACCCGGCTGGCTCAGCTGGAGTGCTGGGAGATGAGG
GCCTCCTGGATCCTGCTCCCTTCTGGGCTCTGACTCTCCTGGAAATCTCTCCAAGGCCAGAGCTATGCTTTAGGT
CTCAATTTTGGAATTTCAAACACCAGCAAAAAATTGAAATCGAGATAGGTTGCTGACTTTTATTTTGTCAAATA
AAGATATTAAAAAAGGC

WO 2004/030615

PCT/US2003/028547

404/6881
FIGURE 374

GGACTGTTGAAGACAGGTCTCCACACACAGCTCCAGCAGCCACATTTGCAACCTTGGCCATCTGTCCAGAACCTG
CTCCCACCTCAGGCCAGGCCAACCGTGCACTGCTGCAATGGGCTCTGAGCTGGAGACGGCGATGGAGACCCTCA
TCAACGTGTTCCACGCCCACTCGGGCAAAGAGGGGGACAAGTACAAGCTGAGCAAGAAGGAGCTGAAAGAGCTGC
TGCAGACGGAGCTCTCTGGCTTCCTGGATGCCCAGAAGGATGTGGATGCTGTGGACAAGGTGATGAAGGAGCTAG
ACGAGAATGGAGACGGGGAGGTGGACTTCCAGGAGTATGTGGTGCTTGTGGCTGCTCTCACAGTGGCCTGTAACA
ATTTCTTCTGGGAGAACAGTGTGAGCAGACAGCCACATTGGGCAGCGCCCTTCCTCTCCACCCTCCCAGACCTGCC
TCTTCCCCCTGCTTCCACCTCACCCCACTTATCCCTCTCCATAACCCCAACCCTTGCCCCACCCCACCCCACCCCA
ACCAAGGGCGCAAGAGTAGCGGTCCAAGCCTGCAACTCATCTTTCAATTAAAGGCTTCTCTCTACCAGCAAAAAA
AAAAAAA

WO 2004/030615 .

PCT/US2003/028547

405/6881
FIGURE 375

MGSELETAMETLINVFHAHSGKEGDYKLSKKELKELLQTELSGFLDAQKDVAVDKVMKELDENG DGEVDFQEY
VVLVAALTVACNNFFWENS

WO 2004/030615

PCT/US2003/028547

406/6881
FIGURE 376

TCAGACAAGCACTGGACGTGGCGGCCATTTTGTGTTTGGACACCGAGCAGGAGCTGGCGGCCGCTGCAGACGAAAG
GCAGGAAAGGGCAGGCCGGGTGAGCAGACGGATCGGCCGACTAGACAGCCAACCAGCAACAACGAAGTGAAGCTCG
CATACTACCGCTTACGCATCTAACCAACCGCCCATCTAGCTAACCCGAGCCCCTCCACCGTCAACTCAGGTTCCG
CCGGTCCCCCGGCCCGCTGCCGGAGCCGTGGTGGCAGCCCCGGGAGGAGCACTGGCGTCTGTTTCCTTCGATTCT
CGGGATTCTGAAGATGGCTGCACAGTCAGCGCCGAAAGTTGTGCTAAAAAGCACCACCAAGATGTCTCTAAATGAG
CGCTTTACTAATATGCTGAAGAACAACAGCCGACGCCAGTGAATATTCGGGCTTCGATGCAGCAACAACAGCAG
CTAGCCAGTGCCAGAAACAGAAGACTGGCCCAGCAGATGGAGAATAGACCCTCTGTCCAGGCAGCATTAAACTT
AAGCAGAGCTTAAAGCAGCGCCTGGGTAAGAGTAACATCCAGGCACGGTTAGGCCGACCCATAGGGGGCCCTGGCC
AGGGGAGCAATCGGAGGACGAGGCCTACCCATAATCCAGAGAGGCTTGCCCAGAGGAGGACTACGTGGGGGACGT
GCCACCAGAACCCTACTTAGGGGCGGGATGTCACTCCGAGGTCAAAACCTGCTCCGAGGTGGACGAGCCGTAGCT
CCCCGAATGGGCTTAAGAAGAGGTGGTGTTCGAGGTCTGAGAGGTCTGGGAGAGGGGGCCTAGGGCGTGGAGCT
ATGGGTCGTGGCGGAATCGGTGGTAGAGGTGCGGGTATGATAGGTGCGGGGAAGAGGGGGCTTTGGAGGCCGAGGC
CGAGGCCGTGGACGAGGGAGAGGTGCCCTTGCTCGCCCTGTATTGACCAAGGAGCAGCTGGACAACCAATTGGAT
GCATATATGTCGAAAACAAAAGGACACCTGGATGCTGAGTTGGATGCCTACATGGCGCAGACAGATGCCGAAACC
AATGATTGAAGCCTGCCCATCCTCCCATGAGAGACTCTTGTTAGTCAACACATCTGTAAATAACCTTGAGATAAC
AGATGAGAAGAAATCTGATTGATGCTGGATGGACCTATCACAATAGGCTGTGGACTTACTTGCCACCAGCTTGTG
CATTTAGTGTGTTCTTTTACTTTTTGATACTGTGTTGTATGAAACCCTTTTGTCTTTGATTGTTTGTGTT
TTTGTTTTTTTAGGGGGGAGGGGGGGTTTTCCCTCCTTTGCCAGACTTCTCTTTGAACACAAATGCATTAGCCT
TGTGGCTAGAACACCCTCTTCTACCTCTGTCTCCCTCACTTGTCTATGCTCTGACATGCTAACATTTCTTT
GTTTCATCCCTGTTGCCCCACAGAAACATCCAGAAAAACCGGTCAGTGTTCCTTCCTCCCTGATCCTTAGGTTT
CTGAAATAGGGTTCTGTTACATCCTCTTCGATAGCCTGTTTAAATGTTTAGAAGGTCTGGAGCTCAAAATGCG
TTCTTCC

WO 2004/030615

PCT/US2003/028547

407/6881
FIGURE 377

AGGGGTGACAGAGGCCGTGGTCTGGTGGGCGCTTTGGTTCCAGAGGAGGCCAGGAGGAGGGTTCAGGCCCTTT
GTACCACATATCCCATTTGACTTCTATTTGTTGTTTACTTCTGGTTTAGTGTGAAATGGCCTTTCCCGGGTCAA
GCCAGCACCTGATGAACTTCCTTCAGTGAGGCCTTGCTGAAGAGGAATCAGGACCTGGCTCCCAATTCTGCTGA
ACAGGCATCTATCCTTTCTCTGGTGACAAAAATAACAATGTGATTGATAATCTGATTGTGGCTCCAGGGACATT
TGAAGTGCAAATTGAAGAAGTTCGACAGGTGGGATCCTATAAAAAGGGGACAATGACTACAGGACACAATGTGGC
TGACCTGGTGGTGATACTCAAGATTCTGCCAACGTTGGAAGCTGTTGCTGCCCTGGGGAACAAAGTCGTGGAAAG
CCTAAGAGCACAGGATCCTTCTGAAGTTTTAACCATGCTGACCAACGAACTGGCTTTGAAATCAGTTCTTCTGA
TGCTACAGTGAAGATTCTCATTACAACAGTGCCACCCAATCTTCGAAACTGGATCCAGAACTCCATTTGGATAT
CAAAGTATTGCAGAGTGCCTTAGCAGCCATCCGACATGCCCGCTGGTTTCGAGGAAAATGCTTCTCAGTCCACAGT
TAAAGTTCTCATCAGACTACTGAAGGACTTGAGGATTCTGTTTTCTGGCTTTGAGCCCCTCACACCCTGGATCCT
TGACCTACTAGGCCATTATGCTGTGATGAACAACCCACCAGACAGCCTTTGGCCCTAAACGTTGCATACAGGCG
CTGCTTGCAGATTCTGGCTGCAGGACTGTTTCTGCCAGGTTTCAGTGGGTATCACTGACCCCTGTGAGAGTGGCAA
CTTTAGAGTACACACAGTCATGACCCTAGAACAGCAGGACATGGTCTGCTATACAGCTCAGACTCTCGTCCGAAT
CCTCTCACATGGTGGCTTTAGGAAGATCCTTGGCCAGGAGGGTGATGCCAGCTATCTTGCTTCTGAAATATCTAC
CTGGGATGGAGTGATAGTAACACCTTCAGAAAAGGCTTATGAGAAGCCACCAGAGAAGAAGGAAGGAGAGGAAGA
AGAGGAGAATACAGAAGAACCACCTCAAGGAGAGGAAGAAGAAAGCATGGAACTCAGGAGTGACATTCCCTTCA
CTCCTTTTCTACCCAAGGGGGAAGACTGGAGCTAAGCTGCCTGCTACTGGGCTTTACATGGTGACAGACATTT
CCGTGGGATAGGGAAGATAGCAGGAAGAAAAGTAACTCCATAGAAGTGTCATTCCACTGGGTTTTGATATTGGC
TTAGCTGCCAGTCTCCCATTTGTGACCTATGCCATCCATCTATAATGGAGGATACCAACATTTCTTCCTAATATT
CTATAATCTCCAACCTCTGAAAACCCCTCTCTCAACTAATACTTTGCTGTTGAAATGTTGTGAAATGTTAAGTGT
CTGGAAATTTTTTTTTCTAAGAAAACTATTAAAGTACTT

WO 2004/030615

PCT/US2003/028547

408/6881

FIGURE 378

MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDLYLCEMAFPRVKPAPDETSFSEALLKRNQDLAPNSAEQASIL
SLVTKINNVIDNLIVAPGTFEVQIEEVRQVGSYKKGTTGHNVDLVVILKILPTLEAVAALGNKVVESLRAQD
PSEVLTMLTNETGFEISSSDATVKILITVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEENASQSTVKVLIR
LLKDLRIRFPGFEP LTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGLFLPGSVGITDPCESGNFRVHT
VMTLEQQDMVCYTAQTLVRILSHGGFRKILGQEGDASYLASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTE
EPPQEEEEESMETQE

WO 2004/030615

PCT/US2003/028547

409/6881
FIGURE 379

CACACCCGCACTCCTCCCGGGTTTCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTTCGGAAGGGAGGAT
CAGGGATGTTTTGCGAGCGGCTGGAACGAGACGGTGCCGATAGAGGAAGCGGGCTCCATGGCTGCCCTCCTGCTGC
TGCCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGAAAGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGG
ACTTGGCCTTTGCGGTGCGAGCTCTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCG
ACCCGGAAGGTCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAAGTGGCCAGCAGCGCGCCGCGCACA
CCTTTCTCATTACAGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAACAGGGCTGCACGCGCCT
TCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAGCGGCGAGGGGAGCGCTGGAGAAGGCGAGC
GGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCGGAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAG
GTGGAGGAGCCGCCGCCCTCTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTTCTGT
GGCTCTGGTTGGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCCCCCTGC
TGCACTGCCTCCGCGAGCTGCGGCGCGCGCGCGCTGGTGTGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACC
TGCCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATT
TGCTGGCTGAAGTGTCCGCTGAAGTGGATGGGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAAACAGACA
CGTGCCCTGTACATCTTACCTCTGGCACCAGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGC
AATGCCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCACTCTACCACA
TGTCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTGGTGTGAAATCCAAGTTCTCGG
CTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCAGTACATTGGGGAGCTGTGCCGATACC
TTGTCAACCAGCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAG
ATACCTGGGAGCGTTTTGTGCGGCGCTTCGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACG
TGGCCACCATCACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGCATATCTTCCCT
TCTCCTTGATTGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCCCAGGGGCACTGTATGGCCACATCTC
CAGGTGAGCCAGGGCTGCTGGTGGCCCCGTAAGCCAGCAGTCCCCATTCCTGGGCTATGCTGGCGGGCCAGAGC
TGGCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCT
GCGATGACCAAGGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGAGAATGTGGCCA
CAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGTGCCAG
GGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCCCACGCTTTGGACCTTATGCAGCTCTACA
CCCACGTGCTGAGAACTTGCCACCTTATGCCCGGCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAG
AGACCTTCAAACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCGACCCACAGACCCTGTCTGACCCACTGTACG
TTCTGGACCAGGCTGTAGGTGCCTACCTGCCCCTCACTGCCCCGTACAGCGCCCTCCTGGCAGGAAACCTTC
GAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACCTGTGTGGGGTGGGGGCGGTTGCAGGTGTACTGG
GCTGTGAGGGATCTTTTCTATACCAGAACTGCGGTCATATTTGTAAATAAATGTGGCTGGAGCTGATCCAGCTG
TCTCTGACCTACAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

410/6881
FIGURE 380

MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLPPLLLPLLLKLHLWPQLRW
LPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQRAAHTFLIHGSRFSYSEAERESNR
ARAFRLALGWDWGPDDGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLPAGP
EFLWLWFGGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG
ISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYLALP
LYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVR LAVSG
LRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRD PQGHCM
ATSPGEPGLLVAPVSQQSPFLGYAGGP ELAQGKLLKD VFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGE
NVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYPARPRFLRLQESL
ATTETFKQQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI

WO 2004/030615

PCT/US2003/028547

411/6881
FIGURE 381

GGCACGAGGGGGCTTCAGGACAATTCGTGATGCGGGGGCTGGTTCCGCCGCTGTATCGGGGGCAGGGACCCCGG
TGGCGGGGGCCACAGGCCGCGACCTTTTCGCCGAAGGGCTGCTGGAGTTCCTGCGACCCGCTGTGCAGCAGCTCG
ACTCTCACGTACACGCCGTAGAGAGAGCCAGGTAGAGCTCCGGGAACAAATTGACAACCTAGCCACAGAACTGT
GCCGCATAAATGAGGATCAGAAGGTGGCCCTGGATCTTGACCCCTATGTTAAGAAGCTACTTAATGCCCCGGCGAC
GCGTTGTCTTGGTTAACAACATTCTACAGAATGCTCAGGAACGACTGAGACGGCTAAACCACAGTGTTGCCAAGG
AAACAGCCCCGAGGAGAGCAATGCTGGATTCCGGGAATTTACCCCCCTGGCTCCCCAGGCATAACAGATGAGCC
TATGGACTCAGTAGCACAACTACTGTTCCCCAGCTGCCTTGTTTCAACAGACATGCAAAGATCCTAGGAGACAGT
CCCCATAGACCTTCAGACATTAATAAAGGGAGCCGTACAGTTTGTTTGAAGCACTTCGTCTTACCCATTTATGTAG
GGGCCCCAGGAAACCTACACACAGCCAGAATGAGGTTCCCAAAGGACTTACATTAATTATGGCTCTTGCTTCCTT
TCACAAATGAGCTGAGGCCTCTACTTTTTTTTTTTTAAAGCTGCATACTTGAGGCTTACCTTCTTCAGGACTAGTT
AACCAGAGGGGGCTTCCTTTGTATGTTACATGCCTGGTTACATGGGCCTGGACAGCATGTCCTCTACCTGTGACTT
CTCATTTTCTGTGTTTACACTGGGGATTTGGAGGGGGCAGGCAAAGTCAAAGTGAATGACCTCTGTCCACCCACTT
TTTTATTGCACTGGCTTGAATACAGTAGCAGTGTGATAGAATCATTTTATTCAATAAAATACTTAAATGAAAAA
AAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

412/6881
FIGURE 382

MAGAGSAAVSGAGTPVAGPTGRDLFAEGLLEFLRPAVQQLD SHVHAVRESQVELREQIDNLATELCRINEDQKVA
LDLDPYVKKLLNARRRVVLVNNILQNAQERLRRLNHSVAKETARRRAMLDSGIYPPGSPGK

WO 2004/030615

PCT/US2003/028547

413/6881
FIGURE 383

CTATGATAAGCTAATTATTTATGTTTGCATAATATTTATGTTTGCATGTTAGTGACATATATTTTAAAAATGTGAT
ACACTCCTGTAATTTATGAGAGTATGTTTCATTGCTGTGAGCTTTGAAGGTGCTCTAATCCTTCCTCATATTTGGC
CTTAGAATGCACCTCGGATCCCCAAGGTTTAGGCTTTCTTCATTTGTCTTTGAAACTATATCTTCTGTCTCTTG
TCATATCTGCTTATTGCGTGTTTTTCATACCTTCCACCTCTCTAAAAGCCGTTACCTGAGCCCTCGTTATCACTT
TTGGTTGAATGTGCTGCACTTAGCTGCATTTCTAAGTTTCTGATTCTTGCAAGTTTGTGGAAACAGAGGAGTCTT
TAACCCACATCAGCCTTGATCTAAGTGTACCACTTTACTTAAAAGTTCTGTTGGGATCTGGAGCTCCTGGTCTAGCA
AGCCATGAAAATGCCAATAAATGTTTGTAAATAAGCTTTTATTTAAACATCCATTTTGTTCGACCTTGAAGCTTT
ACTAATATGCTGAAGAACAACAGCCGACGCCAGTGAATATTCGGGCTTCGATGCAGCAACAACAGCAGCTAGCC
AGTGCCAGAAACAGAAGACTGGCCCAGCAGATGGAGAATAGACCCTCTGTCCAGGCAGCATTAAAACCTTAAGCAG
AGCTTAAAGCAGCGCCTGGGTAAGAGTAACATCCAGGCACGGTTAGGCCGACCCATAGGGGGCCCTGGCCAGGGGA
GCAATCGGAGGACGAGGCCTACCCATAATCCAGAGAGGCTTGCCCAGAGGAGGACTACGTGGGGGACGTGCCACC
AGAACCCTACTTAGGGGCGGGATGTCACCTCCGAGGTCAAACCTGCTCCGAGGTGGACGAGCCGTAGCTCCCCGA
ATGGGCTTAAGAAGAGGTGGTGTTCGAGGTCTGTTGAGGTCTGTTGAGAGGGGGCCCTAGGGCGTGGAGCTATGGGT
CGTGGCGGAATCGGTGGTAGAGGTCTGGGGTATGATAGGTCTGGGGAAGAGGGGGCTTTGGAGGCCGAGGCCGAGGC
CGTGGACGAGGGAGAGGTGCCCTTGCTCGCCCTGTATTGACCAAGGAGCAGCTGGACAACCAATTGGATGCATAT
ATGTGAAAAACAAAAGGACACCTGGATGCTGAGTTGGATGCCTACATGGCGCAGACAGATCCCGAAACCAATGAT
TGAAGCCTGCCCCATCCTCCCATGAGAGACTCTTGTTAGTCAACACATCTGTAAATAACCTTGAGATAACAGATGA
GAAGAAATCTGATTGATGCTGGATGGACCTATCACAATAGGCTGTGGACTTACTTGCCACCAGCTTGTGCATTTA
GTGTGTTCCCTTTTACTTTTTGATACTGTGTTGTATGAAACCCTTTTGTCTTTGATTTGGTTTTTTGTTTTTGT
TTTTTAGGGGGGAGGGGGGGTTTTCCCTCCTTTGCCAGACTTCTCTTTGAACACAAATGCATTAGCCTTGTGGC
TAGAACACCCTCTTCCTACCTCTGTCTCCCTCACTTGTCTATGCTCTGACATGCTAACATTTCTTTGTTTCAT
CCCTGTTGCCCCCACAGAAACATCCAGAAAAACCGGTGAGTGTCTCTCCTCCCTGATCCTTAGGTTTCTGAAA
TAGGGTTCTGTTACATCCTCTTCGATAGCCTGTTTAAATGTTTAGAAGGTCTGGAGCTCAAAAATGCGTTCTTC
C

WO 2004/030615

PCT/US2003/028547

414/6881
FIGURE 384

CCACAGATCCATGATGTGCAGTTCTCTGGAGCAGGCGCTGGCTGTGCTGGTCACTACCTTCCACAAGTACTCCTG
CCAAGAGGGCGACAAGTTCAAGCTGAGTAAGGGGGAATGAAGGAACTTCTGCACAAGGAGCTGCCCAGCTTTGT
GGGGGAGAAAGTGGATGAGGAGGGGCTGAAGAAGCTGATGGGCAGCCTGGATGAGAACAGTGACCAGCAGGTGGA
CTTCCAGGAGTATGCTGTTTTCTGGCACTCATCACTGTCAATGCAATGACTTCTTCCAGGGCTGCCCAGACCG
ACCCTGAAGCAGAACTCTTGACTTCCTGCCATGGATCTCTTGGGCCAGGACTGTTGATGCCTTTGAGTTTGTGTA
TTCAATAAACTTTTTTTGTCTGTTGAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

415/6881
FIGURE 385

MMCSSLEQALAVLVTTTFHKYSCQEGDKFKLSKGEMKELLHKELPSFVGEKVDEEGLKKLMGSLDENSQQVDFQE
YAVFLALITVMCNDFQGCPRP

WO 2004/030615

PCT/US2003/028547

416/6881
FIGURE 386

GCGCCAGACTTGCTGCCGGGCTGGACGGTCCGCACGGTGCTGGGCAGCAGCGAAAACGCGCTGGGCGTGTGCTC
CGACACCGCAGCGCCCTGGCCGCGGTGGACCTCAAGTGGGAGCACAACCCCGCTGTGTTCTGGGCCCCGGCTG
CGTGACGCCGCCGCCAGTGGGGCGCTTACC CGC GACTGGCGGGTCCCGCTGTGACCGCCGGCGCCCCGGC
GCTGGGCTTCGGTGTCAAGGACGAGTATGCGCTGACCACCGCGCGGGGCCAGCTACGCCAAGCTGGGGGACTT
CGTGGCGGCGCTGCACCGACGGCTGGGCTGGGAGCGCCAAGCGCTCATGCTCTACGCCTACCGGCCGGGTGACGA
AGAGCACTGCTTCTTCTCGTGGAGGGGCTGTTTCATGCGGGTCCGCGACCGCCTCAATATTACGGTGGACCACCT
GGAGTTCGCGGAGGACGACCTCAGCCACTACACCAGGCTGCTGCGGACCATGCCGCGCAAAGGCCGAGTTATCTA
CATCTGCAGCTCCCTGATGCCTTCAGAACCCTCATGCTCCTGGCCCTGGAAGCTGGCTTGTGTGGGGAGGACTA
CGTTTTCTTCCACCTGGATATCTTTGGGCAAAGCCTGCAAGGTGGACAGGGCCCTGCTCCCCGAGGCCCTGGGA
GAGAGGGGATGGGCAGGATGTGAGTGCCTGCCAGGCCCTTTCAGGCTGCCAAAATCATTACATATAAAGACCCAGA
TAATCCCGAGTACTTGAATTCCTGAAGCAGTTAAACACCTGGCCTATGAGCAGTTCAACTTCACCATGGAGGA
TGGCCTGGTGAACACCATCCCAGCATCCTTCCACGACGGGCTCTGCTCTATATCCAGGCAGTGACGGAGACTCT
GGCACATGGGGGAAGTGTACTGATGGGGAGAATCACTCAGCGGATGTGGAACCGAAGCTTTCAAGGTGTGAC
AGGATACCTGAAAATTGATAGCAGTGGCGATCGGGAAACAGACTTCTCCCTCTGGGATATGGATCCCGAGAATGG
TGCCTTCAGGGTGTACTGAACTACAATGGGACTTCCCAAGAGCTGGTGGCTGTGTCGGGGCGCAAAGTGAAGT
GCCCCGAGGGTACCTCCTCCTGACATCCCCAAATGTGGCTTTGACAACGAAGACCCAGCATGCAACCAAGATCA
CCTTTCACCCCTGGAGGTGCTGGCTTTGGTGGGCAGCCTCCTTGGCTCGGCATTCTGATTGTCTCCTTCTTCAT
ATACAGGAAGATGCAGCTGGAGAAGGAAGTGGCCTCGGAGCTGTGGCGGGTGCGCTGGGAGGACGTTGAGCCAG
TAGCCTTGAGAGGCACCTGCGGAGTGCAGGCAGCCGGCTGACCTGAGCGGGAGAGGCTCCAATTACGGCTCCCT
GCTAACACAGAGGGCCAGTTCCAAGTCTTTGCCAAGACAGCATATTATAAGGGCAACCTCGTGGCTGTGAAACG
TGTGAACCGTAAACGCATTGAGCTGACACGAAAAGTCCGTGTTGAACTGAAGCATATGCGGGATGTGCAGAATGA
ACACCTGACCAGGTTTGTGGGAGCCTGCACCGACCCCCCAATATCTGCATCCTCAGAGTACTGTCCCCGTGG
GAGCCTGCAGGACATTCTGGAGAATGAGAGCATCACCTGGACTGGATGTTCCGGTACTCACTACCAATGACAT
CGTCAAGGGCATGCTGTTTCTACACAATGGGGCTATCTGTTCCCATGGGAACCTCAAGTCATCCAAGTGCCTGGT
AGATGGGCGCTTTGTGCTCAAGATCACCGACTATGGGCTGGAGAGCTTCAGGGACCTGGACCCAGAGCAAGGACA
CACCGTTTATGCCAAAAGCTGTGGACGGCCCTGAGCTCCTGCGAATGGCTTCACCCCTGTGCGGGGCTCCCA
GGCTGGTGACGTATACAGCTTTGGGATCATCTTCAGGAGATTGCCCTGAGGAGTGGGGTCTTCCACGTGGAAGG
TTTGGACCTGAGCCCCAAGAGATCATCGAGCGGGTACTCGGGGTGAGCAGCCCCCTTCCGGCCCTCCCTGGC
CCTGCAGAGTCACCTGGAGGAGTTGGGGCTGCTCATGCAGCGGTGCTGGGCTGAGGACCCACAGGAGAGGCCACC
ATTCCAGCAGATCCGCTGACGTTGCGCAAATTTAACAGGGAGAACAGCAGCAACATCCTGGACAACCTGCTGTC
CCGCATGGAGCAGTACGCGAACAATCTGGAGGAAGTGGTGGAGGAGCGGACCCAGGCATACCTGGAGGAGAAGCG
CAAGGCTGAGGCCCTGCTCTACCAGATCCTGCCCTCACTCAGTGGCTGAGCAGCTGAAGCGTGGGGAGACGGTGCA
GGCCGAAGCCTTTGACAGTGTACCATCTACTTCAGTGACATTGTGGGTTTCACAGCGCTGTGCGCGGAGAGCAC
ACCCATGCAGGTGGTGACCTGCTCAATGACCTGTACACTTGCTTTGATGCTGTCATAGACAACCTTTGATGTGTA
CAAGGTGGAGACAATTGGCGATGCCTACATGGTGGTGTGAGGGCTCCCTGTGCGGAACGGGCGGCTACACGCCTG
CGAGGTAGCCCGCATGGCCCTGGCACTGCTGGATGCTGTGCGCTCCTTCCGAATCCGCCACCGGCCCCAGGAGCA
GCTGCGCTTGCGCATTGGCATCCACACAGGACCTGTGTGTGCTGGAGTGGTGGGACTGAAGATGCCCGTTACTG
TCTCTTTGGGGATACAGTCAACACAGCCTCAAGAATGGAGTCTAATGGGGAAGCCCTGAAGATCCACTTGTCTTC
TGAGACCAAGGCTGTCTGAGGAGTTTGGTGGTTTCGAGCTGGAGCTTCGAGGGGATGTAGAAATGAAGGGCAA
AGGCAAGGTTTCGACCTACTGGCTCCTTGGGGAGAGGGGGAGTAGCACCCGAGGCTGACCTGCCTCCTCTCTAT
CCCTCCACACCTCCCTACCCTGTGCCAGAAGCAACAGAGGTGCCAGGCCTCAGCCTCACCCACAGCAGCCCCATC
GCCAAAGGATGGAAGTAATTTGAATAGCTCAGGTGTGCTGACCCCAAGTGAAGACACCAGATAGGACCTCTGAGAG
GGGACTGGCATGGGGGATCTCAGAGCTTACAGGCTGAGCCAAGCCCCACGGCCATGCACAGGGACACTCACACAG
GCACACGCACCTGCTCTCCACCTGGACTCAGGCCGGGCTGGGCTGTGGATTCTGATCCCCCTCCCCCTCCCATGC
TCTCCTCCCTCAGCCTTGCTACCCTGTGACTTACTGGGAGGAGAAAGAGTCACCTGAAGGGGAACATGAAAAGAG
ACTAGGTGAAGAGAGGGCAGGGGAGCCACATCTGGGGCTGGCCACAATACCTGCTCCCCCGACCCCTCCACC
CAGCAGTAGACACAGTGCACAGGGGAGAAGAGGGGTGGCGCAGAAGGGTTGGGGGCTGTATGCCTTGCTTCTAC
CATGAGCAGAGACAATTAATAATCTTTATTCCAGTG

WO 2004/030615

PCT/US2003/028547

417/6881
FIGURE 387

MPGPRRPAGSRLRLLLLLLLPPLLLLLLRGSHAGNLTAVVLPPLANTSYPWSWARVGPAVELALAQVKARPDLLPG
WTVRTVLGSSSENALGVCSDTAAPLAAYDLKWEHNPAVFLGPGCVYAAAPVGRFTAHWRVPLLTAGAPALGFGVKD
EYALTTRAGPSYAKLGDFVAALHRRRLGWERQALMLYAYRPGDEEHCFLLVEGLFMRVRDRNLITVDHLEFAEDDL
SHYTRLLRTMPRKGRVIYICSSPDAFRTLMLLALAEAGLCGEDYVFFHLDIFGQSLQGGQGPAPRRPWERGQDV
SARQAFQAAKIITYKDPDNPEYLEFLKQLKHLAYEQNFMTEDGLVNTIPASFHDGLLLYIQAVTETLAHGGTGT
DGENITQRMWNRSFQGVGTGYLKIDSSGDRETDFSLWMDMPENGAFRVVLNYNGTSQELVAVSGRKLNWPLGYPPP
DIPKCGFDNEDPACNQDHLSTLEVLALVGSLSLLGILIVSFFIYRKMQLKELASELWVRWEDVEPSSLERHLR
SAGSRLTSLGRGSNYGSLLTTEGQFQVFAKTAYYKGNLVAVKRVNRKRIELTRKVL FELKHM RDVQNEHLTRFVG
ACTDPPNICILTEYCPRGSLQDILENESITLDWMFRYSLTNDIVKGMLFLHNGAICSHGNLKSNCVVDGRFVLK
ITDYGLESFRDLDP EQGHTVYAKKLWTAPELLRMA SPVVRGSQAGDVYSFGIILQEIALRSGVFHVEGLDLSPE
I IERVTRGEQPPFRPSLALQSHLEELGLLMQRCWAEDPQERPPFQQIRLTLRKFNRENSNILDNLLSRMEQYAN
NLEELVEERTQAYLEEKRAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTPMQVVTL
LNDLYTCFDAVIDNFDVYK VETIGDAYMVVSGLPVRNGRLHACEVARMALALLDAVRSFRIRHRPQEQLRLRIGI
HTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGEALKIHLSSSETKAVLEEFGGFELELRGDVEMKGKGVRTYW
LLGERGSSTRG

WO 2004/030615

PCT/US2003/028547

418/6881
FIGURE 388

CTGGGTGGCGGTATGTTGGTGGGGCCAGCGGCATGGGAGGCATCACCGCAGTCATGGTCAACCAGAACCTGCTGAGC
CCCCTTGTCCTGGAGGTGGACCCCAACATCCAGGCCGTGTGCACCCAGGAGAAGGAGCCGATCAAGACCCTCAAC
AACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAGCAGCAGAACAAGATGCCGGAGACCAAGTGGAGC
CTCCTGCAGCAGCAGAAGACGGCTCGGAGCAACATGGACAAGTTCGAGAGCTACATCAACAACCTTAGGCAGCAG
CTGGAGATTCTGGGCCAGGAGAAGCTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGGGGCTGGTGGAGGACTTC
AAGAACAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAATGAATTTGTGCTCACCAAGAAGGATGTG
GATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTTACTGAAGAGATCAGCTTCCTCAGG
CAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCCAGATCTCAGACACATCATTGCTGAGGTCAAGGCACAGT
ACGAGGACCGCCAGCCGAGCCAGGCTGAGGCTGAGAGCATGTACCAGATCAAGAATGAGGAGCTGCAAGAGCCT
GGCTGGGAAGCACGGGGATGA

WO 2004/030615

PCT/US2003/028547

419/6881
FIGURE 389

TTGCCCGGGACTAGGAGCTTAAGTGAAGAGGTACGCCTTGTTCCGGTGGAAATCAGCCGTAGCCATGAGTTTCTGC
CGGGGCTAGCCCTAGAGTACGGAGCAGGCGGACTTTTCGGTTCCCCGCCCCGCCAGGTGGCGGGGCTACTAGGC
CTCCGGGCATCCCCGGTCTCAAGTAGGCCTCATCTGCCGGCAAGGGCGCCCGAAACGCGGGAGGCGCCATGTCGC
TGGTTGCTTACGCCAGCAGCGATGAGAGCGAGCCGGATGAGGCTGAGCCCCGAGCCGGAGGAAGAGGAGGCGGTGG
CTCCTACATCTGGGCCCCGCTTTAGGGGGCTTGTTTCGCTTCTCTCCCTGCGCCCAAGGGTCCGGCCTTGCTGCCTC
CGCCCCCTCAGATGCTGGCGCCAGCCTTTCCCCCGCCGCTGTTGCTTCCCCACCCACCGGAGACCCCAAGGCTTC
AGCCTCTCTCCCCCTTGCCCTTCGGCCTGGGAGGCTTCCCCCACCTCCAGGCGTGAGCCCGGCTGAAGCGGCGG
GAGTTGGGGAGGGACTGGGATTGGGGTTGCCCTCGCCCCGAGGCCCTGGCCTCAATCTGCCCCCTCCAATTGGCG
GTGCCGGTCCCCCGCTGGGGCTTCCCAAGCCAAAGAAGAGGAAAGAGCCCGTGAAGATCGCGGCGCCGGAGTTGC
ATAAGGGAGATTGAGATTCTGAGGAAGATGAACCCACAAAGAAGAAACTATCCTTCAGGGATCCAGTGAGGGGA
CTGGTTTGTCTGCCTTGCTTCCCCAACCTAAAACCTGACTGTGAAAGAGACTAACAGGTTGCTCCTGCCCATG
CCTTCTCCCGCAAACCTTCGGATGGCTCCCTGATACTAAGCCCTCCAGACTGGCTTCTAAGACCAAGACTTCTCT
CTCTTGCCCCCTGTTGTGGGCACCACAACCACCACTCCGTCGCCCCCTGCTATCAAGGCTGCTGCCAAGAGTGCTG
CCCTGCAGGTGACAAAGCAGATCACGCAGGAAGAAGACGACAGTGATGAGGAAGTAGCCCCCGAAAACCTTTTCT
CCCTCCCTGAAAAGGCTGAGCCACCTGGAGTTGAGCCATACCTTTACCCCATCCCCACTGTCCCTGAAGAGCTGC
CTCCAGGCACGGAACCAGAGCCGGCTTTCCAGGACGATGCAGCCAATGCCCCCTTGAATTCAAGATGGCAGCAG
GTTCAAGTGGGGCCCCCTTGGATGCCTAAGCCTGGGGACGACTACAGCTACAATCAGTTTCCACATATGGCGATG
CCAATGCCGCTGGTGCTTATTATCAGGATTATTACAGTGGTGGCTACTATCCTGCACAGGACCCGGCCCTGGTCC
CCACCCAGGAAATTGCCCCAGATGCCTCCTTCATCGATGACGAAGCATTAAAGCGGCTGCAGGGCAAGAGGAACC
GAGGGAGAGAAGAAATCAACTTTGTGGAGATCAAAGGTGATGACCAGCTCAGTGGGGCCAGCAATGGATGACTA
AGTCATTGACAGAAGAGAAAACCATGAAGTCATTACGCAAAAAGAAAGGTGAGCAGCCAACAGGCCAGCAGCGGC
GGAAACACCAGATCACATATCTTATTCATCAGGCCAAGGAGCGGGAGCTGGAAGTGAAGAACACCTGGTCAGAGA
ACAAGCTCAGCCGCGCTCAGACCCAAGCCAAATATGGATTCTAGGGCTCTGGAAGTGAATGCTCCCAGGATCTCC
TGCCAGCCCAGCTGGCCTGGCCCCCAGCTTACCTCTGGGACCCAGCTGCTCTAAGCCCAGGATCTCTTTCCCC
AAGGACCCAGCCCTCGCCTCTGCGAGAATGAACATATTTGATAGATTTTCTTAACAAGTTAGAAAATTCAGCTC
CTTTCTGTCTGGAGCTAGCAAAGACTTGTGTGATGCCTCCGAAGGGGCTCTGAGTTCTGGGGTGGGAGTTTGC
TCTCTGTCTAGGTGTGATAAAATGTTGAACCTCCCCACCACCACTTTTTTTTTTTTTTAAACCAGGGATGTCTGTT
GAAATAAAACATTTCAGTCTGACAAAAA

WO 2004/030615

PCT/US2003/028547

420/6881
FIGURE 390

MSLVAYASSDESEPDEAEPEPEEEEEAVAPTSGPALGGLFASLPAPKGPALLPPPPQMLAPAFPPPLLLPPPTGDP
RLQPPPLPFLGLGGFPPPGVSPAEEAGVGEGGLGLGLPSRGPGLNLPPPIGGAGPPLGLPKPKKRKEPVKIAAP
ELHKGDSDEEPTKKKTIQGSSEGTGLSALLPQPKNLTVKETNRLLLPHAFSRKPSDGSPTKPSRLASKTK
TSSLAPVVGTTTTTTPSPSAIKAAKSAALQVTKQITQEEDDSDEEVAPENFFSLPEKAEPPGVEPYYP IPTVPE
ELPPGTEPEPAFQDDAANAPLEFKMAAGSSGAPWMPKPGDDYSYNQFSTYGDANAAGAYYQDYYSGGYYP AQDPA
LVPTQEIAPDASFIDDEAFKRLQGKRNRGREEINFVEIKGDDQLSGAQQWMTKSLTEEKTMKSFSSKKKGEQPTGQ
QRRKHQITYLIHQAKERELELKNWSENKLSRRQTQAKYGF

WO 2004/030615

PCT/US2003/028547

421/6881
FIGURE 391

GAGGAGGAGTGGGGACCGGGCGGGGGGTGGAGGAAGAGGCCTCGCGCAGAGGAGGGAGCAATTGAATTTCAAACA
CAAACAACCTGCACGAGCGCGCACCCACCGCGCCGGAGCCTTGCCCCGATCCGCGCCCGCCCCGTCCGTGCGGGCGC
GCGGGCGGAGACGCCGTGGCCGCGCCGGAGCTCGGGCCGGGGGCCACCATCGAGGCGGGGGCCGCGCGAGGGCCG
GAGCGGAGCGGCGCGCCACCGCCGACGCGCAAACCTTGGGCTCGCGCTTCCCGGCCCGGCGCGGAGCCCCGGGGC
GCCCGGAGCCCCGCCATGTCGCGATCCAACCGGCAGAAGGAGTACAAATGCGGGGACCTGGTGTTCGCCAAGATG
AAGGGCTACCCACACTGGCCGGCCCGGATTGACGAGATGCCTGAGGCTGCCGTGAAATCAACAGCCAACAAATAC
CAAGTCTTTTTTTTTCGGGACCCACGAGACGGCATTCTTGGGCCCCAAAGACCTCTTCCCTTACGAGGAATCCAAG
GAGAAGTTTGGCAAGCCCAACAAGAGGAAAGGGTTGAGCGAGGGGCTGTGGGAGATCGAGAACAACCCCTACTGTC
AAGGCTTCCGGCTATCAGTCTCTCCAGAAAAGAGCTGTGTGGAAGAGCCTGAACCAGAGCCCCGAAGCTGCAGAG
GGTGACGGTGATAAGAAGGGGAATGCAGAGGGCAGCAGCGACGAGGAAGGGAAGCTGGTCATTGATGAGCCAGCC
AAGGAGAAGAACGAGAAAGGAGCGTTGAAGAGGAGAGCAGGGGACTTGCTGGAGGACTCTCTTAAACGTCCCCAAG
GAGGCAGAAAACCTTGAAGGAGAGGAGAAGGAGGCAGCCACCTTGGAGGTTGAGAGGCCCCCTTCTATGGAGGTG
GAAAAGAATAGCACCCCTCTGAGCCCGGCTCTGGCCGGGGGCTCCCCAAGAGGAAGAAGAGGAGGAGGATGAA
GAGGAAGAGGCTACCAAGGAAGATGCTGAGGCCCCAGGCATCAGAGATCATGAGAGCCTGTAGCCACCAATGTTT
CAAGAGGAGCCCCCACCCTGTTCTGCTGCTGTCTGGGTGCTACTGGGGAACCTGGCCATGGCCTGCAAACTGGG
AACCCTTTTCCACCCCAACCTGCTCTCTCTTCTACTACTTTTCCCACTCCAAGCCAGCCCCATGGAGATTGA
CCTGGATGGGGCAGGCCACCTGGCTCTCACCTCTAGGTCCCCATACTCTATGATCTGAGTCAGAGCCATGTCTT
CTCCCTGGAATGAGTTGAGGCCACTGTGTTTCTTCCGCTTGGGAGGGGCAATCCTCAAATGCGGGGTGGGGGCAG
CACAGGAGGGCGGCCTCCTTCTGAGCTCCTGTCCCCTGCTACACCTATTATCCCAGCTGCCTAGATTACAGGGAAA
GTGGGACAGCTTGTAGGGGAGGGGCTCCTTTCCATAAATCCTTGATGATTGACAACACCCATTTTCTTTTGCC
GACCCCAAGAGTTTGGGAGTTGTAGTTAATCATCAAGAGAATTGGGGCTTCCAAGTTGTTGGGGCCAAGGACC
TGAGACCTGAAGGGTTGACTTTACCCATTTGGGTGGGAGTGTGAGCATCTGTCCCCCTTTAGATCTCTGAAGCC
ACAAATAGGATGCTTGGGAAGACTCCTAGCTGTCCTTTTTCTCTCCACACAGTGCTCAAGGCCAGCTTATAGTC
ATATATATACCCAGACATAAAGGAAAAGACACATTTTTTAGGAAATGTTTTAATAAAAAGAAAATTACAAAAAA
AAATTTTAAAGACCCCTAACCTTTGTGTGCTCTCCATTCTGCTCCTTCCCCATCGTTGCCCCCATTTCTGAGGT
GCACTGGGAGGCTCCCTTCTATTTGGGGCTTGATGACTTTCTTTTGTAGCTGGGGCTTTGATGTTCTCTCCAG
TGTCATTTCTCATCCACATACCCTGACCTGGCCCCCTCAGTGTGTGTCACCAGATCTGATTTGTAACCCACTGAGA
GGACAGAGAGAAATAAGTGCCCTCTCCACCCCTCTTCTACTGGTCTCTCTATGCCTCTCTACAGTCTCGTCTCT
TTTACCCTGGCCCTCTCCCTTGGGCTCTGATGAAAATTGCTGACTGTAGCTTTGGAAGTTTAGCTCTGAGAAC
CGTAGATGATTTAGTTCTAGGAAAATAAAACCCGTTGATTACT

WO 2004/030615

PCT/US2003/028547

422/6881
FIGURE 392

AGCTTTGGGGTTGTCCCTGGACTTGTCTTGGTTCCAGAACCTGACGACCCGGCGACGGCGACGTCTCTTTTGA
AAAAGACAGTGTCCAGTGTCCAGCCTAGGAGTCTACGGGGACCGCTCCCGCGCCGCCACCATGCCCCAACTTCT
CTGGCAACTGGAAAATCATCCGATCGGAAAACCTCGAGGAATTGCTCAAAGTGCTGGGGGTGAATGTGATGCTGA
GGAAGATTGCTGTGGCTGCAGCGTCCAAGCCAGCAGTGGAGATCAAACAGGAGGGAGACACTTTCTACATCAAAA
CCTCCACCACCGTGCGCACCACAGAGATTAACTTCAAGGTTGGGGAGGAGTTTGAGGAGCAGACTGTGGATGGGA
GGCCCTGTAAGAGCCTGGTGAATGGGAGAGTGAGAATAAAATGGTCTGTGAGCAGAAGCTCCTGAAGGGAGAGG
GCCCCAAGACCTCGTGGACCAGAGAACTGACCAACGATGGGGAAGTATCCTGACCATGACGGCGGATGACGTTG
TGTGCACCAGGGTCTACGTCCGAGAGTGAGTGGCCACAGGTAGAACC GCGCCGAAGCCCACCACTGGCCATGCT
CACCGCCCTGCTTCACTGCCCCCTCCGTCCCACCCCTCCTTCTAGGATAGCGCTCCCCCTTACCCCACTCACTTC
TGGGGGTCACTGGGATGCCTCTTGCAGGGTCTTGCTTTCTTTGACCTCTTCTCTCTCCCTACACCAACAAAGA
GGAATGGCTGCAAGAGCCCAGATCACCCATTCCGGGTTCACTCCCCGCTCCCCAAGTCAGCAGTCCTAGCCCCA
AACCAGCCCAGAGCAGGGTCTCTCTAAAGGGGACTTGAGGGCTGAGCAGGAAAGACTGGCCCTCTAGCTTCTAC
CCTTTGTCCCTGTAGCCTATACAGTTTAGAATATTTATTTGTTAATTTTATTAAATGCTTTAAAAAAA

WO 2004/030615

PCT/US2003/028547

423/6881
FIGURE 393

MPNFSGNWKIIRSENFEELLKVLGVNVMLRKIAVAAASKPAVEIKQEGDTFYIKTSTTVRTTEINFKVGEEFEEQ
TVDGRPCKSLVKWESENKMOVCEQKLLKGEGPKTSWTRELTNDGELILMTADDVVCTRVYVRE

WO 2004/030615

PCT/US2003/028547

424/6881
FIGURE 394

GCAGTCTCCGCCGAGTCTCAGCTGCAGCTGCAGGACTGAGCCGTGCACCCGGAGGAGACCCCCGGAGGAGGCGA
CAAACCTTCGAGTGCCGCGACCCAACCCAGCCCTGGGTAGCCTGCAGCATGGCCCCAGCTGTTCTTCTGCCCCTGCT
GGCAGCCCTGGTCTTGGCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAGAGGACCGCGC
TTTTCGCGTGCGCATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGCGGGCCCTACCATCCCTTGCCACGT
CCACTACCTGCGGCCACCGCCGAGCCGCGGGCTGTGCTGGGCTCTCCGCGGGTCAAGTGGAATTTCTGTCCCCG
GGGCCGGGAGGCAGAGGTGCTGGTGGCGCGGGGAGTGC CGCTCAAGGTGAACGAGGCCTACCGGTTCCGCGTGGC
ACTGCCTGCGTACCCAGCGTGCCTACCGACGTCTCCCTGGCGCTGAGCGAGCTGCGCCCCAACGACTCGGGTAT
CTATCGCTGTGAGGTCCAGCACGGCATCGATGACAGCAGCGACGCTGTGGAGGTCAAGGTCAAAGGGGTGCTCTT
TCTCTACCGAGAGGGCTCTGCCCCGCTATGCTTTCTCTTTCTGGGGCCCAGGAGGCCTGTGCCCCGATTGGAGC
CCACATCGCCACCCCGGAGCAGCTCTATGCCGCCTACCTTGGGGGCTATGAGCAATGTGATGCTGGCTGGCTGTC
GGATCAGACCGTGAGGTATCCCATCCAGACCCACGAGAGGCCTGTTACGGAGACATGGATGGCTTCCCCGGGGT
CCGGAACATATGGTGTGGTGGACCCGGATGACCTCTATGATGTGTAAGTGTGTTATGCTGAAGACCTAAATGGAGA
GTTCCTGGGTGACCTCCAGAGAAGCTGACATTGGAGGAAGCACGGGCGTACTGCCAGGAGCGGGGTGCAGAGAT
TGCCACCACGGGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCCAGGGTGGCTAGCTGATGG
CAGTGTGCGCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGGCTTGCTGGTGTCAAGACTCTCTTCTCT
CTTCCCCAACAGACTGGCTTCCCCAATAAGCACAGCCGCTTCAACGTCTACTGCTTCCGAGACTCGGCCCCAGCC
TTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGCCTCTGATGGACTAGAGGCTATCGTCACAGTGAC
AGAGACCCTGGAGGAAGTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAAATCCCGTGGGGCCATCTACTCCATCCC
CATCATGGAGGACGGAGGAGGTGGAAGCTCCACTCCAGAAGACCCAGCAGAGGCCCTAGGACGCTCCTAGAAAT
TGAAACACAATCCATGGTACCGCCACGGGGTCTCAGAAGAGGAAGGTAAAGGCATTGGAGGAAGAAGAAATA
TGAAGATGAAGAAGAGAAAGAGGAGGAAGAAGAAGAGGAGGAGGTGGAGGATGAGGCTCTGTGGGCATGGCCAG
CGAGCTCAGCAGCCCGGGCCCTGAGGCCTCTCTCCCACTGAGCCAGCAGCCAGGAGAAGTCACTCTCCAGGC
GCCAGCAAGGGCAGTCTGTCAGCCTGGTGCATCACCATTCTGATGGAGAGTCAGAAGCTTCCAGGCCTCCAAG
GGTCCATGGACCACCTACTGAGACTCTGCCCACTCCAGGGAGAGGAACCTAGCATCCCCATCACCTTCCACTCT
GGTTGAGGCAAGAGAGGTGGGGGAGGCAACTGGTGGTCTTGAGCTATCTGGGGTCCCTCGAGGAGAGAGCGAGGA
GACAGGAAGCTCCGAGGGTGCCCTTCCCTGCTTCCAGCCACACGGGCCCTGAGGGTACCAGGGAGCTGGAGGC
CCCCTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGAGCACTCAGTGCAGGCCAGCCAGTGCTGCCCACTGA
CAGCGCCAGCCGAGGTGGAGTGGCGTGGTCCCCGCATCAGGTGACTGTGTCTCCCAAGCCCTGCCACAATGGTGG
GACATGCTTGGAGGAGGAGGAAGGGGTCCGCTGCCCTATGTCTGCTGGCTATGGGGGGGACCTGTGCGATGTTGG
CCTCCGCTTCTGCAACCCCGGCTGGGACGCCTTCCAGGGCGCTGCTACAAGCACTTTTCCACACGAAGGAGCTG
GGAGGAGGCAGAGACCCAGTGCCGGATGTACGGCGCGCATCTGGCCAGCATCAGCACACCCGAGGAACAGGACTT
CATCAACAACCGGTACCGGGAGTACCAGTGGATCGGACTCAACGACAGGACCATCGAAGGCGACTTCTTGTGGTC
GGATGGCGTCCCCCTGCTCTATGAGAACTGGAACCTGGGCAGCCTGACAGCTACTTCTGTCTGGAGAGAACTG
CGTGGTCACTGGTGTGGCATGATCAGGGACAATGGAGTGACGTGCCCTGCAACTACCACCTGTCTTACACCTGCAA
GATGGGGCTGGTGTCTGTGGGCCGCCACCGGAGCTGCCCTGGCTCAAGTGTTCGGCCGCCACGGCTGCGCTA
TGAGGTGGACACTGTGCTTCGCTACCGGTGCCGGGAAGGACTGGCCAGCGCAATCTGCCGCTGATCCGATGCCA
AGAGAACGGTCTGTTGGGAGGCCCCCAGATCTCCTGTGTGCCAGAAAGACCTGCCCGAGCTCTGCACCCAGAGGA
GGACCCAGAAGGACGTGAGGGGAGGCTACTGGGACGCTGGAAGGCGCTGTTGATCCCCCTTCCAGCCCCATGCC
AGGTCCCTTAGGGGGCAAGGCCTTGAACACTGCCGGCCACAGCACTGCCCTGTACCCCAAATTTCCCTCACACCC
TGCGCTCCCGCCACCACAGGAAGTGACAACATGACGAGGGGTGGTGTGGAGTCCAGGTGACAGTCTCTGAAGGG
GCTTCTGGGAAATACCTAGGAGGCTCCAGCCAGCCAGGCCCTCTCCCCCTACCTGGGCACCAGATCTTCCAT
CAGGGCCGGAGTAAATCCCTAAGTGCCTCAACTGCCCTCTCCCTGGCAGCCATCTGTGCCCTCTATCTCTAG
GGAGCACTGTGCCACTCTTTCTGGGTTTTCCAAGGAATGGGCTTGCAAGATGGAGTGTCTGTAAATCAACAG
GAAATAAACTGTGTATGAGCCCAGGCAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

425/6881
FIGURE 395

MAQLFLPLLAALVLAQAPAAALADVLEGDSSSEDRAFRVRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRAVLGSP
RVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQHGIDDSSDAV
EVKVKGVVFLYREGSARYAFSFGAQEACARIGAHIAITPEQLYAAYLGGEQCDAGWLSAQPSAIPASNPASNPASD
GDMDGFPVGRNYGVDPDDLYDVICYAEDLNGELFLGDPPEKLTLEEERAYCQERGAETATTGQLYAAWDGGLDH
CSPGWLADGSRYPVITPSQRCGGGLPGVKTLFLFPNQTGFNPKHSRFRNVYCFRDSAQPSAIPASNPASNPASD
GLEAIVTVTETLEELQLPQEATESESRGAIYSIPIMEDGGGGSSTPEDPAEAPRTLLEFETQSMVPPTGFSSEEG
KALEEEEEKYEDEEEKEEEEEVEDEALWAWPSELSSPGPEASLPTEPAAQEKSLSQAPARAVLQPGASPLPDG
ESEASRPPRVHGPPTETLPTPRERNLASPSPSTLVEAREVGEATGGPELSGVPRGESEETGSSEGAPELPLPATRA
PEGTRELEAPSEDNSGRTAPAGTSVQAQPVLPDTSASRGGVAVVPASGDCVPSCHNGGTCLEEEEGVRCCLCPG
YGGDLCDVGLRFCNPGWDAFQGACYKHFSRRSWEAAETQCRMYGAHLASISTPEEQDFINNRYREYQWIGLNDR
TIEGDFLWSDGVPLLYENWNPGQPDYFLSGENCVMVWHDQGWSDVPCNYHLSYTCKMGLVSCGPPPELPLAQ
VFGRPRLRYEVDTVLRYRCREGLAQRLPLIRCQENGRWEAPQISCVPRRPARALHPEEDPEGRQGRLLGRWKAL
LIPPSSPMFPGP

WO 2004/030615

PCT/US2003/028547

426/6881
FIGURE 396

CTCCTCACAGAAGCCTGGAGCTGGGCATCCAAGAAGAAGCAGCCTCATTGTGTTTTCTGGTGTCATCGTAGGTGGC
CACCTATGGCTTTTGGGAATGTAAAAAGGGCAGCTCTCTGGCATGTTCCTGACTGAGGATCTCATAACATTTAAC
TTGAGGAACCTTCCTCCTTTTCCAGCTTTGGGAGTCAAGCTTCTCACCTGGGGCGGGTGGGTCTGCACCACCCTC
CCACCCTCCTTCCTCCGTGTGGACGATAGAGCCACATCCAGCACCACGGACAGCTCCCGGGCGCCTTCATCTCCT
CGTCTCCAGGCAGCACAAAGCCATTGTGGAATCTCCACCAGGTGTACAGAACGGTGCCTCTGCGTCCTGCCACTC
AGGACCTCTCAAGTCCCCGATGTGATGGCTCCTCAGCATGATCAGGAGAAAATTCCATGATCTTGCTTATTCCTGT
CTTGGGAAGTCCTTCTCCATGTCTAACCAAGATCTATATGGCTATAGCACCAGCTCTTTGGCTCTTGGCTTGGCA
TGGCTAAGTTGGGAGACCAAAAAGAAGAATGTACTTCATCTGGTTGGGCTGGATTCCCTCTTGATAAAGCCTTCCCA
GTTGACTGAAAGATGAGGCTAGGCTCTAGCAAGTTGAAGTCAAACCAGCTCCTTCAAGAAGCTTTGAGCAGAATG
AAGTGGGGAGGACCCAGCTTCCAGCCCAGGAAGCCCACTGTACCTGGAGCCATCTGGGATAAGACTTTGACCCAT
GACTCCCATATCCACAGCCTGTCCATCCTAGCCCATCCCAGTTTATCCTGTATCATTTGAGCTGGGATTCCCACA
TCCTCTGAGTTGGAAGTCCCATCTCAAGTCTTCAATAAAGACTCTTGAATATTG

WO 2004/030615

PCT/US2003/028547

427/6881
FIGURE 397

MFLTEDLITFNLRNFFLLFQLWESSFSPGAGGFCTTLPPSFLRVDDRATSSSTDSSRAPSSPRPPGSTSHCGISTR
CTERCLCVLPLRTSQVPDVMAPQHDQEKFDLAYSCLGKSFMSNQDLYGYSTSSLALGLAWLSWETKKKNVLHL
VGLDSL

WO 2004/030615

PCT/US2003/028547

428/6881
FIGURE 398

TTGCGTAGGGGGCGGGACTAAGGCTGTCAATTGGTCTGTTTTGTGCCGATCAATGAGATGGGTGCGGTGATTGG
CGACTACCTTGAGAGTAGCGGGTTGAGGTGTAAGCCCTGAGGAGGCAGCGTTTTCTGGGCTTCTGTCTGGTTCTC
TCTCTCCAGAAGGTTCTGCCGGTTCCCCCAGCTCTGGGTACCCGGCTCTGCATCGCGTCGCCATGATGGGCCATC
GTCCAGTGCTCGTGCTCAGCCAGAACACAAAGCGTGAATCCGGAAGAAAAGTTCAATCTGGAAACATCAATGCTG
CCAAGACTATTGCAGATATCATCCGAACATGTTTGGGACCCAAAGTCCATGATGAAGATGCTTTTGGACCCAATGG
GAGGCATTGTGATGACCAATGATGGCAATGCCATTCTTCGAGAGATTCAAGTCCAGCATCCAGCGGCCAAGTCCA
TGATCGAAATTAGCCGGACCCAGGATGAAGAGGTTGGAGATGGGACCACATCAGTAATTATTCTTGACGGGGAAA
TGCTGTCTGTAGCTGAGCACTTCCTGGAGCAGCAGATGCACCCAACAGTGGTGATCAGTGCTTACCGCAAGGCAT
TGGATGATATGATCAGCACCTAAAGAAAATAAGTATCCAGTCGACATCAGTGACAGTGATATGATGCTGAACA
TCATCAACAGCTCTATTACTACCAAAGCCATCAGTCGGTGGTCACTTTGGCTTGCAACATTGCCCTGGATGCTG
TCAAGATGGTACAGTTTGAGGAGAATGGTCGGAAAGAGATTGACATAAAAAAATATGCAAGAGTGGAAAAGATAC
CTGGAGGCATCATTGAAGACTCCTGTGTCTTGCGTGGAGTCATGATTAACAAGGATGTGACCCATCCACGTATGC
GGCGCTATATCAAGAACCCTCGCATTGTGCTGCTGGATTCTTCTCTGGAATACAAGAAAGGAGAAAGCCAGACTG
ACATTGAGATTACACGAGAGGAGGACTTCACCCGAATTCTCCAGATGGAGGAAGAGTACATCCAGCAGCTCTGTG
AGGACATTATCCAAGTGAAGCCCGATGTGGTCATCACTGAAAAGGGCATCTCAGATTTAGCTCAGCACTACCTTA
TGCGGGCCAATATCACAGCCATCCGCAGAGTCCGGAAGACAGACAATAATCGCATTGCTAGAGCCTGTGGGGCCC
GGATAGTCAGCCGACCAGAGGAAGTGAAGAGATGATGTTGGAACAGGAGCAGGCCTGTGGAAATCAAGAAAA
TTGGAGATGAATACTTTACTTTTCACTGACTGCAAAGACCCCAAGGCCTGCACCATTCCTCCGGGGGGCTA
GCAAAGAGATTCTCTCGGAAGTAGAACGCAACCTCCAGGATGCCATGCAAGTGTGTCGCAATGTTCTCCTGGACC
CTCAGCTGGTGCCAGGGGTGGGGCCTCCGAGATGGCTGTGGCCCATGCCTTGACAGAAAAATCCAAGGCCATGA
CTGGTGTGGAACAATGGCCATACAGGGCTGTTGCCAGGCCCTAGAGGTCATTCTCGTACCCTGATCCAGAAGT
GTGGGGCCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAACTGTGAGACCTGGGGTG
TAAATGGTGAGACGGGTACTTTGGTGGACATGAAGGAAGTGGGCATATGGGAGCCATTGGCTGTGAAGCTGCAGA
CTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGACATCGTTTCAGGCCACAAAAAGAAAG
GCGATGACCAGAGCCGGCAAGGCGGGGCTCCTGATGCTGGCCAGGAGTGAGTGCTAGGCAAGGCTACTTCAATGC
ACAGAACCAGCAGAGTCTCCCTTTTCTGAGCCAGAGTGCCAGGAACACTGTGGACGTCTTTGTTGAGAAGGGA
TCAGGTGGGGGGCAGCCCCCAGTCCCTTTCTGTCCAGCTCAGTTTTCCAAAAGACACTGACATGTAATTCTTC
TCTATTGTAAGGTTTCCATTTAGTTTGCTTCCGATGATTAAATCTAAGTCATTTG

WO 2004/030615

PCT/US2003/028547

429/6881
FIGURE 399

MGHRPVLVLSQNTKRESGRKVQSGNINA AKTIADI IRTCLGPKSMMKMLLDPMGGIVMTNDGNAILREIQVQHPA
AKSMIEISRTQDEEVGDGTTSVIILAGEMLSVAEHFLEQQMHPTVVISAYRKALDDMISTLKKISIPVDISDSM
MLNI INSSITTKAISRWSSLACNIALDAVKMVQFEENGRKEIDIKKYARVEKIPGGI IEDSCVLRGVMINKDVTH
PRMRRYIKNPRIVLLDSSLEYKKGESQTDIEITREEDFTRILQMEEYIQQLCEDI IQLKPDVVITEKGISDLAQ
HYLMRANITAIRRVKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTF ITDCKDPKACTILL
RGASKEILSEVERNLDAMQVCRNVLLDPQLVPGGGASEMAVAHALTEKSKAMTGVEQWPYRAVAQALEVIPRTL
IQNCGASTIRLLTSLRAKHTQENCETWGVNGETGTLVDMKELGIWEPLAVKLQTYKTAVETAVLLLRIDDIVSGH
KKKGDDQSRQGGAPDAGQE

WO 2004/030615

PCT/US2003/028547

430/6881
FIGURE 400

GAATTGCGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCCCAGCCCCCTGCTCCT
TTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGAAGACCCGCCAGGTGTCTCTGGAGGTCA
CCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTCATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGT
GTGGAGCAGCCTGGGGCCTCTGGCAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCGTCAACTG
GAGCCTCCTGCTATCCCTGAGCCCGATGGGGGCTGATGGTGTCCCTAAGGACAGCATTCACTTTTTCTTCTGC
CCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGCCTTTGGGAAGACC
ATATCCTCCATACTCCTTGCCGATTTCTCTTGGAACAACATCACTGATTCAATTGGATCCTGCCACCCTGAGTGC
CACATTTCAAGGCCACCCCATGAACGACCCCTACCAGGACTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGC
CTTTTCCAGGTCCAGCCGACCAGCCCAACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGC
CCTGATTGGAGCCTCTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGA
CTGCCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGGACCAGCTACT
GTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCCAGAAGCCGGGGGGCCGAGAATC
AGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAGCATACTCTCTTCCCCAGTCACCCATTGTCCGAGC
CTTCTTTGGGTCCCAGAATAACTTCTGTGCCTTCAATCTGACGTTCCGGGGCTTCCACAGGCCCTGGCTATTGGGA
CCAACACTACCTCAGCTGGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCTCCACTAGTCTT
GGGCATCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGCTGCACCA
CAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGGACATTACTGAACCTGTCTT
GCTGTGCCTCGAACTCTGGAGGTTGGAGCATCAAGTTCCAGCCGGCCCTTCACTCCCCATCTTGCTTTTCTG
TGGAACTCAGAGGCCAGCCTCGACTTCCCTGGAGACCCCCAGGTGGGGCTTCCCTCATACTTTGTTGGGGGACTT
TGGAGCGGGCAGGGGACAGGGCTATTGATAAGGTCCCCTTGGTGTTCCTTCTTGATCTCCACACATTTCCCT
TGGATGGGACTTGCAAGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGATTTA
TTTTTTTTT

WO 2004/030615

PCT/US2003/028547

431/6881
FIGURE 401

MRGSVECTWGWGHCAPSPLLLWTLFFFAPFGLLGKTRQVSLEVIPNWLGPLQNLHRAVGTNSTLHYVWSSL
GPLAVVMVATNTPHSTLSVNWSLLLSPEPDGGLMVLPKDSIQFSSALVFTRLLEFDSTNVSDTAAPLGRPYPPY
SLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGSLAFRVQAFSRSSRPAQPPRLHTADTCQLEVALIGA
SPRGNRSLFGLEVATLGQGPDCPSMQEQHSIDDEYAPAVFQLDQLLWGSLSGFAQWRPVAYSQKPGGRESALPC
QASPLHPALAYSLPQSPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMMLLGVGFPVPDGLSPLVLGIMA
VALGAPGLMLLGGGLVLLLHHKKYSEYQSIN

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

433/6881
FIGURE 403

MTEQETLALLEVKRSDSPEKSSPQALVPNGRQPEGEGGAESPGAESLRVGSSAGSPTAIEGAEDGLDSTVSEAA
LPWGTGPQPSAPFPDPPGWRDIEPEPPESEPLTKLEELPEDDANLLPEKAARAFVPIDLQCIERQPQEDLIVRCE
AGEGECRTFMPPRVTHPDPTERKWAEAVVRPPGCSCGGCGSCGDREWLRAVASVGAALILFPCLLYGAYAFLPFD
VPRLPTMSSRLIYTLRCGVFATFPIVLGILVYGLSLLCF SALRPFGEPRREVEIHRRYVAQSVQLFIFYFFNLAV
LSTYLPQDTLKLLPLLTGLFAVSRLIYWLTFAVGRSFRGFGYGLTFLPLLSMLMWNLYYMFVVEPERMLTATESR
LDYDPDHARSASDYRPRPWG

WO 2004/030615

PCT/US2003/028547

434/6881
FIGURE 404

ACTCAGTGTTTCGCGGGAGCCGCACCTACACCAGCCAACCCAGATCCCGAGGTCCGACAGCGCCCCGGCCAGATCC
CCACGCCGTGCCAGGAGCAAGCCGAGAGCCAGCCGGCCGGCGCACTCCGACTCCGAGCAGTCTCTGTCTTCGACC
CGAGCCCCCGCGCCCTTTCCGGGACCCCTGCCCGCGGGCAGCGCTGCCAACCTGCCGGCCATGGAGACCCCGTCC
CAGCGGGCGGCCACCCGCAGCGGGGCGCAGGCCAGTCCACTCCGCTGTCGCCCACCCGCATCACCCGGCTGCAG
GAGAAGGAGGACCTGCAGGAGCTCAATGATCGCTTGGCGGTCTACATCGACCGTGTGCGCTCGCTGGAAACGGAG
AACGCAGGGCTGCGCCTTCGCATCACCGAGTCTGAAGAGGTGGTCAGCCGCGAGGTGTCCGGCATCAAGGCCGCC
TACGAGGCCGAGCTCGGGGATGCCCGCAAGACCCTTGACTCAGTAGCCAAGGAGCGCGCCCGCTGCAGCTGGAG
CTGAGCAAAGTGCGTGAGGAGTTTAAGGAGCTGAAAGCGCGCAATACCAAGAAGGAGGGTGACCTGATAGCTGCT
CAGGCTCGGCTGAAGGACCTGGAGGCTCTGCTGAACTCCAAGGAGGCCGCACTGAGCACTGCTCTCAGTGAGAAG
CGCACGCTGGAGGGCGAGCTGCATGATCTGCGGGGCCAGGTGGCCAAGCTTGAGGCAGCCCTAGGTGAGGCCAAG
AAGCAACTTCAGGATGAGATGCTGCGGGCGGTGGATGCTGAGAACAGGCTGCAGACCATGAAGGAGGAACTGGAC
TTCCAGAAGAACATCTACAGTGAGGAGCTGCGTGAGACCAAGCGCCGTCTATGAGACCCGACTGGTGAGATTGAC
AATGGGAAGCAGCGTGAGTTTGAGAGCCGGCTGGCGGATGCGCTGCAGGAAGTGCGGGCCCCAGCATGAGGACCAG
GTGGAGCAGTATAAGAAGGAGCTGGAGAAGACTTATCTGCCAAGCTGGACAATGCCAGGCAGTCTGCTGAGAGG
AACAGCAACCTGGTGGGGGCTGCCCACGAGGAGCTGCAGCAGTCGCGCATCCGCATCGACAGCCTCTCTGCCCAG
CTCAGCCAGCTCCAGAAGCAGCTGGCAGCCAAGGAGGCGAAGCTTCGAGACCTGGAGGACTCACTGGCCCCGTGAG
CGGGACACCAGCCGGCGGCTGCTGGCGGAAAAGGAGCGGGAGATGGCCGAGATGCGGGCAAGGATGCAGCAGCAG
CTGGACGAGTACCAGGAGCTTCTGGACATCAAGCTGGCCCTGGACATGGAGATCCACGCCTACCGCAAGCTCTTG
GAGGGCGAGGAGGAGAGGCTACGCCTGTCCCCAGCCCTACCTCGCAGCGCAGCCGTGGCCGTGCTTCCTCTCAC
TCATCCCAGACACAGGGTGGGGGCAGCGTACCAAAAAGCGCAAAGTGGAGTCCACTGAGAGCCGCAGCAGCTTC
TCACAGCACGCACGCACTAGCGGGCGCGTGGCCGTGGAGGAGGTGGATGAGGAGGGCAAGTTTGTCCGGCTGCGC
AACAAGTCCAATGAGGACCAGTCCATGGGCAATTGGCAGATCAAGCGCCAGAATGGAGATGATCCCTTGCTGACT
TACCGGTTCCACCAAAGTTACCCCTGAAGGCTGGGCAGGTGGTGACGATCTGGGCTGCAGGAGCTGGGGCCACC
CACAGCCCCCTACCGACCTGGTGTGGAAGGCACAGAACCTGGGGCTGCGGGAACAGCCTGCGTACGGCTCTC
ATCAACTCCACTGGGGAAGAAGTGGCCATGCGCAAGCTGGTGCGCTCAGTGACTGTGGTTGAGGACGACGAGGAT
GAGGATGGAGATGACCTGCTCCATCACCACCATGTGAGTGGTAGCCGCCGCTTGAGGCCGAGCCTGCACTGGGGCC
ACCCAGCCAGGCCTGGGGGCAGCCTCTCCCCAGCCTCCCCGTGCCAAAATCTTTTCATTAAAGAATGTTTGGAA
CTTT

WO 2004/030615

PCT/US2003/028547

435/6881
FIGURE 405

METPSQRRATRSGAQASSTPLSPTRITRLQEKEDELQELNDRLAVYIDRVRSLETENAGLRRLRITESEEVVSREVS
GIKAAEAEELGDARKTLDSVAKERARLQLELSKVREEFKELKARNTKKEGDLIAAQARLKDLEALLNSKEAALST
ALSEKRTLEGELHDLRGQVAKLEAALGEAKKQLQDEMLRRVDAENRLQTMKEELDFQKNYSEELRETKRRHETR
LVEIDNGKQREFESRLADALQELRAQHEDQVEQYKKELEKTYSAKLDNARQSAERNSNLVGAAHEELQQSRIRID
SLSAQLSQLQQLAAKEAKLRDLEDLARERDTSRRLAEKEREMAEMRARMQQQLDEYQELLDIKLALDMEIHA
YRKLEGEERLRLSPSPTSQRSRGRASSHSSQTQGGGSVTKKRKLESTESRSSFSQHARTSGRVAVEEVDEEGK
FVRLRNKSNEDQSMGNWQIKRQNGDDPLLTYRFPKFTLKAGQVVTIWAAGAGATHSPPTDLVWKAQNTWGCGNS
LRTALINSTGEEVAMRKLVRSVTVVEDDEDEDGDDLLHHHHVSGSRR

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

437/6881
FIGURE 407

LRLKGSSNTTECVPTSEHVAEIVGRQGCKIKALRAKTNTYIKTPVRGEEPVFMVTGRREDVATARREIISAAE
HFMSIRASRNKSGAAGVAPALPGQVTIRVRVPYRVVGLVVGPKGATIKRIQQQNTYIIITPSRDRDPVFEITGA
PGNVERAREEIEITHIAVRTGKILEYNNENDFLAGSPDAAIDSRYSDAWRVHQPCKPLSTFRQNSLGCIGECGVD
SGFEAPRLGEQGGDFGYGGYLFPGYGVGKQDVYYGVAETSPPLWAGQENATPTSVLFSSASSSSSSSAKARAGPP
GAHRSPATSAGPELAGLPRRPPG

WO 2004/030615

PCT/US2003/028547

438/6881
FIGURE 408

GGAGGAGCCGGGCGGGCTGGCGGGCGGCCGGGTGGCGGGCGGGCGGCATGGCGGAGCCGAGCGGGGCGGAGACGAGG
CCCCCATTCGGGTCACCGTCAAGACCCCCAAGGACAAGGAGGAAATTGTGATCTGCGATCGAGCCTCGGTCAAG
GAGTTCAAAGAGGAAATCTCCCGAGGTTTAAGGCTCAGCAGGATCAGCTGGTCTGATCTTCGAGGCAAGATC
CTCAAGGATGGGGACACACTGAACCAGCACGGAATCAAGGACGGGCTCACTGTCCATCTGGTCATCAAGACCCCT
CAGAAGGCTCAAGATCCAGCTGCTGCCACTGCTTCTTCCCCCTCCACACCTGACCCTGCCTCAGCACCCCTCCACC
ACGCTTGCTTACCCGCCACCCCTGCCAGCCCTCCACCTCTGGCAGTGCCTCTTCAGATGCTGGCAGTGAAGC
CGGAGGAGCAGTGGTGGGGGGCCCTCTCCGGGGGCTGGGGAGGGATCCCCAGTGCTACTGCGTCCATACTCTCT
GGCTTTGGGGGCATCCTGGGGCTGGGCAGCCTAGGCCTGGGCTCTGCCAACTTCATGGAGCTGCAGCAGCAGATG
CAGCGGCAGCTGATGTCCAATCCTGAGATGCTGTACAGATCATGGAGAACCCCTGGTCCAGGATATGATGTCT
AACCTTGATCTGATGCGTCACATGATTATGGCCAACCCCAAGATGCAGCAGTTGATGGAGCGGAACCTGAGATC
AGCCACATGCTCAATAACCTGAACCTCATGAGGCAGACAATGGAGCTTGCTCGGAATCCAGCCATGATGCAAGAG
ATGATGCGGAACCAGGACCGGGCCCTGAGCAACCTTGAGAGCATCCCTGGAGGGTATAATGCCCTCCGCCGCATG
TACACGGACATCCAGGAGCCCATGTTCACTGCTGCCCGGGAACAGTTTGGCAACAATCCCTTCTCTTCCCTGGCC
GGGAACCTCCGACAGCTCATCTCCAGCCCTCTGCCGACTGAGAATCGAGAGCCCCCTCCCTAACCCCTGGAGCCCC
TCGCCCCCACCTCCAGGCCCCCGGGTCCGGTGGGGAGGGACCCGGAGGATCGGGGACCAGCCAGGTGCACCCG
ACAGTCTCGAACCCCTTTGGGATCAATGCGGCTAGCCTGGGGTCAGGGATGTTCAATAGCCCAGAAATGCAAGCC
CTCCTCCAGCAGATCTCTGAGAACCCCAAGCTGATGCAGAATGTGATCTCAGCACCCCTACATGCGCAGCATGATG
CAGACGCTTGCCCAGAACCCCGACTTTGCTGCTCAGATGATGGTGAATGTGCCGCTCTTCGCGGGGAACCCCCAA
CTGCAGGAGCAGCTCCGCTGCAGCTCCAGCTTTCCTGCAGCAGATGCAGAACCCAGAGTCACTCTCCATCCTT
ACCAATCCCCGAGCCATGCAGGCATTGCTGCAGATCCAGCAGGGACTACAGACCTTGACAGCCGAGGCCCTGGG
CTGGTACCCAGCCTTGGCTCCTTTGGGATATCCCGGACCCAGCACCCCTCAGCAGGCAGCAACGCAGGGTCTACG
CCCGAGGCCCCCACTTCCCTACCAGCCACGCCAGCCACATCTTCTCCAACAGGGGCTTCCAGCGCCAGCAGCAA
CTCATGCAGCAGATGATCCAGCTTTTGGCTGGAAGTGGAACTCACAGGTGCAGACGCCAGAAGTGAGATTTAG
CAGCAGCTGGAGCAGCTCAACTCCATGGGCTTCATCAATCGTGAGGCTAACCTGCAGGCCCTGATTGCCACAGGA
GGGGACATCAACGCAGCTATCGAGAGACTGCTGGGCTCCAGCTCTCCTAATCCCTCGGCCCATGCCTCCTGCCT
CTCCCCCTCCCTCGATGTCAGCATTCCGTTCTTCTGTCAATCCTTACCCTCTGCAGCTTGCTCCTCCCTTCCGTCTT
CTCCCTCATCCTTTCCAAACAGCAGGGTGACTTTAGAGGCATGGGCTCCAACCCCTTAGCTCTGTCTGAGAATTA
TGGTTTTACTGCTACGTCTCTAACAGACTCTTCTCTCCTGGTCTCCTTGAGCAGTGCTACTTAACAGTTTTTAC
AGTTTCATTGATTGACTCTACCTCCTTGCCCCACACCACTTTTGCAATCTTTAACTTTTCACTGGCTGTGCAGAG
TCGAGGGAGGAACCAGCTCTCTGGTTTACTGGAACATAGTCTTCCATCTATACCACTAGGGTTTTGTCTTATGTT
TACTTTTGGTAACTCTCTTCCCTCTTTTCTCCCTACCCCCCAACCCCTAGCCCAACCAATGCTAGAAATTTCTG
CTCTGAAGGAGGAGCAGGTGAACAGGTGGTAATTTTCTTCTCGGCCCTATTCTGGTTCATTACGACTTTTTT
GGTGGGAACGTGTGGAATTCAGGGTAAGGAGGAAGATGCCTGTTCTCCCTGTCTGAAGAGGGAGATGAGACAG
CTCTCTGGACAGGAATTAACAAACGCTGGAGCAGCCAGAGGAAATTCGTGTGAAAGAGGAGGAATGAGATTAT
TCGGAGGAAGGGAATGGGGGAGACAGCCTGAGTAAAGGCTTGAAGTTGGAATTAACAGTGGGGAGCAGAAGCA
CTCATAGCTCTTTTAGGCAGAAGAATCCAGGCCCGAGCTGGCAGAAGAGACTTAGAGATGCTAATGGAATTTAAA
CTGAAAAAAGGAGCCCAATGAAGCTAAGCGCCACGCCCAAGGGGTCATATTGGCTTTAGTTCTTCAAGCATA
TGTGCTTATATGCACACACACACATTTCCATGGACCCAGGCTTGCTTGTGTCCCCAGGCACCAAGTAGTTTGA
GCCCCCTCAAAAGACATGAAGGGGGTGGGGTCTGTGTGAGTAGTGGGGAGGTGCATGTGTATCCACATGTGTG
CATACTCTTAAGTTGGGTGGGAAGTGGATTCTTGTGTTTCTGGTTCAGAGTGCTCTCCCACCACCAGAGA
CAAGTGGGTAAAAAGGTCAGTCCATTGCAGGAATATATATCCGGGAGAGCTAGGTCCCTTGGGGCTCTGGATGCT
GGGTAACCCGAGTAATGTGGGTACCTTTCTGAAGCTGTACAGGGCTGTGACTAGCACCCCTATACCCCTCAC
TGCTTGTGGGAATAGTAGAGGGTTTTTCTCCAGAGCCCTGGCCTTTTCACTTCTTAATTTTCCCTCCAG
GCCAGAAAGTTTTCTTTGAGGAAGGAGAGAGGGTGGAATGATGCCTTTGATCTGGAATTTGACATTTCTCT
GTCAGAGCACAGAGGAGGCTCATATCACCTCTTCCCTCTCCTACTTGGCCAGCTGCTTGGAGGACCGACCCAT
GGCTGAGAATATGACGGCAAGAGGAACAGAGTTTGTCTCAAGTGGGAAAGGGTCCCAAGCAGTCCAGAGAAGATG
TCTGTGTGGCTTTCCCTCCCTGCCTCCCCAGCTCCACACTGGCCTTTGTAAATAAATGGCGTGGTCTTTGTTG
TG

WO 2004/030615

PCT/US2003/028547

439/6881
FIGURE 409

GGCTCTCTTCCTGTCTTTGTGGCTCCGGAAAGGCGTTTGGGATGCCAACCGATGAGGCTGCTGTCAATTTGTGGTGT
TGGCTCTATTTGCTGTCACTCAAGCAGAGGAAGGAGCCAGGCTTTTGGCTTCCAAATCACTGCTGAACAGATACG
CCGTGGAGGGACGAGACCTGACCTTGCAGTACAACATCTACAATGTTGGCTCAAGTGCTGCATTAGACGTGGAAC
TATCTGATGATTCCTTCCCTCCAGAAGACTTTGGCATTGTGTCTGGAATGCTCAATGTCAAATGGGACCGGATTG
CCCCTGCTAGCAATGTCTCCCACACTGTGGTCCTGCGCCCTCTCAAGGCTGGTTATTTCAACTTCACCTCGGCAA
CAATTACTTACCTGGCCCAGGAGGATGGGCCCCGTTGTGATTGGCTCTACCAGTGCACCTGGACAGGGAGGAATCC
TGGCTCAGCGGGAGTTTGACAGGCGATTCTCCCCCTCATTTTCTGGACTGGGCAGCCTTTGGGGTCATGACCCTTC
CCTCCATCGGCATCCCCCTGCTATTGTGGTACTCCAGCAAGAGGAAATATGACACTCCCCAAAACGAAGAAGAACT
GATTGGGGCTTCCACAGCCCTCCTCTCCCAAGAAATCCAGGCTCCTCTCCCAAGAAATCCAGGTGCTTTCCAGAC
TCCAAAGGGTATCTTAAATGCAATCTCTTCTCTCTTAGCCCTTGGCCACTTCTCCTGGATCCTGCCCTGCTCTC
AGCCATAGTGAAGGACCAGCCCTAGGAGTCTGCGAGAGCCTCCTTGGTTCCATCGTGAAGCCATAAACAGGAATG
CCTTTGGCAATAGCCTTGAGCCTAGAGGGCCCTCTGATGCCCACTGAGGTGCTGTTGGTTTATTGCTGGCAACG
TGAATTCTCTCAGGGGTCTAGGAGGGGCATTTTGGAGACTGCCTGACACCACCCCTATCCCCTGCCTCCCCCTCT
CAGAAGAGGGTGGAAGATGAAATGAAAGCTATGGGACTCTTGGAGGATACCCAGTGTCTATTCTGGGTTAGAGAA
GTGCTTACTAAGGGGTTTTCTAATAAAAACAAATGCCAATTGC

WO 2004/030615

PCT/US2003/028547

440/6881
FIGURE 410

MRLLSFVVIALFAVTQAEEGARLLASKSLLNRYAVEGRDLTLQYNIYNVGSSAALDVELSDDSFPPEDFGIVSGM
LNVKWDRIAPASNVSHTVVLRPLKAGYFNFTSATITYLAQEDGPVVGSTTSAPGGGILAQREFDRRFSPHFLDW
AAFVMTLP SIGIPLLLWYSSKRKYDTPKTKKN

PCT/US2003/028547

GAGACCAACGCGTGCGGGCCGAACCCCTCCCCCGCCTTCCCCCAACAATACAGGACGCCGGGGTCCGCGCCGCG
TCCTCCCTGGTCCCCCGTCCGATTATGTCTCGGATCGAATCCCTCAGCGGGGCGCGGATCGACCGGAGCAGAGA
GCTGGCGAGCAAGACCCGGGAAAAGGAAATGAGAAAGCCAAGGATGCCCGCTATACAAATGGGCACCTCTT
CACCACCATTTAGTTTTCAGGCTATGACCATGTGCTATGCTTGTAAACAAGAGCATCACAGCCAAGGAAGCCCTCAT
CTGCCCCAACCTGCAATGTGACTATCCACAACCGCTGTAAAGACACCCCTCGCCAACTGTACCAAGGTCAAGCAGAA
GCAACAGAAAGCGGCCCTGTCTGAAGAACAACACCGCCTTGCAGTCCGTTTCTCTTCGAAGTAAGACAACCATCCG
GGAGCGGCCAAGCTTCGGCCATCTACCCCTCCGACAGCTTCCGGCAGTCCCTCCTGGGCTCCCCCGGTGGCCGCTC
CTCCTTGTCTTTAGCCAAGAGTGTCTTCTACCACCAACATTGCTGGACATTTCATATGATGAGTCTCCCCGTGGGGCT
GCGCCGGATCCTCTCACAGTCCACAGACTCCCTCAACATGCGGAACCGAACCCCTATCCGTGGAATCCCTCATTGA
CGAAGAGGTAATCTACAGTGAGCTGATGAGTGACTTTGAGATGGATGAGAAGGACTTTGCAGCTGACTCTTGGAG
TCTTGCTGTGGACAGCAGCTTCTGTCAGCAGCATAAAAAGGAGGTGATGAAGCAGCAAGATGTCATCTATGAGCT
AATCCAGACAGAGCTGCACCATGTGAGGACACTGAAGATCATGACCCGCCCTCTTCCGCACGGGGATGCTGGAAGA
GCTACACTTGGAGCCAGGAGTGGTCCAGGGCCTGTTCCCTGCGTGGACGAGCTCAGTGACATCCATACAGCTT
CCTCAGCCAGCTATTAGAACGCCGACGCCAGGCCCTGTGCCCTGGCAGCACCCGGAACTTTGTATCCATCGCTT
GGGTGATCTGCTCATCAGCCAGTTCTCAGGTCCTAGTGCGGAGCAGATGTGTAAGACCTACTCGGAGTCTGTCAG
CCGCCACAGCAAGGCCTTAAAGCTCTATAAGGAGCTGTACGCCCGAGACAAACGCTTCCAGCAATTCTATCCGGAA
AGTGACCCGCCCGCCGTGCTCAAGCGGCACGGGGTACAGGAGTGCATCCTGCTGGTGACTCAGCGCATACCAA
GTACCCGTTACTCATCAGCCGATCCTGCAGCATTCCACGGGATCGAGGAGGAGCGCCAGGACCTGACCACAGC
ACTGGGGCTAGTGAAGGAGCTGCTGTCCAATGTGGACGAGGGTATTTATCAGCTGGAGAAAGGGGCCCGTCTGCA
GGAGATCTACAACCGCATGGACCCCTCGGGCCCAAACCCCAAGTGCCTGGCAAGGGGCCCTTTGGCCGAGAGGAAC
TCTGAGGCGCAAACATCATCCACGATGGCTGCCTGCTCTGGAAGACAGCGACGGGGCGCTTCAAAGATGTGCTAGT
GCTGCTGATGACAGATGTACTGGTGTCTTCTCCAGGAAAAGGACCAGAAGTACATCTTTCCTACCCGTGGACAAGCC
TTCAGTGGTATCGCTGCAGAATCTAATCGTACGAGACATTGCCAACCAAGGAGAAAGGGATGTTTCTGATCAGCGC
AGCCCCACCTGAGATGTACGAGGTGCACACAGCATCCCGGGATGACCGGAGCACCTGGATCCGGGTCAATTCAGCT
GAGCGTGCGCACATGCCATCCAGGGAGGACTTCCCCCTGATTGAGACAGAGGATGAGGCTTACCTGCGGGCAAT
TAAGATGGAGTTGCAGCAGAAGGACCGGGCACTGGTGGAGCTGCTGCGAGAGAAGGTGCGGGCTGTTTGTGAGAT
GACCCATTTCCAGGCCGAAGAGGATGGTGGCAGTGGGATGGCCCTGCCACCCTGCCAGGGGCCCTTTCCGCTC
TGAGTCCCTTGAGTCCCTCGTGCGCAGCGGCTGCTGCAGGATGCCATCCGTGAGGTGGAGGGTCTGAAAGACCT
GCTGGTGGGGCCAGGAGTGAACCTGCTCTTGACACCCCGAGAGCCAGCCCTGCCCTTGGAACCAGACAGCGGTGG
TAACACGAGTCCCTGGGGTCACTGCCAATGGTGAGGCCAGAACCCTTCAATGGCTCCATTGAACTCTGCAGAGCTGA
CTCAGACTCTAGCCAGAGGGATCGAAATGGAAATCAGCTGAGATCACCGCAAGAGGAGGCGTTACAGCGATTGGT
CAATCTCTATGGACTTCTACATGGCCTACAGGCAGCTGTGGCCAGCAGGACACTCTGATGGAAGCCCGGTTCC
TGAGGGCCCTGAGCGGCGGGAGAAGCTGTGCCGAGCCAACCTCGGGATGGGGAGGCTGGCAGGGCTGGGGCTG
CCCTGTGGCCCCCTGAAAAGCAGGCCACGGAACCTGGCATTACTGCAGCGGCAACATGCGCTGCTGCAGGAGGAGT
ACGGCGCTGCCGGCGGGCTAGGTGAAGAACGGGCAACCGAAGCTGGCAGCCTGGAGGCCCGGCTCCGGGAGAGTGA
GCAGGCCCGGGCACTGCTGGAGCGTGAGGCCGAAGAGGCTCGAAGGCAGCTGGCGCCCGGCTGGGGCCAGACCGAGCC
ACTCCAGCTGAGGCCCCCTGGGGCCGCAGACCTGTGGATCCTCGCGGCGCAGCCTCCCCGCAGGCGATGCCCT
GTACTTGAGTTTCAACCCCCCACAGCCAGCCGAGGCATGACCGCTGGATCTACCTGTCACTACTCGCTCTGT
CCATCGAAACTTTGAGGACCGAGAGAGGCAGGAATGAGCAGCGCTGAGCCCTGGATCTACCTGTCACTACTCGCTCTGT
TGACACTGGCAGCGAGGAGGAAGGTAGCAGCGCTGTCTCCGCCCCACAGTCCACGAGACTTTACCAGAATGCA
GGACATCCCGGAGGAGAGCAGGAGCGCAGCAGGGGAGGCTGTAGCCTCCGAGAGCTAAGGGGGCCCCCTCCCCCT
GCCCTGTCGCCCATGAAGAACATTACTGAGGGGGCTAACCTTGGGGACTCCAATTTGCCAATGATGAGGGAACA
TTTGAAAGAACATGCAATTGTCTTGCCAGCTCTTGGGATCCTTGATACCTGGGGCCATTTAAGAAGCTAGGGG
AATTAGGCCACAACACCCCTGGGACATCCGAAAGCTACACCACAGATGCCAGTGGTTTATGCTTCTTCCGCA
ACTTTAGGAAAATTTATTTATTTATTTAGTTATGGGGGAGAGGGGAGATTTAAAGGACCAGGGACATG
GGAACCAAGCCATAGGGATCAGAGGGCCTTGTCTTGAACACTACTGGGGTATATTAGGCTCATCCACGCAGCT
GCTGGGTTCTTGCCCTAACGGCCCTCCCTGCAACATCCGTCTTGAGGAGAGGGCTGCAGCCACAGCACCCCTACT
GCCCTTTAAATAAAGGAGGGCTGTGGGCAGGGCCATGTCCCTTTCTCCTCTCCCTCAACCTCTTACTGCTGTTT

WO 2004/030615

PCT/US2003/028547

442/6881
FIGURE 411B

TCCCTTTCTCCGTCCTTCATGGAAGCCCTGGGAGATAACCTGGCTTCCTGGAGTTGATGGAATAAAGGTTGGGGT
GGCCATAATGGTTTGTGGGGGTGAGGGAAAAACCCACAGGGACCAGAATGTTTGTGTTCTTTGTTTTCTT
TTTTGTACCAAAGTCAACTGCACGTGTTTTATATTTTAAGAGATCGTAGGCAATTAGAGATCGAAGCCTCCTAT
CTCCACATCTCTGAAGAAGTTGAGGGGTGGGGGAGAGAATGACTTCTGCCTTCATCTGCAGTAACGGGGGGACCT
ATACTGACCTCTTCCCCAGCCATTTAGAAACAAGTTCTAGGGTGGGTTGGAAAATCTCCAAGAGCCCTGACCTCA
TCTTCCACCTCAGCAACCATGACCTGAAACCTCAGCGTGAATTTGGGGGATTTTTCAGTGAACCCCTGCCCCCA
AATGTCGACCAGCCCCCAAATGTCGAAGAATTTCTTCTTGCCAATTTTGTGTTTAAAAAAAAAATTGAGGGAA
AATTAAAAACCTGGAACCTCA

WO 2004/030615

PCT/US2003/028547

443/6881
FIGURE 412

ATGCAGCAGCACGTTTCAGCTCTTGACCCAAATCCACCTTCTTGCCACCTGCAACCCCAACCTCAATCCGGAGGCC
ACTACCACCAGGATATTTCTTAAAGAGCTGGGAACCTTTGCTCAAAGCTCCATCGCCCTTCACCATCAGTACAAC
CCCAAGTTTCAGACCCTGTTCCAACCCTGTAACTTGATGGGAGCTATGCAGCTGATTGAAGACTTCAGCACACAT
GTCAGCATTGACTGCAGCCCTCATAAACTGTCAAGAAGACTGCGAATGAATTTCCCTGTTTGCCAAAGCAAGTG
GCTTGGATTCTGGCCACAAGCAAGGTTTTTCATGTATCCAGAGTTACTTCCAGTGTGTTCCCTGAAGGCAAAGAAT
CCCCAGGATAAGATCGTCTTCACCAAGGCTGAGGACAATTTGTTAGCTTTAGGACTGAAGCATTTTGAAGGAACT
GAGTTTCCTAATCCTCTAATCAGCAAGTACCTTCTAACCTGCAAACTGCCACCAACTGACAGTGAGAATCAAG
AACCTCAACATGAACAGAGCTCCTGACAACATCATTAAATTTTATAAGAAGACCAAACAGCTGCCAGTCCTAGGA
AAATGCTGTGAAGAGATCCAGCCACATCAGTGAAGCCACCTATAGAGAGAGAAGAACACCGGCTCCCATTCTGG
TTAAAGGCCAGTCTGCCATCCATCCAGGAAGAAGCTGCGGCACATGGCTGATGGTGCTAGAGAGGTAGGAAATATG
ACTGGAACCACTGAGATCAACTCAGATCGAAGCCTAGAAAAAGACAATTTGGAGTTGGGGAGTGAACTCGGTAC
CCACTGCTATTGCCTAAGGGTGTAGTCTGAAACTGAAGCCAGTTGCCACCCGTTTCCCCAGGAAGGCTTGGAGA
CAGAAGCGTTTCATCAGTCTGAAGCCCCTCCTTATCCAACCCAGCCCCTCTCTCCAGCCCAGCTTCAACCCCTGGG
AAAACACCAGCCCAGTCAACTCATTGAGAAGCCCCTCCGAGCAAAATGGTGCTCCGGATTCTCACCCAATACAG
CCAGCCACTGTTTTACAGACAGTTCCAGGTGTCCCTCCACTGGGGGTGAGTGGAGGTGAGAGTTTGTGCTCTCT
GCAGCACTGCCTGCTGTGCCCCCTGAGGCCAGGACAAGCTTCCCTCTGTCTGAGTCCCAGACTTTGCTCTCTCT
GCCCCGTGTGCCCAAGGTAATGCTGCCCTCCCTTGCCCCCTTCTAAGTTTCGAAAGCCATATGTGAGACGGAGACC
TCAAAGAGAAGAGGAGTCAAGGCCTCTCCCTGTATGAAACCTGCCCTGTTATCCACCACCTGCATCTGTTATC
TTCAGTGTTCCTGCTACCACTGTGAAGATTGTGAGCCTTGGCGGTGGCTGTAACATGATCCAGCCTGTCAATGCG
GCTGTGGCCAGAGTCCCAGACTATTTCCCATCACTACCTCTTGGTTAACCTACTTCCCTCCCCTGTCCATTG
AACCAGTCCCTTGTGGCCTCCTCTGTCTCACCTTAATTGTTTCTGGCAATTCTGTGAATCTTCTATACCATCC
ACCCCTGAAGATAAGGCCACAGTGAATGTGGACATTGCTTGTGCTGTGGCTGATGGGGAAATGCCTTTCAGGGC
CTAGAACCCAAATTAGAGCCCCAGGAAGTATCTCTCTCTCTGCTACTGTTTTCCCGAAAGTGAACATAGCCCA
GGGCTCCACTAGCAGATGCAGAGTGCCAAGAAGGATTGTGAGAGAATAGTGCTGTGCTGGACCGTTGTGAAA
ACAGAGGAGGGGAGGCAAGCTCTGGAGCCGCTCCCTCAGGGCATCCAGGAGTCTCTAAACAACCTACCCCTGGG
GATTTAGAGGAAATTGTCAAGATGGAACCTGAAGAAGCTAGAGAGGAAATCAGTGGATCCCCTGAGCGTGATATT
TGTGATGACATCAAAGTGGAACATGCTGTGGAATTGGACACTGGTGCCCCAAGCGAGGAGTTGAGCAGTGCTGGA
GAAGTAACGAAACAGACAGTCTTACAGAAGGAAGAGGAGAGTCAAGCAACTAAACCCCTTCTCTCTCAA
GAGCCCCCTGATGAAGGAACCTCAGGGACAGATGTGAACAAAGGATCATCAAAGAATGCTTTGTCTCAATGGAT
CCTGAAGTGAGGCTTAGTAGCCCCCAGGGAAGCCAGAAGATTCTCCAGTGTGATGGTCAGTCAAGTGGGACT
CCAGTTGGGCCAGAACTGGAGGAGAGAAGAATGGGCCAGAAGAAGAGGAAGAAGAGGACTTTGATGACCTCAC
CAAGATGAGGAAGATGAAATGTCATCAGCTTCTGAGGAATCTGTGCTTTCTGTCCAGAACTCCAGGTGAGAGCT
GGAGAATATTCTCAAGTATTTCTGTGGACTCAGTAATATGTATCACTTATTGATATGCCACCTGCTTGCTTGCTGC
ACTATGGATAGTCTAAATCATTGTATTTGA

WO 2004/030615

PCT/US2003/028547

444/6881
FIGURE 413

MQQHVQLLTQIHLLATCNPNLNPEATTTRIFLKELGTFQAQSSIALHHQYNPKFQTLFQPCNLMGAMQLIEDFSTH
VSIDCSPHKTVKKTANEFPCLPKQVAWILATSKVFMYPELLEVC SLKAKNPQDKIVFTKAEDNLLALGLKHFEGT
EFPNPLISKYLLTCKTAHQLTVRIKNLNMNRAPDNIKFYKKTQLEVLGKCCEEIQPHQWKPPIEREEHRLPFW
LKASLPSIQEELRHMA DGAREVG NMTGTTEINSDRSLEKDNLELGSESRYPLLLPKGVVLKLPVATRFPRKAWR
QKRSSVLKPLLIQPSPSLQPSFNPGKTPARSTHSEAPPSKMVLRIHPHIQPATVLQTVPGVPPLGVSGGESFESP
AALPAVPPEARTSFPLSESQTLLSSAPVPKVMLPSLAPSKFRKPYVRRRPSKRRGVKASPCMKPAPVIHHPASVI
FTVPATTVKIVSLGGGCNMIQPVNAAVAQSPQTIPITITLLVNPTSFPCPLNQSLVASSVSPLIVSGNSVNLPIPS
TPEDKAHVNVDIACAVADGENAFQGLEPKLEPQELSPLSATVFPKVEHSPGPPLADAECQEGLESENSACRWTVVK
TEEGRQALEPLPQGIQESLNNPTPGDLEEIVKMEPEEAREEISGSPERDICCDDIKVEHAVELDTGAPSEELSSAG
EVTKQTVLQKEEERSQPTKTPSSSQEPPEDEGTSGTDVNKGSSKNALSSMDPEVRLSSPPGKPEDSSSVVGQSVGT
PVG PETGGEKNGPEEEEEEDFDDLTQDEEDEMSSASEESVLSVPELQVRAGEYSQVFRGLSNMYHLLICHLLACC
TMDSPKIICI

PCT/US2003/028547

FIGURE 414

GCCTTTTTTGCAGTCTCAGGACGGGGCGCTTTGGAGCCGGCCCCAGGCAGCGTGTGTGCGGTGCGCTAGTCTGGAGA
ACTAGTCCCTCGACTCACGTGCAAGGATGATGCTGAAAGGAATAACAAGGCTTATCTCTAGGATCCATAAGTTGGA
CCCTGGGCGTTTTTTTACACATGGGGACCCAGGCTCGCCAAAGCATTGCTGCTCACCTAGATAACCAGGTTCCAGT
TGAGAGTCCGAGAGCTATTTCCCGCACCAATGAGAATGACCCGGCCAAGCATGGGGATCAGCACGAGGGTCAGCA
CTACAACATCTCCCCCAGGATTGGAGACTGTATTTCCCATGGCCTTCTCTCTGCTTTGTGATGCAGGTGAA
GACATTCAGTGAAGCTTGCCTGATGGTAAGGAAACCAGCCCTAGAACTTCTGCATTACCTGAAAAACACCAGTTT
TGCTTATCCAGCTATACGATATCTTCTGTATGGAGAGAAGGGAAACAGGAAAAACCCTAAGTCTTTGCCATGTTAT
TCATTTCTGTGCAAAACAGGACTGGCTGATACTACATATTCCAGATGCTCATCTTTGGGTGAAAAATTGTGCGGA
TCTTCTGCAGTCCAGCTACAACAAACAGCGCTTTGATCAACCTTTAGAGGCTTCAACCTGGCTGAAGAATTTCAA
AACTACAAATGAGCGCTTCTTGAACCAGATAAAAGTTCAAGAGAAGTATGTCTGGAATAAGAGAGAAAGCACTGA
GAAAGGGAGTCCCTCTGGGAGAAGTGGTTGAACAGGGCATAACACGGGTGAGGAACGCCACAGATGCAGTTGGAAT
TGTGCTGAAAGAGCTAAAGAGGCCAAAGTTCTTTGGGTATGTTTCACCTCCTAGTGGCCGTGGATGGAATCAATGC
TCTTTGGGGAAGAACCCTCTGAAAAGAGAAGATAAAAGCCCGAFTGCCCCCGAGGAATTAGCACTTGTTACAA
CTTGAGGAAAAATGATGAAAAATGATTGGCATGGAGGCGCCATTGTGTGCGCTTTGAGCCAGACTGGGTCTCTCTT
TAAGCCCCGGAAAGCCTATCTGCCCCAGGAGTTGCTGGGAAAGGAAGGATTGATGCCCTGGATCCCTTTATTCC
CATCTTGTTTTCCAACATAACCCAAAGGAATTTGAAAGTTGTATTCACTATTATTGAAAAACAATTGGCTTCA
ACATGAGAAAGCTCCTACAGAAGAAGGGAAAAAAGAGCTGCTGTTCTTAAGTAACGCCAACCCCTCGCTGCTGGA
GCGGCACTGTGCCTACCTCTAAAGCCAAGATCACAGCATGTGAGGAAGACAGTGGACATCTGCTTTATGCTGGACC
CAGTAAGATGAGGAAGTCGGGCAGTACACAGGAAGAGGAGCCAGGCCCTTGACCTATGGGATTGGACAGGACTG
CAGTTGGCTCTGGACCTGCATTAAAAATGGGTTTTCACTGTGAATGCGTGACAATAAGATAATCCCTTGTTCCTAAA
ACTTTATATCAGTTTATGGAATGTGGTTTTTACATTTAAGATAATTATGGCTCTTTTCTAAAAAATAAAATAT
CTTTCTAAAAA

WO 2004/030615

PCT/US2003/028547

446/6881
FIGURE 415

MMLKGITRLISRIHKLDPGRFLHMGTOARQSIAAHLDNQVPVESPRAISRNTNENDPAKHGDQHEGQHYNISPQDL
ETVFPHGLPPRFVMQVKTSEACLMVRKPALELLHYLKNTSFAYPAIRYLLYGEKGTGKTLCHVIHFCAKQDW
LILHIPDAHLWVKNCRDLLQSSYNKQRFQDQPLEASTWLKNFKTTNERFLNQIKVQEKYVWNKRETEKGSPLGEV
VEQGITVRNATDAVGIVLKEKLRQSSLGMFHLVAVDGINALWGRTTLKREDKSPIAPEELALVHNLKMMKND
WHGGAIVSALSQTGSLFKPRKAYLPQELLGKEGFDALDPFIPILVSNYNPKFESCIQYYLENNWLQHEKAPTEE
GKKELLFLSNANPSLLERHCAYL

WO 2004/030615

PCT/US2003/028547

447/6881
FIGURE 416

TCTTCACCACTGCTCTCCCAGAGGTCCAGGTCCGGGAGATGACAGTGGCTCCCAGAAAGCCCAGGATTCAATCGC
TGAGAGAGTGCTTAGGCCCGAATGCCGGCCAAATCGTTCTACTCACCGTGTCGGAGGCCGAGAGCGATGAGAGT
ACAGGGAAGTGAGGAAGAGGGGTGGCCGCCAGGCTCCTCCGCTTCCCTGGGTCCACCGCGGATCCCTCCCGCTT
GTCAGGAGGCGGCCAGCGGGTAAGCCGACTGGCGGAAATGCGAGAGAGGAGAAGGGAAAGGTGGAGGGCTAAAGG
GGCAAAGTGAGAGGAGGCGGATCCCGCAACCGACACTGGGATCGTTTCCCTCGCAAAGCGAACCACAAATGGCG
GCGGCAGCGGCGGCAGCAGAGTGGCCGCGGCAGCTCCTCCAGAGGGAGGGAGCTAAGGGCGCCTAGCGACACCCC
CAACCTCCCCTCCTCCCTCCTCGCTTCTTCCCCACGGTCCCCCGCTTCGCCCCACTCCGGCCATGTAGCGCGC
ACGTACGCCCGCACGCGTACGAGTGTCTACGGGCTCGTGGCTGCTCCCACCAACCACACCTTCGGCCGTC
CTGCGAGCCAGCCATCCCGTACGCGCTACCCACGGGAACCTCCTCGCCCAGTTCTCCACTCCCCCTCAGACCTT
GTCAAGCCGGCTCCAGCGCAGGCCCTCAGCGTACCTCAGCGGCGCGAGCCCAAGCCTTCTCCACCTCCTCTTC
TCTCCTCCCCCTCCTCCCCGCGCACGGCCACCAACCGCGCCAAAGCAGCCGCCGCGCAGCACCCCCACCTA
CACTCCTCGCGCTGCGCCTCCACAGTCCCCACCGCGGGACTGTTCCATTCTGGCGGCTGCAGGGGCGAGGAGA
GGAAGGGACCGCAAAGCGAGTCTGGCTTGCCGTTTACTGGAATTGCCAGGGTGGCCGGCGGAGTCCCATGACA
ACCTACCTCCCTGGGTTCGTGCGCGCGCGCTGCGGCTCGCTCCTCCTCCATGGGACCGCGCGAGGGGATCGA
GGGCGGCTAGCGCCCTCTGCCGGCCGGTGGTTGGAGGCCGCGCGGCTGCGCGTTGAGTCGTTTCTGCGCGA
TGACCCGACCCTTTTTTGAGTCTCAGGACGGGCGCTTGGAGCGGCCCCAGGCAGCGTGTGTCGGTCGCGCTAG
TCTGGAGAAGTCTCCTCGACTACGGTGAGGGAATGGACCGACACGGGTATTGTACCGCTGAGGGAAGGAGCG
GGACTCCGGACCTCCAGGAGGTAGGGAGTGAGGCCGGTAGACGGCGCGCCTCCGGGGGGGATTCTCCCCGGCG
TTGAGTTGCCAACCTGGGACCCGAGGAAGTTCGGCGTGGTGGTGTGCTTTTTGTTGTTGTTAACCTCCTCGGAT
TTCTCGAATTTACACCACTGTCCATATGCGATGATGTTTGTGTTGCCCTTGACGCACTTACTCATGGATGGTACT
TCAGCCTCGTTAGACAGCCTGGTGATGGAGGATGAAGAAACCATGTGCTTCTCATTAGTTCTGGACTCAGTTTC
CCTTGCTTTCAGCAAGTTATTTTTGTTAGTTCTTTATCAAAAAGTGATACATAAAAATTAGGCACTCCAAACATG
CCTCCAGGGTTGGTGTGTGAAATAATAAGATAGGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGG
GAGGCCGAGGCAGGTGGATGACAAGGTGAAGAGATCGAGACAATCCTGGCCAACATGGTGAAACCCCGTCTCTAC
TAAAAATACAAATATTAGCCGGCCGTGGTGGCGGGCGCTGTAGCCCCAGCTACTCGGGAGGCTGAGGCAGGAGA
ATTGCTTGAACCCGGGCGGCGGAAGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGCGACAAAGCG
AGACTCCGTCACACACACACACACACGAAATAATAATATATGTAAAGTGGAATTAGCTCCAAGTCGTTAAT
AAAACAAAGCAGGCCGGCGCTTGTGTTAAATAGTTGTATCAATGACTTGATTTAGATTAAATGAGGATATATTTTT
CAAATTTATGCCTTTTACAAAATTTTTAAAGAGTAGGTAATGTGCGTGATAGATATAAAGAAAGGAAAAGATCTC
CAGATGTGGAATCTTCTACTGGATCCTGTAAACAGAAAGAAGACATTAGGCTGGGCGCAGTGGCTCACACCTGTAA
TCTCAGCACTTTGGGAGGCGGAGGAGGGCGCATTGCTTGAGCCTAGGAGTTCGAGACCAGCTTAGGCAACACGGT
GAAACCCCATCTCTACAAAAGACACAAAATTAGACAGGTGTGGCACACGCTTGTAGTCTGAGCTACTTGGGAG
GCTGAAGCAGGAGGATTGAGGAAGAGGTTGCAAAGTTAGCCGAGATCACGCCATCACACTGCAGCCTAGGTGACA
GAGCGAGACCTGTCTCAAAAAAAGAAAGAAGACATTAGCAGAAAAGCTGAGGAAATGCAAATAAAGTCTGCAAT
TTTTAAAT

WO 2004/030615

PCT/US2003/028547

448/6881
FIGURE 417

MTRPFFAVSGRALWSRPQAACVGRLVWRTPRLTVREWTDTGIVPLRERSGTPDLQEVGSEAGRPARLRGGFLPG
VELPTWDPRKFGVVVCFLLLLTLLGFLEFHTTVHMR

PCT/US2003/028547

[illegible]

WO 2004/030615

PCT/US2003/028547

450/6881
FIGURE 419

MGFSNMEDDGPEEEERVAEPQANFNTPQALRFEELLANLLNEQHQIAKELFEQLKMKKPSAKQQKEVEKVKPQCK
EVHQTLILDPAQRKRLQQQMQQHVQLLTQIHLLATCNPNLNPEASSTRICLKELGTFAQSSIALHHQYNPKFQTL
FQPCNLMGAMQLIEDFSTHVSIDCSPHKTVKKTANEFPCLPKQVAVILATSKVFMYPELLPVCSLKAKNPQDKIL
FTKAEDNLLALGLKHFEGTEFLNPLISKYLLTCKTARQLTVRIKNLNMNRAPDNI IKFYKKTQQLPVLGKCCEEI
QPHQWKPPIEREEHRLPFWLKASLPSIQEELRHMDGAREVGNMTGTTEINSDQGLEKDNSELGSETRYPLLLPK
GVVLKLPVADRFPPKAWRQKRSSVLKPLLIQSPSLQPSFNPGKTPAQSTHSEAPPSKMVLRIHPHIQPATVLQ
TVPGVPPLGVSGGESFESPAALPAMPPEARTSFPLSESQTLSSAPVPKVMMPSPASSMFRKPYVRRRPSKRRGA
RAFRCIKPAPVIHPASVIFTVPATTVKIVSLGGGCNMIQPVNAAVAQSPQTIPIATLLVNPTSFPCPLNQPLVAS
SVSPLIVSGNSVNLP IPSTPEDKAHMNVDIACAVADGENAFQGLEPKLEPQELSPLSATVFPKVEHSPGPPPVDK
QCQEGLSENSAYRWTVVKTEEGRQALEPLPQGIQESLNNSSPGDLEEVVKMEPEDATEEISGFL

WO 2004/030615

PCT/US2003/028547

451/6881
FIGURE 420

AGCGCAGTATGCGGGCGGGGCCGGGAGGTGCTCACA CTGCAGTTGGGACATTTTGCCGGTTTCGTGGGCGCGC
ACTGGTGGAAACCAGCAGGATGCTGCGCTGGGCGGAGCGACCGATTCCAAGGAGCCCCGGGAGAGCTGTGCCCGG
ACGTCCTGTATCGTACGGGCGGGACGCTGCACGGCCAGGAGACCTACACGCCGCGACTCATCTCATGGATCTGA
AGGGTAGTTTGAGCTCCCTAAAAGAGGAAGGTGGACTCTACAGGGACAAACAGTTGGATGCTGCAATAGCATGGC
AGGGGAAGCTCACCACACACAAAGAGGAAGTCTATCCCAAGAACCCTTATCTCCAAGACTTTCTGAGTGCAGAGG
GAGTGCTGAGTAGTGATGGTGCTGGAGGGTCAAATCCATTCCCAATGGCAAAGGTTCCCTCACCCTCCCCACCG
CTACAACCTCCAAAACCACTTATCCCTACAGAGGCCAGCATCAGGGTCTGGTTCAGACTTCCTCAGAGTCCATCTCC
ATCCCCGGAGCATCTGTATGATTGAGAAGTACAACCACGATGGGGAAGCAGGTTCGGCTGGAGGCTTTTGGCCAAG
GGGAAAGTGTCTTAAAGGAACCCAAGTACCAGGAAGAGCTGGAGGACAGGCTGCATTTCTACGTGGAGGAATGTG
ACTACTTGCAGGGCTTCCAGATCCTGTGTGACCTGCACGATGGCTTCTCTGGGGTAGGCGCGAAGGCGGCAGAGC
TGCTACAAGATGAATATTACAGGGCGGGGAATAATAACCTGGGGCCTGCTACCTGGTCCCTACCATCGTGGGGAGG
CCCAGAGAAACATCTATCGTCTATTAAACACAGCTTTTGGTCTCGTGCACCTGACTGCTCACAGCTCTCTTGTCT
GCCCCCTGTCTTGGGTGGGAGCCTGGGCCTGCGACCCGAGCCACCTGTCAGCTTCCCTTACCTGCATTATGATG
CCACTCTGCCCTTCCACTGCAGTGCCATCCTGGCTACAGCCCTGGACACAGTCACTGTTCCCTTATCGCCTGTGTT
CCTCTCCAGTTTCCATGGTTTCATCTGGCTGACATGCTGAGCTTCTGTGGGAAAAGGTGGTGACAGCAGGAGCAA
TCATCCCTTTCCCTTGGCTCCAGGCCAGTCCCTTCTGATTCCCTGGTGCAGTTTGGAGGAGCCACCCCATGGA
CCCCACTGTCTGCATGTGGGGAGCCTTCTGGAACACGTTGCTTTGCCAGTCAGTGGTGCTGAGGGGTATAGACA
GAGCATGCCACACAAGCCAGCTCACCCAGGGACACCTCCACCCTCTGCCCTTCATGCATGTACCACTGGGGAAG
AAATCTTGGCTCAGTATTTACAACAGCAGCAGCCTGGAGTCA TGAGTTCTTCCCATCTGCTGCTGACTCCCTGCA
GGGTGGCTCCTCCTTACCCCCACCTCTTCTCAAGCTGCAGTCCACCGGTATGGTTCTGGATGGTTCCCCCAAGG
GAGCAGCAGTGGAGAGCATCCAGTGTTTGGGGCACTGTGTTCTTCTCGTCCCTGCACCAGACCCTGGAAGCCT
TGGCCAGAGACCTCACCAAAC TCGACTTGGCGCGCTGGGCCAGCTTCATGGATGCTGGAGTGGAGCACGATGACG
TAGCAGAGCTGCTGCAGGAGCTACAAAGCCTGGCCCAGTGCTACCAGGGTGGTGACAGCCTCGTGGACTTAAAGTT
CCCAGTGTGGGAGAAAGGAGCTAGTTTGCAATAAAAACAGCTGGATGCAGGAGCCAGTGTCTTCATGCAGAGGA
GCTCAATGTGCGGGGACTAGCTACACCAACATATGCACTTTTACATTTAGAAACACTGTGATTAGACCACAGAA
CAATAAATATGTGCCATCAGACC

WO 2004/030615

PCT/US2003/028547

452/6881
FIGURE 421

MAGGAREVLTTLQLGHFAGFVGAHWWNQDAAALGRATDSKEPPGELCPDVLYRTGRTLHGQETYTPRLIILMDLKGS
LSSLKEEGGLYRDKQLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRVKSIPNGKGSSPLPTATT
PKPLIPTASIRVWSDFLRVHLHPRSICMIQKYNHDGEAGRLEAFQGGSVLKEPKYQEELEDRLHFYVEECDYL
QGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLPGPYHRGEAQORNIYRLLNTAFGLVHLTAHSSLVCPL
SLGGSGLRPEPPVSFPYLHYDATLPFHCSAILATALDVTVPYRLCSSPVSMVHLADMLSFCGKKVVTAGAIIP
FPLAPGQSLPDSLVQFGGATPWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPTGTPPPSALHACTTGEEIL
AQYLQQQPGVMSSSHLLLTPCRVPYPHFLFSSCSPPGMVLDGSPKGAAVESIPVFGALCSSSSLHQTLEALAR
DLTKLDLRRWASFMDAGVEHDDVAELLQELQSLAQCYQGGDSLVD

WO 2004/030615

PCT/US2003/028547

453/6881
FIGURE 422

AGGTGAGAGAGGATGTGTGCTGGGCCTTGGAGGAAGGGGGCCGAGACCGGGCCTTACTTCTGTAACGATACTGTG
AGGCATCGGAAGGCCAGCCTGTTGTGTCCGTTTTGAAGGATGCCCCCTGTCCCGCTGGTTGAGATCTGTGGGGGTC
TTCCTGCTGCCAGCCCCCTACTGGGCACCCCGGGAGAGGTGGCTGGGTTCCTACGGCGGGCCCTCCCTGGTGAC
GGGTACCCAGTCTGGCCTGGCACAGTGCCCGCTGCTGGTGCCAAGCGTGGACAGAGGAACCTCGAGCCCCTTTGC
TCCTCCCTCAGAATGAACGGAGACCAGAATTCAGATGTTTATGCCCAAGAAAAGCAGGATTTCTGTTTCAGCACTTC
TCCAGATCGTTAGGGTGTGACTGAGGATGAGATGGGGCACCCAGAGATAGGAGATGCTATTGCCCGGCTCAAG
GAGGTCTGGAGTACAATGCCATTGGAGGCAAGTATAACCGGGGTTTGACGGTGGTAGTAGCATTCCGGGAGCTG
GTGGAGCCAAGGAAACAGGATGCTGATAGTCTCCAGCGGGCCTGGACTGTGGGCTGGTGTGTGGAACCTGCTGCAA
GCTTTCTTCTGGTGGCAGATGACATCATGGATTCATCCCTTACCCGCCGGGGACAGATCTGCTGGTATCAGAAG
CCGGGCGTGGGTTTGGATGCCATCAATGATGCTAACCTCCTGGAAGCATGTATCTACCGCCTGCTGAAGCTCTAT
TGCCGGGAGCAGCCCTATTACCTGAACCTGATCGAGCTCTTCTGCGAGAGTTCCTATCAGACTGAGATTGGGCAG
ACCCTGGACCTCCTCACAGCCCCCAGGGCAATGTGGATCTTGTGAGATTCACTGAAAAGAGGTACAAATCTATT
GTCAAGTACAAGACAGCTTTCTACTCCTTCTACCTTCTATAGCTGCAGCCATGTACATGGCAGGAATTGATGGC
GAGAAGGAGCACGCCAATGCCAAGAAGATCCTGCTGGAGATGGGGGAGTTCTTTCAGATTTCAGGATGATTACCTT
GACCTCTTTGGGGACCCAGTGTGACCGGCAAAATTGGCACTGACATCCAGGACAACAAATGCAGCTGGCTGGTG
GTTCAGTGTCTGCAACGGGGCACTCCAGAACAGTACCAGATCCTGAAGGAAAATTACGGGCAGAAGGAGGCTGAG
AAAGTGGCCCGGGTGAAGGCGCTATATGAGGAGCTGGATCTGCCAGCAGTGTCTTGCAATATGAGGAAGACAGT
TACAGCCACATTATGGCTCTCATTGAACAGTACGCAGCACCCCTGCCCCAGCCGTCTTCTGGGGCTTGCGCGC
AAAATCTACAAGCGGAGAAAGTGACCTAGAGATTGCAAGGGCGGGGAGAGGAGGCTCTCAATAAAATAATCGTGTA
ACCTT.

WO 2004/030615

PCT/US2003/028547

454/6881
FIGURE 423

MPLSRWLRSVGVFLLPAPYWAPRERWLGSRLRRPSLVHGYPVLAWSARCWCQAWTEEPRALCSSLRMNGDQNSDV
YAQEKQDFVQHFSQIVRVLTEDEMGHPEIGDAIARLKEVLEYNAIGGKYNRGLTVVVAFRELVPRKQDADSLQR
AWTVGWCVELLQAFFLVADDIMDSSLTRRGQICWYQKPGVGLDAINDANLLEACIYRLLKLYCREQPYYLNLI
FLQSSYQTEIGQTLDLLTAPQGNVDLVRFTKRYKSIVKYKTAFYSFYLP IAAAMYMAGIDGEKEHANAKKILLE
MGEFFQIQDDYLDLFGDPSVTGKIGTDIQDNKCSWLVVQCLQRATPEQYQILKENYGQKEAEKVARVKALYEELD
LPAVFLQYEEDSYSHIMALIEQYAAPLPPAVFLGLARKIYKRRK

WO 2004/030615

PCT/US2003/028547

455/6881
FIGURE 424

GGTAGTTGGTTGTGGGCACTGGGTTAGAGGTATCACGTGGGGCACTTTCGTCTTAGCTTTTGGACAAGACGCAG
GCGCAACCCACGGCTGCTGCGGGGATCCTTGTGGCCCTTCCGGTCGGTGGAACCAATCCGTGCACAGAGAAGCGG
GGCGAACTGAGGCGAGTGAAAGTGGACTCTGAGGGCTACCGCTACCGCCACTGCTGCGGCAGGGGCGTGAGGGCA
GAGGGCCGCGGAGGCCGAGTTGCAAACATGGCTCAGAGCAGAGACGGCGGAAACCCGTTCCGCCGAGCCCAGCGA
GCTTGACAACCCCTTTTTCAGGACCCAGCTGTGATCCAGCACCGACCCAGCCGGCAGTATGCCACGCTTGACGTCTA
CAACCCTTTTTCAGACCCGGGAGCCACCACCAGCCTATGAGCCTCCAGCCCCCTGCCCCATTGCCTCCACCCTCAGC
TCCCTCCTTGCAGCCCTCGAGAAAGCTCAGCCCCACAGAACCTAAGAACTATGGCTCATACAGCACTCAGGCCTC
AGCTGCAGCAGCCACAGCTGAGCTGCTGAAGAAACAGGAGGAGCTCAACCGGAAGGCAGAGGAGTTGGACCGAAG
GGAGCGAGAGCTGCAGCATGCTGCCCTGGGGGGCACAGCTACTCGACAGAAACAATTGGCCCCCTCTACCTTCTTT
TTGTCCAGTTTCAGCCCTGCTTTTTTCCAGGACATCTCCATGGAGATCCCCCAAGAATTTTCAGAAGACTGTATCCAC
CATGTACTACCTCTGGATGTGCAGCAGCTGGCTCTTCTCCTGAACTTCTTCGCCTGCCTGGCCAGCTTCTGTGT
GGAAACCAACAATGGCGCAGGCTTTGGGCTTTCTATCCTCTGGGTCTCCTTTTTCACTCCCTGCTCCTTTGTCTG
CTGGTACCGCCCCATGTATAAGGCTTTCCGGAGTGACAGTTCAATTCATTTCTTCGTTTTCTTCTTCATTTTCTT
CGTCCAGGATGTGCTCTTTGTCTCCAGGCCATTGGTATCCCAGGTTGGGGATTTCAGTGGCTGGATCTCTGCTCT
GGTGGTGCCGAAGGGCAACACAGCAGTATCCGTGCTCATGCTGCTGGTCGCCCTGCTCTTCACTGGCATTGCTGT
GCTAGGAATTGTCATGCTGAAACGGATCCACTCCTTATACCGCCGCACAGGTGCCAGCTTTCAGAAGGCCAGCA
AGAATTTGCTGCTGGTGTCTTCTCCAACCCTGCGGTGCGAACCAGCTGCCAATGCAGCCGCTGGGGCTGCTGA
AAATGCCCTTCCGGGCCCCGTGACCCCTGACTGGGATGCCCTGGCCCTGCTACTTGAGGGAGCTGACTTAGCTCCC
GTCCCTAAGGTCTCTGGGACTTGGAGAGACATCACTAACTGATGGCTCCTCCGTAGTGCTCCCAATCCTATGGCC
ATGACTGCTGAACCTGACAGGCGTGTGGGGAGTTCACTGTGACCTAGTCCCCCATCAGGCCACACTGCTGCCAC
CTCTCACACGCCCCAACCAGCTTCCCTCTGCTGTGCCACGGCTGTTGCTTCGGTTATTTAAATAAAAAGAAAGT
GGAAGTGGAACTGACAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

456/6881
FIGURE 425

MAQSRDGGNPFAEPSELDNPFQDPAVIQHRPSRQYATLDVYNPFETREPPPAYEPPAPAPLPPPSAPSLQPSRKL
SPTEPKNYGSYSTQASAAAATAELLKKQEELNRKAEELDRRERELQHAALGGTATRQNNWPPLPSFCPVQPCFFQ
DISMEIPQEFQKTVSTMYYLWMCSTLALLLNFLACLASFCVETNNGAGFGLSILWVLLFTPCSFVCWYRPMYKAF
RSDSSFNFFVFFFIFFFVQDVLFLVLAIGIPGWGFSGWISALVVPKGNTAVSVLMLLVALLFTGIAVLGIVMLKRI
HSLYRRTGASFQKAQQEFAAGVFSNPAVRTAAANAAAGAAENAFRAP

WO 2004/030615

PCT/US2003/028547

457/6881
FIGURE 426

GGTAGTTGGTTGTGGGCACTGGGTAGAGGTATCACGTGGGGGCACTTTTCGTCTTAGCTTTTGGACAAGACGCAG
GCGCAACCCACGGCTGCTGCGGGGATCCTTGTGGCCCTTCCGGTCGGTGGAACCAATCCGTGCACAGAGAAGCGG
GGCGAACTGAGGCGAGTGAAGTGGACTCTGAGGGCTACCGCTACCGCCACTGCTGCGGCAGGGGCGTGGAGGGCA
GAGGGCCGCGGAGGCCGAGTTGCAAACATGGCTCAGAGCAGAGACGGCGGAAACCCGTTTCGCCGAGCCCAGCGA
GCTTGACAACCCCTTTTCAGCCACCACCAGCCTATGAGCCTCCAGCCCCCTGCCCCATTGCCTCCACCCTCAGCTCC
CTCCTTGAGCCCTCGAGAAAGCTCAGCCCCACAGAACCTAAGAACTATGGCTCATAACAGCACTCAGGCCTCAGC
TGCAGCAGCCACAGCTGAGCTGCTGAAGAAACAGGAGGAGCTCAACCGGAAGGCAGAGGAGTTGGACCGAAGGGA
GCGAGAGCTGCAGCATGCTGCCCTGGGGGGCACAGCTACTCGACAGAACAAATTGGCCCCCTCTACCTTCTTTTTG
TCCAGTTTCAGCCCTGCTTTTTTCCAGGACATCTCCATGGAGATCCCCCAAGAATTTTCAGAAGACTGTATCCACCAT
GTACTACCTCTGGATGTGCAGCACGCTGGCTCTTCTCCTGAACCTTCCTCGCCTGCCTGGCCAGCTTCTGTGTGGA
AACCAACAATGGCGCAGGCTTTGGGCTTTCTATCCTCTGGGTCCCTTTTCACTCCCTGCTCCTTTGTCTGCTG
GTACCGCCCCATGTATAAGGCTTTCCGGAGTGACAGTTCATTCAATTTCTTCGTTTTCTTCTTCAATTTCTTCGT
CCAGGATGTGCTCTTTGTCTCCAGGCCATTGGTATCCCAGGTTGGGGATTTCAGTGGCTGGATCTCTGCTCTGGT
GGTGCCGAAGGGCAACACAGCAGTATCCGTGCTCATGCTGCTGGTCGCCCTGCTCTTCACTGGCATTGCTGTGCT
AGGAATTGTCATGCTGAAACGGATCCACTCCTTATACCGCCGCACAGGTGCCAGCTTTCAGAAGGCCAGCAAGA
ATTTGCTGCTGGTGTCTTCTCCAACCCTGCGGTGCGAACCAGCTGCCAATGCAGCCGCTGGGGCTGCTGAAAA
TGCCTTCCGGGCCCCGTCAGCCCTGACTGGGATGCCCTGGCCCTGCTACTTGAGGGAGCTGACTTAGCTCCCGTC
CCTAAGGTCTCTGGGACTTGGAGAGACATCACTAAGTATGGCTCCTCCGTAGTGCTCCCAATCCTATGGCCATG
ACTGCTGAACCTGACAGGCGTGTGGGGAGTTCAGTGTGACCTAGTCCCCCATCAGGCCACACTGCTGCCACCTC
TCACACGCCCCAACCCAGCTTCCCTCTGCTGTGCCACGGCTGTTGCTTCGGTTATTTAAATAAAAAGAAAGTGGA
ACTGGAAGTGAATAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

458/6881
FIGURE 427

MAQSRDGGNPFAEPSELDNPFQPPPAYEPPAPAPLPPPSAPSLQPSRKLSPTPEPKNYGSYSTQASAAAATAELLK
KQEELNRKAEELDRRERELQHAALGGTATRQNNWPPLPSFCPVQPCFFQDISMEIPQEFQKTIVSTMYYLWMCSTL
ALLLNFLACLASFCVETNNGAGFGLSILWVLLFTPCSFVCWYRPMYKAFRSDSSFNFFVFFFIFFVQDVLFLVLA
IGIPGWGFSGWISALVVPKGNTAVSVLMLLVALLFTGIAVLGIVMLKRIHSLYRRTGASFQKAQQEFAAGVFSNP
AVRTAAANAAAGAAENAFRAP

WO 2004/030615

PCT/US2003/028547

459/6881
FIGURE 428

CCTGCGGCAGCCGGAGCTCGGGGAGCGGAGCGTGGTGGGGAGGGGAGCGGGACAGGCGACACAGGAGACAGCGGC
GCCGCGGCTCTCCCCACCAGGCGGCCCCGGATCCTACTGGACGCCCTGAGGGACACCGACCGCGCTCTAGAG
TCACCCACGCGCGACCCCTCCCTCTTCTCTAGACTTATTTCCATCCTTCCCGCTTTTACCCCTCCCCACCCGTC
CTGGGCTCCAGGCGCGCGCCCCCTCCTCACTCCTGGACCGGCCCTTCTCGGTGCCCCCTCTCCCTAGGGAGATGC
GATGAGCCGGTGCCCCCGCGTCTCATCGTCGCCCCGGGCACGGTGCCCCGTCCAGTGCCCGTGGTGGGGAGGGAG
CACTCCGCGGTCCCTCCGTGACGCCCCCTCGCTTGGCCCCCCCCACAGCTGGCGTCCCTCGGCCATGCCCCAGGGG
ACCCAGCCAGGGGGTGGGCTCTAGAGCGAGTGGGGTGGAGAGGAGAAAGGACGGGGCCCTTGGGGGCTCTGAGAT
GCTCCCAAGTGCCAGGGAGGGCCGAGCGAGGCGCAGGCAACCGGGCAGCAGGCATGATGCCCTCGCCTAGTGACT
CCAGCCGCTCGCTGACCAGCGGGCCAGCACCAGGGGCCCTTACCCACCTCCGCCTCCACCGACCCCTGGCTGCAGG
CCCTGCTTACGCTGGGGCTGGTCCAAGTGCTCCTGGGCATCCTGGTGGTCACCTTCAGCATGGTGGCTCTTCCG
TCACCACCACCGAGAGCATCAAGAGGTCTGCCCCGTCTTGGGCTGGGTTCTCGCTGGCGTTCTCCGGGGTGGTTG
GCATTGTGCTCTGGAAGCGGCCATTCACTCTAGTGATCTCCTTCTTCTCCTTGCTTTCGGTGCTCTGTGTCATGC
TTAGCATGGCTGGCTCTGTTCTCTCCTGTAAGAATGCTCAACTGGCCCGAGACTTCCAACAGTGCTCTCTGGAAG
GAAAGGTCTGTGTGTGCTGTCCCTCTGTTCCCTCCTCCGGCCCTGTCCAGAGTCGGGGCAGGAAGTGAAGTTG
CCCCTAACTCCACCTGTGATGAAGCCCCGAGGGGGCCCTCAAGAACCTGCTCTTCAGCGTCTGTGGGCTCACCATT
GTGCCGCTATAATCTGTACACTCTCTGCTATTGTCTGCTGCATCCAAATCTTCTCCCTGGACCTCGTGCAACGC
AGCTGGCCCCCTGAGCGGTCACTCTCAGGCCCCACTGGGACCTCTGGGCTGCACGTCCCCGCCCCCAGCCCCCTCC
TACACACCATGCTGGACCTGGAGGAATTTGTCCCGCTGTGCCCCCACCGCCCTACTATCCCCCAGAGTATACCT
GCAGCTCAGAAACAGATGCACAGAGCATCACGTACAATGGCTCCATGGACAGCCAGTGGCCTTGTACCCTACCG
ATTGCCCCCTTCTTATGAGGCAGTCATGGGACTACGAGGAGACAGCCAGGCCACTCTCTTTGACCCTCAGCTTC
ACGATGGCTCGTGCACTCTGTGAACGAGTGGCCTCCATTGTAGACGTGTCCATGGACAGCGGGTCTCTGGTGCTGT
CAGCCATTGGTGACCTCCCTGGGGGCTCTAGCCCGTCGGAGGACTCGTGCTGCTGGAGCTGCAGGGCTCCGTGC
GCTCCGTGGACTACGTTCTCTTTCGCTCCATCCAGCGCAGCCGTGCCGGCTACTGCCTCAGCCTGGACTGTGGCC
TGCGGGGGCCCCCTTCGAGGAAAGCCCCCTGCCACGGCGCCCCCAGGGCTGCCCGCTCCTATTCTGCTCTGCCC
CTGAAGCTCCACCCCCACTGGGTGCCCCCAGCTGCCCGCAGCTGCCACCGGTTGGAGGGCTGGCCGCCCTGGG
TGGGACCTGCTTCCCCGAGCTGAGGCGGCGGGTCCCCCGGGGAGGGGGCCGCCAGCCGAGCCCCGCCACCC
GAGCCCCGACTCGTCGCTTCAGCGATAGCTCAGGTTCCCTCACCACCGGGGCACCGCCCTCCTCATCCGGCAT
CCCCACCACCGCTGCTGCTGCCACGGTCCCACAGCGACCCAGGCATCACGACCTCCAGTGACACTGCTGACTTCA
GGGACCTTTATACCAAAGTGCTTGAGGAAGAAGCTGCTTCTGTTTCTCTGAGATACAGGGCTCTGCTCTGAAG
CCTGCTCTTCCGCTAGCCCCGTGCCCTTCCCCAAGTTGCTACGTGCCCGGTGAGCCGAGAAACGGCGCCCTG
TGCCACCTTCCAAAAAGTTCCCTGCCCTCGGGCCCTGCACCTGCCACTCCCTGGGGGACCTAAAGGGCAGCT
GGCCAGGTGCGGGGCTGGTCACTCGTTTCTCCAGATATCCAGGAAAGCCCCAGACCCAGTGGGACTGGAGCTC
ATGGACATAAGCAGGTGCCCGGAGCCTGTGGGGCCGGCTGGCCGAGAGAGCCTCCACCTTCGCAGCTGCGGAG
ATCTGAGCTCTAGCTCTTCCCTGCGCGTCTCCTGTCTGGCCGAGGCTGGAGCGTGGTACCCGCCCCACAGCC
TCAGCCTCAACGGGGGAGCCGGGAGACTGGGCTCTGACCTAGGCTTCTTGTACACTGAACACATCCAGCCACA
GGCACCAGCTGGTTGGGACCAGCAGCCCCCAGCATCCTCTTGCAGTGGCTGGCACAAGAAAGAACCTGCTGTATA
CCCCCAAAGTGCTCCCTTCCCTCCTACCTCTGGGGTCTCTTGTGCTTGCCTCTGCTGCTCTGGTCTGGGAGAG
CTTCTGCTCTGTGCTGCATGGGTATTAGACTGTGGGGGAGATGCCCTTCTTATAGCACTGGAGGAGGAAACA
AATTCTTGTCCTCCCTCAGAATGAGAGTGGCTCTTCTGATTGCAAGGGCACTATGGTCAGGGCAAAGGCATGGC
CCAGGTGTTAAGTACAGGGTGACGTGTGCTATGCAATGGGGTGGTAAGGCAGGCACGAAGAGTCCAAAAATC
TAGGTGGCTCTCAGCTCTGCCACCTCTAGCTGCATGACCTTGGGCAAGCTATGTAACCCCAATTGCTGCTCCA
TTAAAGACTGTGAAGGTAGAATGTTGTAAAGCTCTTAACAGTATGTAAGCCTTCAATAAATTTAGTTTTCCCC
TT

WO 2004/030615

PCT/US2003/028547

460/6881
FIGURE 429

MMPSPSDSSRSLTSRPSTRGLTHLRLHRPWLQALLTLGLVQVLLGILVVTFSMVASSVTTTESIKRSCPSWAGFS
LAFSGVVGIVSWKRPFTLVISFFSLLSVLCVMLSMAGSVLSCKNAQLARDFQQCSLEGKVCVCCPSVPLLPCPE
SGQELKVAPNSTCDEARGALKNLFSVCGLTICAAICTLSAIVCCIQIFSLDLVHTQLAPERSVSGPLGPLGCT
SPPAPLLHTMLDLEEFVPPVPPPPYPPEYTCSSSETDAQSITYNGSMDSPVPLYPTDCPPSYEAVMGLRGDSQA
TLFDPQLHDGSCICERVASIVDVSMDSGSLVLSAIGDLPGGSSPSEDSCLLELQGSVRSVDYVLFRSIQRSRAGY
CLSLDCGLRGPFEEsplPRRPPRAARSYSCSAPEAPPLGAPTAARSCHRLEGWPPWVGPCFPPELRRRVPRGGGR
PAAAPPTRAPTRRFSDSSGSLTPPGHRPPHPASPPPLLLPRSHSDPGITTSDDTADFRDLYTKVLEEEAASVSSA
DTGLCSEACLFRLARCPSPKLLRARS AEKRRPVPTFQKVP LPSGPAPAHSLGDLKGSWPGRGLVTRFLQISRKAP
DPSTGTGAHGKQVPRSLWGRPGRESLHLRSCGDLSSSSSLRRLLSGRRLERGTRPHSLSLNGGSRETGL

WO 2004/030615

PCT/US2003/028547

461/6881
FIGURE 430

CAGTGCCCCACAGCTCTTCAGGCCCTTCCTGTGCCTGGCTGCCCTCCCACCCTACCCTTTTGTACCTCTGAGAAG
GCTCTGGCCCCACGCACAGCCCCACTGTACCAGGGCCAGTATCTGTCTCAGGGACCTCCTATCCAGAGCCTGAG
CCAGCCCCAGCCCCAGCCCCAGCTCCAGCTGCTCCATCTGAACCTGTATCTTCTTCCAAGCCACCCATTACCCTC
TTGGAGTCAGACTCACGCATCTCCAAAGAAGAACTTTTGAGAGCCCAGGCGCTGAGAGAGCAGGGTCAGACACTC
CCGAGCCTCTCGGTACAGCTGTAGGGGCGACACAGGTAGGCTTGCAGCTGCGGGAACAGTGCCACCTCCGCACCT
AAGCACTCCCATTCCTGGCCAGCATCCTTGGGGCTCATCTCATAACAATAGCCCCGGTCTCAGAGCTACCTCCTT
CTCCAGCTCTTCTCGTCTCAGGCCTGTGCTCCCCAGTCAGCAGCTGTAGCCGTTCCATGTACTGCCGCTGCAT
GCGGCCAGGCAGGAAGAAGTTGAGGGGAAAGGGCATAGCCTCTGCATAACACTTCCGGGTCACTTCTACGTAGTT
CTTGGTGTCTATCCAAAAAGTATGTACCTGGATTGGGTGGGCAGGAAGAAACAGGCAGGTCTGAGCCAGTGCACC
TGTCTGATTCAAGGTGGGCTTCTGACCTCCATGCTCTCTGAGTCTCTGTGTGGGTCTGTGTGTTCCCGTCCCTT
CCCCGGCTGGCCATGGATGCTGGGAGGTCTGGGCACACTCACCAGCACCAGGATCAACTTCTCCTCCAGGAGAGA
CATGAAGGCCAGGGTGTCTGCCCTTGCTGAGCTGACAGATCATAATCAGCATTGTACTTCTGTGGAGGAAATAT
CCATCGCGTGGACGCTGGGGAGCTGCAAGGGCACTTACCAGGGAGGAAGGAGTCTGTCTGGTACCCCCCTCAC
TGGCCTCTGAGTGCAGTGGAGGTACAGCAAGGAACCTTTCTGCAAGGCCCTTGCTGGGCCCAGCCAGTAG
CCTGTTGCTGTTGGCAAAAAGCCTGGGCCTTGGAGCCCGTGGCCGTCAAGGTCTGGGCCCATTGAGAAGAAGG
AAGAAAGGTTGGGCCGCAAACTAGGAGCAGCTCCCAGAAATTTCCATGGAAAGCTGGAAACAATGCCTGCTGACAGC
AACTTTCTAACAGTAACTTTCCCGACCCAGACACCACAAAGCTAGCACAAAGGAGCTCAGATGCAGGCTAGGACT
CGGTCCATGCCTCAGGAACCAGGGAAAGCCATCCTCACACTCCCTGGATCCAGGGAAACCCACGCCCAGGGCCCCC
CAGCTTGTTCCTCAGTGCCAGCTCTTGGCTATTTCTTTCACTTCATTCCATCGCCCAGACACCATTACCACAT
ACACATTCCATCCATACCCCCAGGTCTCAGCCTGCCCTACCTTCCCAGGCTCCAGTCCCTGTTCTCAGCATCCC
CCACCACATCCTGAGTAAGCTTTGTCCCCAGATAACCTCTTCAGCATGATCCTTAAATCTCCCTAAGCCTCAGTT
TCTCCCCTGTGGAATGGGGGTAAGAATCTTTCTCTGAATGCCCTGTGTTAGGAAATAATTTAGAATACTTCG
GAAACAAAAAGCTCTGTTACACCTAAGCAATCAGGGCAGTGGCCCTGGCCTTGCCAGGAACTTAGGCTTTTATC
TGGATCCTCTTTCCAGGCCTCTCAATTAATTCCCCAGGTCCTTAACCTTTGGGAAATTAGAAATTAGGAAGAGTG
TCCCACCTCTGACACTGTGTTCCCTCTTGGAACCTGACCGTCAATGCTAGAGAACCCTTGGAACACATGCTGGC
CCAGCCCTCTAGTTTTACAAATAAGGGAGTGACAGCCCTGAGAGGTTACATGGCCTGCCCAAGATCACGCAGTC
AATGGCAGAGTAAAGAGCATAGCCTAGGCCTCCCCACTCCTCTAGTAATGCTCTTTCATCTTCTCCAACTGGCT
CTAAGCCTTGTCCATCCTGAGCCCCATATCTAGCCCAACCTAGTCCCTGAAAACAAGAAGTGGCCCTTAGAAATC
TCTCTCCAGTCCCCTATCAGAGGCCAACTGCTGTCTTCCAGTCTCCTTCAGCCTGTGCTCCTCTCCCTCCCTGA
CTGACAGGCAGAAGGTACCGTGCCTCTGGATATCCCCACAGTGGCCTGAGCTGCATCTCTTGCCGACTGCTTTAA
TACATCACAGTGACATTGTGTGTGTCTCTGCCACCAGACTATTGCTCCTTGATGCTCTGGGTACCTGCATCTAG
CATGGCATATATCTAGTGCTCAATAAATGTGTATTGTACGG

WO 2004/030615

PCT/US2003/028547

462/6881
FIGURE 431

MAWTLGSCKGTSPGRKESCLVPPSLASECSGGTARNFSCQGPLAWAQPVACCCWQKAWALEPAGRQGPPIEKKE
ERLGRKLGAAPRISMESWNNAC

WO 2004/030615

PCT/US2003/028547

463/6881
FIGURE 432

AAGCCCCAGCCCGGCCTCCGCTCCGGCCGCGCCACCGCCCCTGTTTTGTTTCCATGGCGACAGGCGGCGCAGGG
CCCCTCCAAACATAACGCGCTGTGGAAAACATGCTGCTCGGGGGACCCCCCGCAGTCCCCGCTCGGGGACGAG
CCCCAAGGGGGCCCTGGAGCAGTACAGGCCACGTGCAGTTTGGCAAGAGCCCCAGACCTGGCCCCAGGCGCACAAAG
ACCCCGCTCTCCAGAGCCTGCCGCGCCTTCAAGGGTTCCGGGGCTCCACTTGACGAGGCGCCGTGACTCTCCGAG
GCGCGCCGGGGCCGACAGCGCTGTCCCGCTACGTGGGCCACCTCTGGATGGGCGGCGGCGCCCTCCCCGAGGC
CCGCGGCCAGTCCCCCGCAGTTTCACTGCCAGTGGGCCAGAGAAGCCTCGCCTCCCCGGGGATCTCCCCAGG
CCCCCTGACCGCAACGATCGGAGGGGCGGTGGCGGGGGCGGGCCCAGGCAGGGGAGGGCAGAAGCACACAAGGA
AGTGTTCGGGACAGAGGGTGGGCAAGATGGCGGCGCCATGGAGCTGTTCTGCTGGTCAGGGGGCTGGGGGCT
GCCGTCACTGGACCTGGACAGCCTGGCCGTGCTGACCTATGCCAGATTTACTGGTGCTCCACTGAAGGTACACAA
GATCAGCAACCCCTGGCAGAGCCCTTCAGGAACCTCTGCCTGCCCTTCGGACCAAGTCATGGAGAGGTATCTCAGT
TCCACACAAGATCATCACCCACCTTCGAAAAGAGGTACATACTTTTTGGATAGACACCAAGAACTACGTGGAAGT
GACCCGGAAGTGGTATGCAGAGGCTATGCCCTTTCCCTCACTTCTTCTGCTGGCCGCATGCAGCGGCAGTA
CATGGAACGGCTACAGCTGCTGACTGGGGAGCACAGGCCTGAGGACGAGGAAGAGCTGGAGAAGGAGCTGTACCG
AGAGGCTCGGGAGTGTCTGACCCTGCTCTCTCAGCGCCTGGGCTCTCAAAAGTTCTTCTTTGGAGATGCCCCGTC
CTCCTTGGACGCCTTCGTCTTCAGCTACTTGGCCCTGCTGCTGCAGGCAAGCTGCCCAGTGGGAAGCTGCAGGT
CCACCTGCGTGGGCTGCACAACCTCTGTGCCTATTGTACCCACATTCTCAGTCTCTACTTCCCCTGGGATGGAGC
TGAGGTACCACCGCAACGCCAGACACCAGCAGGCCCAGAGACTGAGTGAGTGAGCCATACCGGCGCCGGAACCAAG
ATCCTATCTGTGCTGGCAGTGACTGGCAGCCATGGTGGGCTACGCCTTGCTCAGCGGCATTGTCTCCATCCAGCG
GGCAACGCCTGCTCGTGGCCCCAGGCACCCGGACCCTGGGCATGGCTGAGGAGGATGAAGAGGAATGATTTGTCC
TCACGCTCCCAAGACTGGTTTTTCTACTCTCATGCATTCCAGAGGCCCCGTGCCTCCTCGTTGTTGGTACAGCC
GGACACGGGGTGTGCCACCCAGAATAAAGCCACTCACACTG

WO 2004/030615

PCT/US2003/028547

464/6881
FIGURE 433

GCCGGAAGCGCGCGGAGACCATGTAAGTGAAGACCTCGCGAGGTCTGAGAGTCACTGGAGCTACCAGAAGCATCAT
GGGGCCCTGGGGGAGAGCCAGAGCTCCTGGTGTGGCGCCCCGAGGCGGTAGCTTCAGAGCCTCCAGTGCCTGTGGG
GCTGGAGGTGAAGTTGGGGGCCCTGGTGTCTGCTGCTGGTGTCTACCTCCTCTGCAGCCTGGTGCCCATCTGTGT
GCTGCGCCGGCCAGGAGCTAACCATGAAGGCTCAGCTTCCCGCCAGAAAGCCCTGAGCCTAGTAAGCTGTTTCGC
GGGGGGCGTCTTTTTGGCCACTTGTCTCCTGGACCTGCTGCCTGACTACCTGGCTGCCATAGATGAGGCCCTGGC
AGCCTTGACAGTGACGCTCCAGTTCCCACTGCAAGAGTTTCATCCTGGCCATGGGCTTCTTCCTGGTCTCTGGTGAT
GGAGCAGATCACACTGGCTTACAAGGAGCAGTCAGGGCCGTACCTCTGGAGGAAACAAGGGCTCTGCTGGGAAC
AGTGAATGGTGGGCGCAGCATTGGCATGATGGGCCAGGGGTCCCACAGGCGAGTGGAGCCCCAGCAACCCCTC
AGCCTTGCGTGCCTGTGTAAGTGGTGTCTCCCTGGCCCTCCACTCCGTGTTTCGAGGGGCTGGCGGTAGGGCTGCA
GCGAGACCGGGCTCGGGCCATGGAGCTGTGCCTGGCTTTGCTGTCTCCACAAGGGCATCCTGGCTGTGAGCCTGTC
CCTGCGGCTGTGTGAGAGCCACCTTAGGGCACAGGTGGTGGCTGGCTGTGGGATCCTCTTCTCATGCATGACACC
TCTAGGCATCGGGCTGGGTGCAGCTCTGGCAGAGTCGGCAGGACCTCTGCACCAGCTGGCCCAGTCTGTGCTAGA
GGGCATGGCAGCTGGCACCTTTCTCTATATCACCTTTCTGGAAATCCTGCCCCAGGAGCTGGCCAGTTCTGAGCA
AAGGATCCTCAAGGTCATTCTGCTCCTAGCAGGCTTTGCCCTGCTCACTGGCCTGCTCTTCATCCAAATCTAGGG
GGCTTCAAGAGAGGGGCGAGGGGAGATTGATGATCAGGTGCCCTGTTCTCCCTTCCCTCCCCAGTTGTGGGGAA
TAGGAAGGAAAGGGGAAGGGAAATACTGAGGACCAAAAAGTTCTCTGGGAGCTAAAGATAGAGCCTTTGGGGCTA
TCTGACTAATGAGAGGGAAGTGGGCAGACAAGAGGCTGGCCCCAGTCCCAAGGAACAAGAGATGGTCAAGTCGCT
AGAGACATATCAGGGGACATTAGGATTGGGGGAAGACACTTGACTGCTAGAATCAGAGGTGGACACTATACATAA
GGACAGGCTCACATGGGAGGCTGGAGGTGGGTACCCAGCTGCTGTGGAACGGGTATGGACAGGTCATAAACCTAG
AGTCAGTGTCTGTGGTCTAGCCATTTACGACCCCTGCCACTTGGAGTGGACCCCTCCTACTCTTCTTAGCG
CCTACCCCTCATACCTATCTCCCTCCTCCCATCTCCTAGGGGACTGGCGCCAAATGGTCTCTCCCTGCCAATTTTG
GTATCTTCTCTGGCCTCTCCAGTCTGCTTACTCCTCTATTTTTAAAGTGCCAAACAAATCCCCTTCTCTTTCT
CAAAGCACAGTAATGTGGCACTGAGCCCTACCCAGCACCTCAGTGAAGGGGGCCTGCTTGCTTTATTTTGGTC
CCGGATCCTGGGGTGGGGCAGAAATATTTTCTGGGCTGGGGTAGGAGGAAGGTTGTTGCAGCCATCTACTGCTGC
TGTACCCTAGGAATATGGGGACATGGACATGGTGTCCCATGCCAGATGATAAACACTGAGCTGCCAAAACATTT
TTTTAAATACACCCGAGGAGCCCAAGGGGAAGGGCAATGCCTACCCCAAGCGTTATTTTTGGGGAGGGAGGGCT
GTGCATAGGGACATATTCTTTAGAATCTATTTTATTAAGTACCTGTTTTGGGACCTGTTACCCAAATAAAGAT
GTTTCTAG

WO 2004/030615

PCT/US2003/028547

465/6881
FIGURE 434

AGAAAGAAAAGGTGTAGTGTGTTGGGGAGGTCAACGGGCTATGCTGGCTTGACAGGGCTGGGCTCTTCAGAACAGA
AGCATGGATCTCGGAATCCCTGACCTGCTGGACGCGTGGCTGGAGCCCCAGAGGATATCTTCTCGACAGGATCC
GTCCTGGAGCTGGGACTCCACTGCCCCCTCCAGAGGTTCCGGTAACTAGGCTACAGGAACAGGGACTGCAAGGC
TGGAAGTCCGGTGGGGACCGTGGCTGTGGCCTTCAAGAGAGTGAGCCTGAAGATTTCTTGAAGCTTTTCATTGAT
CCCAATGAGGTGTACTGCTCAGAAGCATCTCCTGGCAGTGACAGTGGCATCTCTGAGGACCCCTGCCATCCAGAC
AGTCCCCCTGCCCCAGGGCAACCAAGTTCTCCTATGCTCTATGAGGTTGTCTATGAGGCAGGGGCCCTGGAGAGG
ATGCAGGGGGAAACTGGGCCAAATGTAGGCCTTATCTCCATCCAGCTAGATCAGTGGAGCCCAGCATTTATGGTG
CCTGATTCTGTCATGGTCAGTGAGCTGCCCTTTGATGCTCATGCCACATCCTGCCAGAGCAGGCACCGTAGCC
CCAGTGCCCTGTACAACCCTGCTGCCCTGTCAAACCCTGTTCTGACCGATGAGGAGAAGCGTCTGCTGGGGCAG
GAAGGGGTTTCCCTGCCCTCTCACCTGCCCTCACCAAGGCAGAGGAGAGGGTCTCAAGAAGGTCAGGAGGAAA
ATCCGTAACAAGCAGTCAGCTCAGGACAGTCGGCGGCGGAAGAAGGAGTACATTGATGGGCTGGAGAGCAGGGTG
GCAGCCTGTTCTGCACAGAACCAAGAATTACAGAAAAAGTCCAGGAGCTGGAGAGGCACAACATCTCCTTGGA
GCTCAGCTCCGCCAGCTGCAGACGCTAATTGCTCAAACCTCCAACAAAGCTGCCAGACCAGCACTTGTTGTTTG
ATTCTTCTTTTTTCCCTGGCTCTCATCATCCTGCCAGCTTCAGTCCATTCCAGAGTCGACCAGAAGCTGGGTCT
GAGGATTACCAGCCTCACGGAGTGACTTCAGAAATATCCTGACCCACAAGGACGTAACAGAAAATCTGGAGACC
CAAGTGGTAGAGTCCAGACTGAGGGAGCCACCTGGAGCCAAGGATGCAAATGGCTCAACAAGGACACTGCTTGAG
AAGATGGGAGGGAAGCCAAGACCCAGTGGGCGCATCCGGTCCGTGCTGCATGCAGATGAGATGTGAGCTGGAACA
GACCTTCCTGGCCCACTTCCTGATCACAAGGAATCCTGGGCTTCCTTATGGCTTTGCTTCCCACTGGGATTCCTA
CTTAGGTGTCTGCCCTCAGGGGTCCAAATCACTTCAGGACACCCCAAGAGATGTCCTTTAGTCTCTGCCTGAGGC
CTAGTCTGCATTTGTTTGATATATGAGAGGGTACCTCAAATACTTCTGTTATGTATCTGTGATTTTATTTCTTC
TTTGGGTATAGGGTTGAGGGGAAATAAGTTTTGAGTGAGAAATAAACGTTTTAGCTGAAATTGT

WO 2004/030615

PCT/US2003/028547

466/6881
FIGURE 435

MDLGIPDLLDAWLEPPEDIFSTGSVLELGLHCPPPEVPVTRLQEQGLQGWSGGDRGCGLQESEPEDFLKLFIDP
NEVYCSEASPGSDSGISEDPCHPDSFPAPRATSSPMLYEVVYEAGALERMQGETGPNVGLISIQLDQWSPAFMVP
DSCMVSELPFDAHAILPRAGTVAPVPCTLLPCQTLFLTDEEKRLLGQEGVSLPSHLPLTKAEERVLKKVRRKI
RNKQSAQDSRRRKKEYIDGLESRVAACSAQNQELQKKVQELERHNISLVAQLRQLQTLIAQTSNKAQTSTCVLI
LLFSLALIILPSFSFQSRPEAGSEDYQPHGVTSRNILTHKDV TENLETQVVESRLREPPGAKDANGSTRTLLEK
MGGKPRPSGRIRSVLHADEM

WO 2004/030615

PCT/US2003/028547

467/6881

FIGURE 436

GCGAGGCGCCACCGACGCGGAAGACTATAAGCCCCAGCGGGCGACGACCGAACGCCCCGGGAACACCGGGCCCC
GAGCTCGGTCCCGCGCCCGAGGATCCTCCACGGGGCTAGATGGCTGCGTCGGGGGCGGGAGCGGAGGTGAGCGGG
CGCTAGGGCCGCGAGCCCCCGCCGGCCCTTCTCCAGCGCCCTGCGGACCCCGCAGAAGGCGCTCGCCTCCCTAG
CCCGCAAAAACATATCGATTTTCTCGCTGTGGCAACGGGGACGTCCTGATAGATCCTCTGCTCCAATAGGCAAC
TCCGGCCTTCCCTGCCCTGACCTGGAACCTCTGGGAGGGCTGCAGAGTAAGTGCCGCCTCTGCGCTCCGACGGAG
GCACGAGGCCTGTGGAGTAGGTCCCTCTGTTCCGACAGGTGCGACACTTGGCGCTCCATGCTTGCGGGTGCCGGG
AGGCCTGGCCTCCCCCAGGGCCGCCACCTCTGCTGGTTGCTCTGTGCTTTCACCTTAAAGCTCTGCCAAGCAGAG
GCTCCCGTGCGAGGAAGAGAAGCTGTGTCAGCAAGCACCTCAAATTTGCCATGCTGGCTGGTGGAAGAGTTTGTGGTA
GCAGAAAGAGTGCTCTCCATGCTCTAATTTCCGGGGCTAAAACCTACCCCTGAGTGTGGTCCACAGGATATGTAGAG
AAAATCACATGCAGCTCATCTAAGAGAAATGAGTTCAAAGCTGCCGCTCAGCTTTGATGGAACAACGCTTATTT
TGGAAGTTTGAAGGGGCTGTGCTGTGTGTGGCCCTGATCTTCGCTTGTCTTGTTCATCATTGTCAGCGACAATTG
GACAGAAAGGCTCTGGAAAAGGTCCGGAAGCAAATCGAGTCCATATAGCTACATTCCACCCTTGTATCCTGGGTC
TTAGAGACCCTATCTCAGACAGTGAAAGTGAAATGGACTGATTTGCACTCTTGTTCTTTGGAGCCTTGTGGTGG
AATCCCCTTTTCCCCATCTTCTTTTCAGATCATTAATGAGCAGAATAAAAAGAGTAAATGGT

WO 2004/030615

PCT/US2003/028547

468/6881
FIGURE 437

MLAGAGRPGLPQGRHLCWLLCAFTTLKLCQAEAPVQEEKLSASTSNLPCWLVEEFVVAEECSPCSNFRAKTTPECG
PTGYVEKITCSSSKRNEFKSCRSALMEQRLFVKFEGAVVCVALIFACLVIIRQRQLDRKALEKVRKQIESI

WO 2004/030615

PCT/US2003/028547

469/6881
FIGURE 438

GAATTCGAGGATCCGGGTACCATGGGAGGAAAACTTCTTCCTGGCCTGGGCTCCGTGCCGCTCTGTTTGCCAACC
GTCCAGTCCCGCCTACCAAGTGCCGGGCGCTCCCCACCCCTCCCCCGGCTCCCCCGGTGTCCGCCATGGCCAAAGC
CTACGACCACCTCTTCAAGTTGCTGCTGATCGGGGACTCGGGGGTGGGCAAGACTTGTCTGATCATTGCTTTGC
AGAGGACAACCTTCAACAACACTTACATCTCCACCATCGGAATTGATTTCAAGATCCGCACCTGTGGATATAGAGGG
GAAGAAGATCAAACCTACAAGTCTGGGACACGGCTGGCCAAGAGCGGTTCAAGACAATAACTACTGCCTACTACCG
TGGAGCCATGGGCATTATCCTAGTATACGACATCACGGATGAGAAATCTTTCGAGAATATTGAGAACTGGATGAA
AAGCATCAAGGAGAATGCCTCGGCTGGGGTGGAGCGCCTCTTGCTGGGGAACAAATGTGACATGGAGGCCAAGAG
GAAGGTGCAGAAGGAGCAGGCCGATAAGTTGGCTCGAGAGCATGGAATCCGATTTTTTCGAAACTAGTGCTAAATC
CAGTATGAATGTGGATGAGGCTTTTAGTTCCCTGGCCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGG
AAACGGCAACAAGCCTCCCAGTACTGACCTGAAAACTTGTGACAAGAAGAACACCAACAAGTGCTCCCTGGGCTG
AGGACCTTTCTTGCTTCCCCACCCCGGAAGCTGAACCTGAGGGAGACAACGGCAGAGGGAGTGAGCAGGGGAGA
AATAGCAGAGGGGCTTGAGGGGTCACATAGGTAGATGGTAAAGAGAATGAGGAGAAAAAGGAGAAAAGGGAAAAAG
CAGAAAGGAAAAAAGGAAGAGAGAGGAAGGGAGAAGGGAGAGGAATGAATTGAGGAAGTGAAAGAAGGCAAGGA
GGTAGGAAGAGAGGGAGGAGGAAAGGAAGGAGAGAGATGCCTCAGGCTTCAGACCTTACCTGGGTTTTTCAGGGCA
AACATAAATGTAAATACACTGATTTATTCTGTTACTAGATCAGGTTTTAGGGTCCTGCAAAAGGCTAGCTCGGCA
CTACACTAGGGAATTTGCTCCTGTTCTGTCACTTGTGATGGTCTTTCTTGGTATTAAAGGCCACCATTTCACAA
AAAAAAAAAAAAACCATGGTACCCGGATCCTCGAATTC

WO 2004/030615

PCT/US2003/028547

470/6881
FIGURE 439

MAKAYDHLFKLLLLIGDSGVGKTCLIIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKLQVWDTAGQERFKTITT
AYYRGAMGIILVYDITDEKSFENIQNWMKSIKENASAGVERLLLGKNKCDMEAKRKVQKEQADKLAREHGIRFFET
SAKSSMNVDEAFSSLARDILLKSGGRRSGNGNKPPSTD LKTC DKKN TNKCSLG

WO 2004/030615

PCT/US2003/028547

471/6881
FIGURE 440

CCTTTCCGGCGGTGACGACCTACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAG
AGGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCAG
GATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCT
GCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAAGGATGTTCCCTTCAGGAGGAAGCAGCACTTAAAAGCACTCTG
AGTCAAGATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT

WO 2004/030615

PCT/US2003/028547

472/6881
FIGURE 441

MPLAKDLLHPSPEEEKRKHKKKRLVQSPNSYFMDVKCPGCKITTVFSHAQTVVLCVGCSTVLCQPTGGKARLTE
GCSFRRKQH

WO 2004/030615

PCT/US2003/028547

473/6881
FIGURE 442

ACTCAGGCAGCAGCCCCCTTCTTTCTTGCCCCAGTCTCCAGTTCTCCAGTGTTACAGGTGAGCCTACCAACAGCC
ACTGCTCATGATGGAGGCCATCAAGAAAAAGATGCAGATGCTGAAGTTAGACAAGGAGAATGCTCTGGATCGGGC
AGAGCAAGCTGAAGCTGAGCAGAAGCAGGCAGAAGAAAGAAGTAAACAGCTGGAGGATGAGCTGGCAGCCATGCA
GAAGAAGCTGAAAGGGACAGAGGATGAGCTGGACAAGTATTCTGAAGCTTTGAAGGATGCCCAGGAGAAGCTGGA
ACTGGCAGAGAAGAAGGCTGCTGATGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGA
AGAGCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGA
GAGTGAGAGAGGTATGAAGGTTATTGAAAAACGGGCCCTTAAAGATGAAGAAAAGATGGAACTCCAGGAAATCCA
ACTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT
TGAAGGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCTAAGTGTTCTGAGCTGGAGGAGGAGCT
GAAGAATGTCACCAACAACCTCAAGTCTCTTGAGGCTCAGGCGGAGAAGTACTCTCAAAAAGAAGATAAATATGA
GGAAGAAATCAAGATTCTTACTGATAAACTCAAGGAGGCAGAGACCCGTGCTGAGTTTGCTGAGAGATCGGTAGC
CAAGCTGGAAAAGACAATTGATGACCTGGAAGATGAGCTCTATGCCCAGAACTGAAGTACAAGGCCATTAGCGA
GGAGCTGGACCACGCCCTCAATGACATGACCTCTATATTAATTATCACCGTTTCTGCTCTGTTCTGGATCTGCCCC
CTTTACTCCTCGGGGAACCCAAGGCCCCACTCTCGCTCTGGATTCCATTTGGGTGAGCCTGGCTGGTCCCCAAGG
CATTAGGATGGGGGAGCAAAAAGCAACTTATGTATTTTCTTCCACCCCCACCCCAAATTAAATGTTAAGCTGCT
GGA

WO 2004/030615

PCT/US2003/028547

474/6881
FIGURE 443

MMEAIIKKKMQLKLDKENALDRAEQAEAEQQAEEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQEKLELA
EKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENTRALKDEEKMELQEIQLK
EAKHIAEEADRKYEEVARKLVIIIEGDLERTEERAELAESKCSELEEEELKNVTNNLKSLEAQAEKYSQKEDKYEEE
IKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQLKYKAISEELDHALNDMTSI

WO 2004/030615

PCT/US2003/028547

475/6881
FIGURE 444

GTCAGCGGGGAAGCTGGAAGGCGTCGTTCTCCTTTCCAGCTCTCCTGCCTGTCCGCCATGTTTTCAGGCCGGGT
CTGGCTTGGTCTTCCCCCGTAAGGAAATGGCCGGGAGCTCCAGGGGACCCAGGCGCCGTGCTTCCGGCGGAGCT
GGGCTGACCAGCCAGGACAGCGGGGTAAACCCGAACAATTCTGCGCGAGGTAGGGAGGCCATGGCGTCCGGCAGT
AACTGGCTCTCCGGGGTGAATGTCGTGCTGGTGATGGCCTACGGGAGCCTGGACTTGAAAGAGGAGATTGATATT
CGACTCTCCAGGGTTCAGGATATCAAGTATGAGCCCCAGCTCCTTGAGATGATGATGCTAGACTACTACAAGT
GAAACCCAGGAAATCAAAGTTGCTACAACATATCTGTATAGGATGAAAGCTCTGGATGCCATTTCGTACCTCTGAG
ATCCCATTTTCTTCTGAAGGCCGGCATCCCCGTTCTTAATGGGCAAGAATTTCCGCTCCTACCTGCTGGATCTG
CGAAACACTAGTAGCCTTTCAAGGGTGTACGCAAGCACTCATTGATACCCTTTTGGATGGCTATGAAACAGCC
CGCTATGGGACAGGGGTCTTTGGCCAGAATGAGTACCTACGCTATCAGGAGGCCCTGAGTGAGCTGGCCACTGCG
GTTAAAGCACGAATTGGGAGCTCTCAGCGACATCACCAGTCAGCAGCCAAAGACCTAACTCAGTCCCCTGAGGTC
TCCCCAACAACCATCCAGGTGACATACCTCCCTCCAGTCAGAAGAGTAAACGTGCCAAGCACTTCCTTGAATTG
AAGAGCTTTAAGGATAACTATAACACATTGGAGAGTACTCTGTGACGGAGCTGAAGGACTCTTGCCGTAGATTAA
GCCAGTCAGTTGCAATGTGCAAGACAGGCTGCTTGCCGGGCCGCCCTCGGAACATCTGGCCCAGCAGGCCAGAC
TGTATCCATCCAAGTTCCCGTTGTATCCAGAGTTCTTAGAGCTTGTGTCTAAAGGGTAATCCCCAACCCTTCCT
TATGAGCATTTTTAGAACATTGGCTAAGACTATTTTCCCCCAGTAGCGCTTTTTTCTGGATTTGCATTCCGGGTG
TATTCTTAATGTTTCTGTCAAAGCTTCTTAAAAATCTTCACTTGGTTTCAGCCATAGTTCACCTTCCCTGTTCCA
GGTTTATTTAATTCCAAAGGTGAGAGTTGGAGTGAGATGTCTCCATATCTATACCTTTGTGCACAGTTGAATGG
GAACGTGTTTGGGTTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAGGTCAAGTGG
GGAAGTTGGTGAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCCTGACATGC
AAGGATCTACTTTAATTCACACTCTCATTAAATAAATTGAATAAAAGGGAATGTTTGGCACCTGATATAATCTG
CCAGGCTATGTGACAGTAGGAAGGAATGGTTTCCCCTAACAAAGCCCAATGCACTGGTCTGACTTTATAAAATTATT
TAATAAAATGAACATTATCAATAAAACGTATGAATCAGTAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

476/6881
FIGURE 445

MASGSNWLSGVNVVLVMAYGSLDLKEEIDIRLSRVQDIKYEPQLLADDDARLLQLETQGNQSCYNYLYRMKALDA
IRTSEIPFHSEGRHPRSLMGKNFRSYLLDLRNTSTPFKGVRKALIDTLLDGYETARYGTGVFGQNEYLRVQEALS
ELATAVKARIGSSQRHHQSAAKDLTQSPEVSPTTIQVLYLPSSQSKRAKHFLLELKSFKDNYNTLESTL

WO 2004/030615

PCT/US2003/028547

477/6881
FIGURE 446

CCCGACTAAGTGACTTAAACTCCCACCTACTCCTGGAATAAGGAGTCAAAGCCCGGATAGGCGCAGTATTCTACC
TTGTAAATACTGTTATTTGTATATACTGTAAATGATGACATCGGTGGGCACTAACCGAGCCCCGGGAAACTGGGA
ACAACCTCAAAACCAAAACCAGACACAGCACAGCACAAGCAGCGGCCACAGGCCACTGCAGAACAAATTAGACTTGCACA
GATGATTTTCGGACCATAATGATGCTGACTTTGAGGAGAAGGTGAAACAATTGATTGATATTACAGGCAAGAACCA
GGATGAATGTGTGATTGCTTTGCATGACTGCAATGGAGATGTCAACAGAGCTATCAATGTTCTTCTGGAAGGAAA
CCCAGACACGCATTCTCGGGAGATGGTTCGGGAAGAAGAAGGGAGTCTCAGGCCAGAAGGATGGTGGCCAGACGGA
ATCCAATGAGGAAGGCAAAGAAAATCGAGACCGGGACAGAGACTATAGTCGGCGACGTGGTGGGCCACCAAGACG
GGGAGAGGTGCCAGCCGTGGACGAGAGTTTCGAGGTTCAGGAAAATGGATTGGATGGCACCAGAGTGGAGGGCC
TTCTGGAAGAGGAACAGAAAGAGGCAGAAGGGGCCGTGGCCGAGGCAGAGGTGGCTCTGGTAGGCGAGGAGGAAG
GTTTTCTGCTCAAGGAATGGGAACCTTTAACCCAGCTGATTATGCAGAGCCAGCCAATACTGATGATAACTATGG
CAATAGCAGCGGCAATACGTGGAACAACACTGGCCACTTTGAACCAGATGATGGGACGAGTGCATGGAGGACTGC
AACAGAGGAGTGGGGGACTGAAGATTGGAATGAAGATCTTTCTGAGACCAAGATCTTCACTGCCTCTAATGTGTC
TTCAGTGCCTCTGCCTGCGGAGAATGTGACAATCACTGCTGGTCAGAGAATTGACCTTGCTGTTCTGCTGGGGAA
GACACCATCTACAATGGAGAATGATTCACTAATCTGGATCCGTCTCAGGCTCCTTCTCTGGCCCAGCCTCTGGT
GTTTCAGTAATTCGAAGCAGACTGCCATATCACAGCCTGCTTCAGGGAACACATTTTCTCATCACAGTATGGTGAG
CATGTTAGGGAAAGGATTGGTGATGTCGGTGAAGCTAAAGCGGCAGTACTACAGGCTCCAGTTCTTGGAGCA
ATTCAAGACTGCCCAAGCCCTGGCTCAGTTGGCAGCTCAGCATTCTCAGTCTGGAAGCACCACCACCTCCTCTTG
GGACATGGGCTCGACGACACAATCCCCATCACTGGTGCAGTATGATTGAAGAACCCAAGTGATTACAGCAGTGCA
CAGCCCCTTTACAAAGCGCCAGGCTTTTACCCCATCTTCAACCATGATGGAGGTGTTCTTTCAGGAGAAGTCACC
TGCAGTGGCTACCTCCACAGCTGCACCTCCACCTCCGTCTTCTCCTCTGCCAAGCAAATCCACATCGGCTCCACA
GATGTCGCTGGATCTTCAGACAACCAGTCTCTAGCCCTCAGCCGGCTCAGCAGAACTGAAACAGCAGAAGAA
AAAAGCCTCCTTGACTTCTAAGATTCTGCTCTGGCTGTGGAGATGCCTGGCTCAGCAGATATGCTCAGGGCTAAA
CCTGCAGTTTGGGGCATTGCAGTTTGGGTGAGAGCCTGTCTTTCTGATTATGAGTCCACCCCAACCCAGAGCGC
CTCTTCAAGCCAGGCTCCAAGTAGCCTGTATACCAGCAGCGCCAGTGAATCATCCTCTACAATTTCTATCTAACCA
GAGTCAGGAGTCTGGTTATCAGAGCGGCCCAATTCAGTCGACAACCTATACCTCCCAAAATAATGCTCAGGGCCC
TCTTTATGAACAGAGATCCACACAGACTCGGCGGTACCCAGCTCCATCTCTTCATCACCCCAAAAGGACCTGAC
TCAGGCAAAGAATGGCTTCAGTTCTGTGCAGGCCACGCAGTTACAGACCACACAATCTGTTGAAGGTGCTACAGG
CTCTGCAGTGAAATCTGATTACCTTCCACTTCTAGCATCCCCCTCTCAATGAAACGGTATCTGCAGCTTCCTT
ACTGACGACAACCAATCAGCATTCACTCCTCTGGGTGGCTTGAGCCACAGTGAGGAGATTCCAAATACTACCAC
CACACAACACAGCAGCAGTATCTACGCAGCAGAATACCCTTTTCATCATCAACATCTTCTGGGCGCACTTCGAC
ATCCACTCTTTGCACACAAGTGTGGAGAGTGAGGCGAATCTCCATTCTTCTCCAGCACTTTTTCCACCACATC
CAGCACAGTCTCTGCACCTCCCCAGTGGTCAGTGTCTCCTCCAGTCTCAATAGTGGCAGTAGCCTGGGCCTCAG
CCTAGGCAGCAACTCCACTGTCACAGCCTCGACTCGAAGCTCAGTTGCTACGACTTCAGGAAAAGCTCCTCCCAA
CCTCCCTCCTGGGGTCCCGCGTGTGTTGCCTAATCCGTATATTATGGCTCCAGGGCTGTTACATGCCTACCCGCC
ACAAGTATATGGTTATGATGACTTGCAGATGCTTCAGACAAGATTTCCATTGGATTACTACAGCATCCCATTTC
CACACCCACTACTCCGCTGACTGGGAGGGATGGTAGCCTGGCCAGCAACCCTTATTCTGGTGACCTCACAAAGTT
CGGCCGTGGGGATGCCTCCTCCCCAGCCCCGGCCACAACCTTGGCCCAACCCCAACAGAACCAGACGCAGACTCA
CCATACCACGCAGCAGACATTCCTGAACCCGGCGCTGCCTCCTGGCTACAGTTACACCAGCCTGCCATACTATAC
AGGGGTCCCGGCCCTCCCCAGCACCTTCCAGTATGGGCTGCTGTGTTCCCTGTGGCTCCTACCTCTTCCAAGCA
GCATGGTGTGAATGTCAGTGTGAATGCATCGGCCACCCCTTTTCCAACAGCCGAGTGGATATGGGTCTCATGGATA
CAACACTGGAAGAAAATATCCACCCCTTACAAGCATTCTTGACGGCTGAGAGCTAAATTTGGCCCAAGGCTGGG
GGCTGTGTTTTGTGTGTGTGTATAAATTTGCACTGAAGTCTTGTTTTCAGAAACCAGACCACTGAGGAGAGCCTGC
TGAGCTGAGGCCATGGCCTGCGTGGCTTGGGGAATGAGTTGGTGGATACCTTCTGGGCTTTTGAAGTTGCCCT
CCCCCATTTCCCTCTCCCCATGTGTCTGACCCTGTCTTACCCATTTCAAGTTCAAGCGGTGCAGCACCTTCGAA
GCATCAATGCACACACCTGCTGTGCTTTTGATTCTGGAAGGCATGTAGTTTCAACTTGTAACAAAAATATTTG
TAGTCTTCAATAAACTGTGGTATTTCTTTAGCTAAC

WO 2004/030615

PCT/US2003/028547

478/6881

FIGURE 447

MMTSVGTNRARGNWEQPQNQNTQHKQRPQATAEQIRLAQMISDHNDADFEKVKQLIDITGKNQDECVIALHDC
NGDVNRAINVLLEGNDPETHSWEMVGKKKGVSQKDGQTESNEEGKENRDRDRDYSRRRGPPRRGRGASRGREF
RGQENGLDGTKSGGPSGRGTERGRRGRGRGRGSGRRGGRFSAQGMGTFFNPADYAEPANTDDNYGNSSGNTWNNT
GHFEPDDGTSAWRTATEEWGTEDWNEDLSETKIFTASNVSSVPLPAENVITITAGQRIDLAVLLGKTPSTMENDSS
NLDPSQAPSLAQPLVFSNSKQTASQPASGNTFSHHSVMVSLGKGFGDVGEAKGGSTTGSQFLEQFKTAQALAL
AAQHSQSGSTTTSSWDMGTTQSPSLVQYDLKNPSSSAVHSPFTKRQAFTPSSTMMEVFLQEKSPAVATSTAAPP
PPSSPLPSKSTSAPOMSPGSSDNQSSSPQPAQQKLKQQKKKASLTSKIPALAVEMPGSADISGLNLQFGALQFGS
EPVLSDYESTPTTSASSSQAPSSLYTSTASESSSTISSNQSQESGYQSGPIQSTTYTSQNNAQGPLYEQRSTQTR
RYPSSISSSPQKDLTQAKNGFSSVQATQLQTTQSVEGATGSAVKSDSPSTSSIPPLNETVSAASLLTTTNQHSSS
LGGLSHSEEIPNTTTTQHSSSTLSTQONTLSSSTSSGRTSTSTLLHTSVESEANLHSSSSTFSTTSSTVSAPPPVV
SVSSSLNSGSSLGLSLGSNSTVTASTRSSVATTSGKAPPNLP PGVPPLLPNPYIMAPGLLHAYPPQVYGYDDLQ
LQTRFPLDYYSIPFPTPTTPTLTGRDGLASNPYSGDLTKFGRGDASSPAPATTLAQPQONQTQTHHTTQOTFLNP
ALPPGYSYTSLPYYTGVPGLPSTFQYGPVFPVAPTSSKQHG VNVSVNASATPFQQPSGYGSHGYNTGRKYPPPY
KHFWTAES

WO 2004/030615

PCT/US2003/028547

479/6881
FIGURE 448

CCTACAGAGGGGTCCATACCGTGTTGTTCTGGATTCCCGTTGTAACCTAAAGGGAAATTTTCACAATGTCAGAG
CCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGACAGCAGGAACCCACTTAGGTGGCACTA
ATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTACATCATAAAATCTGAAGAGGA
CCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCCATTGTTGCCATTGAAAACCCCTGCTGATGTCAGTGTTATATCCT
CCAGGAATACTGGCCAGAGGGCCATGCTGAAGTTTGTGCTGCCACTGGAGCCACTCCAATTGCTGGCCACTTCA
CTCCTGGAACCTTCACTAACCGGATCCAGGCAGCCTTCCGGGAGCCACAGCTTCCTGTGGTTACTGACCCAGGG
CTGACCACCAGCCTCTCACGGAGGTATCTTATGTTAACTTACCTACCATTGCGCTGTGTAACACAGATTCTCCTC
TGCGCTATGTGGACATTGCCATCCCATGCAACAATAAGGGAGCTCACTCAGTGGGTTGGATGTGGTGGATGCTGG
CTCAGGAAGTTCTGCGCATGCGTGGCACCATTCCCGTGAACACCCATGGGAGGTCATGCCTGATCTCTGCTTCT
ACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAAGAGGCAGTGACCAAGGAGGAATTTCAGG
GTGAATGGACTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGAAGGTCTGCAGG
TGCCCTCTGTGTCTATTTCAGTAGTTCCCTACTGAAGACTGGAGCGCTCAGCCTGCCACGGAAGACTGGTCTGCAG
CTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGAATGGTCTTAAAGCTGTTCTTGCATGGGCTCTTA
AGCAACATGGAAAAATGGTTGATGGAAAATAAATAAACATCAGTTTCT

WO 2004/030615

PCT/US2003/028547

480/6881
FIGURE 449

MSRALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAMLKFAAATGATPIAGHFTPGFTNRIQAAFREPQLPVVTDPRADHQPLTEVSYVNLPTIALCNT
DSPLRYVDIAIPCNNKGAHSGVGMWWMLAQEVLRMRGTISREHPWEVMPDLCFYRDPEEIEKEEQAAAAEEAVTKE
EFQGEWTAPAPEFTATQPEVADWSEGLQVPSVSIQSSLLKTGALS LPRKTGLQLPLLRPLNGVGATTEWS

WO 2004/030615

PCT/US2003/028547

481/6881
FIGURE 450A

CGAAATTGAACCGGAGCCATCTTGGGCCCCGGCGCGCAGACCCGCGGAGTTTCCCGTGCCGACGCCCCGGGGCCAC
TTCCAGTGCGGAGTAGCGGAGGCGTGGGGGCCCTCGAGGGGCTGGCGCGGGCCAGCGGTGCGGGCCAGGGTCGTGCC
GCCGGCGGGTCGGGCCGGGCAATGCCTCGCGGGCGCAATGAATCCGCGGCAGGGGTATTCCCTCAGCGGATACTA
CACCCATCCATTTCAAGGCTATGAGCACAGACAGCTCAGGTACCAGCAGCCTGGGCCAGGATCTTCCCCAGTAG
TTTCCTGCTTAAGCAAATAGAATTTCTCAAGGGGCAGCTCCCAGAAGCACCGGTGATTGGAAAGCAGACACCGTC
ACTGCCACCTTCCCTCCCAGGACTCCGGCCAAGGTTTCCAGTACTACTTGCCTCCAGTACCAGAGGCAGGCAAGT
GGACATCAGGGGTGTCCCCAGGGGCGTGCACTCAGAAAGTCAGGGGCTCCAGAGAGGGTTCCAGCATCCTTCACC
ACGTGGCAGGAGTCTGCCACAGAGAGGTGTTGATTGCCTTTCCTCACATTTCCAGGAAGTGAAGTATCTACCAAGA
TCAGGAACAAAGGATCTTAAAGTTCTGGAAGAGCTTGGGGAAGGGAAGGCCACCACAGCACATGATCTGTCTGG
GAACTTGGGACTCCGAAGAAAGAAATCAATCGAGTTTATACTCCCTGGCAAAGAAGGGCAAGCTACAGAAAGA
GGCAGGAACACCCCTTTGTGGAAAATCGCGGTCTCCACTCAGGCTTGGAAACCAGCACAGCGGAGTGGTAAGACC
AGACGGTCATAGCCAAGGAGCCCCAACTCAGACCCGAGTTTGGAAACCGGAAGACAGAACTCCACATCTGTCTC
AGAAGATCTTCTTGAGCCTTTTATGTCAGTCTCAGCTCAGGCTTGGAAACCAGCACAGCGGAGTGGTAAGACCAGA
CAGTCATAGCCAAGGATCCCCAACTCAGACCCAGGTTTGGAACTGAAGACAGCAACTCCACATCTGCCTTGGA
AGATCCTCTTGAGTTTTAGACATGGCCGAGATCAAGGAGAAAATCTGCGACTATCTCTTAATGTGTCTGACTC
CTCTGCCCTGAATTTGGCTAAAAATATTGGCCTTACCAAGGCCCGAGATATAAATGCTGTGCTAATTGACATGGA
AAGGCAGGGGGATGTCTATAGACAAGGGACAACCCCTCCCATATGGCATTGTGACAGACAAGAAGCGAGAGAGGAT
GCAAATCAAGAGAAATACGAACAGTGTCTTGAACCGCTCCAGCTGCAATCCCTGAGACCAAAAGAAACGCAGA
GTTCTCTACCTGTAATATACCCACATCAAATGCCTCAAAATAACATGGTAACCACAGAAAAAGTGGAGAATGGGCA
GGAACCTGTCTATAAAGTTAGAAAACAGGCAAGAGGCCAGACCAGAACCAGCAAGACTGAAACCACCTGTTTATTA
CAATGGCCCCCTCAAAGCAGGGTATGTTGACTTTGAAAATGGCCAGTGGGCCACAGATGACATCCCAGATGACTT
GAATAGTATCCGCGCAGCACCAGGTGAGTTTCGAGCCATCATGGAGATGCCCTCCTTCTACAGTCATGGCTTGGC
ACGGTGTTCACCCCTACAAGAACTGACAGAGTGCCAGCTGAAGAACCCCATCAGCGGGCTGTTAGAATATGCCCA
GTTTCGCTAGTCAAACCTGTGAGTTCAACATGATAGAGCAGAGTGGACCACCCCATGAACCTCGATTTAAATTCCA
GGTTGTCTAATGGCCGAGAGTTTCCCCCAGCTGAAGCTGGAAGCAAGAAAGTGGCCAAGCAGGATGCAGCTAT
GAAAGCCATGACAATCTGTCTAGAGGAAGCCAAAGCCAAGGACAGTGGAAAATCAGAAAGTATCATCCCACTATT
CACAGAGAAAGAAATCAGAGAAGACTGCAGAGTCCCAGACCCCAACCCCTCAGCCACATCCTTCTTTCTGGGAA
GAGCCCCGTACCCACACTGCTTGAGTGTATGCACAAATGGGGAACCTCCTGCGAATTCCGTCTCCTGTCCAAAGA
AGGCCCTGCCCATGAACCCAGTTCCAATACTGTGTTGAGTGGGAGCCCAACTTTCCCCAGGCGACCAACTCCAT
CAGCAAGAAAGTGGCAAAGCAGATGGCCGCAGAGGAAGCCATGAAGGCCCTGCATGGGGAGGCGACCAACTCCAT
GGCTTCTGATAACCAGCCTGAAGGTATGATCTCAGAGTCACTTGATAACTTGAATCCATGATGCCCAACAAGGT
CAGGAAGATTGGCGAGCTCGTGAGATACTGAACACCAACCCCTGTGGGTGGCCTTTTGGAGTACGCCCGCTCCCA
TGGCTTTGCTGCTGAATTCAGTTGGTTCGACCAGTCCGGACCTCCTCAGGAGCCCAAGTTTCGTTTACCAAGCAAA
AGTTGGGGGTCTGCTGGTTCCAGCCGTCTGCGCACACAGCAAGAAGCAAGGCAAGCAGGAAGCAGCAGATGCGGC
TCTCCGTGTCTTGATTGGGGAGAACGAGAAGGCAGAACGCATGGGTTTACAGAGGTAACCCCAAGTGACAGGGGC
CAGTCTCAGAAGAACTATGCTCCTCCTCTCAAGGTCCCCAGAAGCACAGCCAAAGACACTCCCTCTCACTGGCAG
CACCTTCCATGACCAGATAGCCATGCTGAGCCACCGGTGCTTCAACACTCTGACTAACAGCTTCCAGCCCTCCTT
GCTCGGCCGCAAGATTCTGGCCGCCATCATTATGAAAAAGACTCTGAGGACATGGGTGTCTGCTCAGCTTGGG
AACAGGGAATCGCTGTGTGAAAGGAGATTCTCTCAGCCTAAAAGGAGAAACTGTCAATGACTGCCATGCAGAAAT
AATCTCCCGGAGAGGCTTCATCAGGTTTCTCTACAGTGAAGTAAATGAAATACAACTCCAGACTGCGAAGGATAG
TATATTTGAACCTGCTAAGGGAGGAGAAAAGCTCCAAATAAAAAAGACTGTGTCAATCCATCTGTATATCAGCAC
TGCTCCGTGTGGAGATGGCGCCCTCTTTGACAAGTCTTGCAGCGACCGTGCTATGGAAAGCACAGAATCCCGCCA
CTACCTGTCTTCGAGAATCCCAACAAGGAAAGCTCCGCACCAAGGTGGAGAACGGAGAAGGCACAATCCCTGT
GGAATCCAGTGACATTGTGCCTACGTGGGATGGCATTGGGCTCGGGGAGAGACTCCGTACCATGTCTGTAGTGA
CAAAATCCTACGCTGGAACGTGCTGGGCCTGCAAGGGGCACTGTTGACCCACTTCTGACGCCATTTATCTCAA
ATCTGTACATTGGGTTACCTTTTCAGCCAAGGGCATCTGACCCGTGCTATTTGCTGTCTGTGACAAGAGATGG
GAGTGCATTTGAGGATGGACTACGACATCCCTTTATTGTCAACCAACCCCAAGGTTGGCAGAGTCAGCATATATGA
TTCCAAAAGGCAATCCGGGAAGACTAAGGAGACAAGCGTCAACTGGTGTCTGGCTGATGGCTATGACCTGGAGAT

WO 2004/030615

PCT/US2003/028547

482/6881
FIGURE 450B

CCTGGACGGTACCAGAGGCACTGTGGATGGGCCACGGAATGAATTGTCCCGGGTCTCCAAAAAGAACATTTTTCT
TCTATTTAAGAAGCTCTGCTCCTTCCGTTACCGCAGGGATCTACTGAGACTCTCCTATGGTGAGGCCAAGAAAGC
TGCCCGTGACTACGAGACGGCCAAGAAGTACTTCAAAAAAGGCCTGAAGGATATGGGCTATGGGAAGTGGATTAG
CAAACCCAGGAGGAAAAAGAACTTTATCTCTGCCAGTATAGTATGCTCCAGTGACAGATGGATTAGGGTGTGT
CATACTAGGGTGTGAGAGAGGTAGGTCGTAGCATTCTCATCATAGGTGAGGGGATTTTTTTTTCTCTTTTTT
TTTCTTTTTAAGCCATAATTGGTGATCTGAAACTTTGGGTTCCCATTTATCCTGCTTTCTTTGGGATTGCTAG
GCAAGGTCTGGCCAGGCCCTTTTTTCCCCCAAGTGAAGAGGCAGAAACCTAAGAAGTTATCTTTTCTTTCTA
CCCAAAGCATAACATAGTCACTGAGCACCTGCGGTCCATTTCTCTTAAAAGTTTTGTTTTGATTTGTTTTCCATTT
CCTTTCCCTTTGTGTTTGCTACACTGACCTCTTGCGGTCTTGATTAGGTTTCAGTCAACTCTGGATCATGTCAGG
GACTGATAATTTCAATTTGTGGATTACGCAGACCCCTCTACTTTCCCTCTTTCCCTTCTGAGATTCTTTCTTTGTG
ATCTGAATGTCTCCTTTTCCCCCTCAGAGGGCAAGAGGTGAACATAAAGGATTTGGTGAAACATTTGTAAGGGT
AGGAGTTGAAAAGTGCAGTTCCCAAGTGCCACGGAAGTGTGATTGGAGCCTGCAGATAATGCCAGCCATCCTCCC
ATCCTGCACTTTAGCCAGCTGCAGGGCGGGCAAGGCAAGGAAAGCTGCTTCCCTGGAAGTGTATCACTTTCTCCG
GCAGCTGGGAAGTCTAGAACCAGCCAGACTGGGTAAAGGGAGCTGCTCAAGCAATAGCAGAGGTTTACCCGGCA
GGATGACACAGACCACTTTCCAGGGAGCACGGGCATGCCTTGGAATATTGCCAAGCTTCCAGCTGCCTCTTCTCC
TAAAGCATTCTAGGAATATTTTCCCCGCAATGCTGGGCGTACACCCTAGCCAACGGGACAAATCCTAGAGGGT
ATAAAATCATCTCTGCTCAGATAATCATGACTTAGCAAGAATAAGGGCAAAAATCCTGTTGGCTTAACGTCAC
GTTCCACCCGGTGTAATATCTCTCATGACAGTGACACCAAGGGAAGTTGACTAAGTCACATGTAAATTAGGAGTG
TTTTAAAGAATGCCATAGATGTTGATTCTTAAGTGTACAGATAACCTGTAATTGAGCAGATTTAAAATTCAGGC
ATACTTTTCCATTTATCCAAGTGCTTTCAATTTTCCAGATGGCTTCAGAAGTAGGCTCGTGGGCAGGGCGCAGAC
CTGATCTTTATAGGGTTGACATAGAAAGCAGTAGTTGTGGGTGAAAGGGCAGGTTGTCTTCAAACCTCTGTGAGGT
AGAATCCTTTGTCTATACCTCCATGAACATTGACTCGTGTGTTTCAGAGCCTTTGGCCTCTCTGTGGAGTCTGGCT
CTCTGGCTCCTGTGCATTCTTTGAATAGTCACTCGTAAAACTGTGAGTCTTGAAACTGTTTCTTTTACTCATG
TTGAAGGGACTTTGTGGCTTTTAGAGTGTGGTTCATGACTCCAAGAGCAGAGCAGGGAAGAGCCCAAGCATAGA
CTTGGTGCCGTGGTGATGGCTGCAGTCCAGTTTTGTGATGCTGCTTTTACGTGTCCCTCGATAACAGTCAGCTAG
ACACACTCAGGAGGACTACTGAGGCTCTGCGACCTTCAGGAGCTGAGCCTGCCTCTCTCCTTTAGATGACAGACC
TTCATCTGGGAACGTGCTGAGCCAGCACCCCTCAGATGATTTCCCTCCAACTGCTGACTAGGTCATCCTCTGTCT
GGTAGAGACATTACATCTTTGCTTTTATTCTATGCTCTCTGTACTTTTGACCAAAAATTGACCAAGTAAGAAA
ATGCAAGTTCTAAAAATAGACTAAGGATGCCTTTGCAGAACACCAAGCATCCCAAGGAAGTGGTAGGGAAGTGG
CGCCTGTCTCCTGGAGTGGAAGAGGCCTGCTCCCTGGCTCTGGGTCTGCTGGGGGCACAGTAAATCAGTCTTGGC
ACCCACATCCAGGGCAGAGAGGTCTGTGGTTCTCAGCATCAGAAGGCAGCGCAGCCCTCTCCTCTTCAGGCTAC
AGGGTGTGTCACCTGCTGAGTCTCAGGTTGTTTGGCCTCTCTGGTCCATCTTGGGCATTAGGTTCTCCAGCAGAG
CTCTGGCCAGCTGCCTCTTCTTAAGTGGGAACACAGGCTCTCACAAGATCAGAACCCCACTCACCCCAAGAT
CTTATCTAGCAAGCCTGTAGTATTTCAGTTTCTGTTGTAGGAAGAGAGCGAGGCATCCCTGAATTCCACGCATCTG
CTGGAACAGAGCCGTGTGATATCGCATCCCTGCGCCCCATGCCCTCTGAGTCACACAGGACAGAGGAGGCA
GAGCTTCTGCCACTGTTATCTTCACTTTCTTTGTCCAGTCTTTTGTGTTTTAATAAGCAGTGACCCTCCCTACTC
TTCTTTTTAATGATTTTTGTAGTTGATTTGTCTGAAGTGTGGTACTGTGATTCTTGAATAATCACTTGTA
AATTGTGAGTGTGTAAGCTGTTTCTTTTACTCACATTGAAGGGACTTCGTTGGTTTTTTGGAGTCTTGGTTGTG
ACTCCAAGAGCAGAGTGAGGAAGACCCCAAGCATAGACTCGGGTACTGTGATGATGGCTGCAGTCCAGTTTTAT
GATTCTGCTTTTATGTGTCCCTTGATAACAGTGACTTAACAATATACATTCTCATAAATAAAAAAACAAGA
ATCTGAATTCTT

WO 2004/030615

PCT/US2003/028547

483/6881
FIGURE 451

GAGCCAGCGAGGAGTGAAGCTGAGCCTGGCCTCACACGCTCCTAGAGGACCACCTCCTGAGAGAGTTCTTTACCC
CCCTCTTCTTTCTCCAAGCTCCCCTCCTGCTCTCCCTCCCTGCCCAATACAATGCATTCTTGAGTGGCAGCGTCT
GGACTCCAGGCAGCCCCAGAGAACC GAAGCAAGCCAAAGAGAGGACTGGAGCCAAGATACTGGTGGGGGAGATTG
GATGCCTGGCTTTCTTTGAGGACATCTTTGGAGCGAGGGTGGCTTTGGGGTGGGGGCTTGCTGTCAGGGAATAC
AGCCAGGCCCCAAGATGGACACTTCTGGGCACCTTCATGACTCGGGGGTGGGGGACTTGATGAAGACCCCAAGT
GCCCCGTGTCATCCTCTGGGGATGAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCCACCACCGCCAG
CGCCACCAGCAGCCCCCAGCAGCCCCTGGGACCCTCGCTGCAGCCTCAGCCTCCGCAGCTTCAGCAGCAGCAGC
AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCACCGCATCCCCGTGTCTCAGCTCGCCCAACTCCAGAGCCAGCCCCG
TCCACCCTGGCCTGCTGCACTCCTCTCCCACCGCTTTCAGGGCCCCCCCCCTTCGTCCAATCCACCGCCATCCTCC
ACCTTTCCTCCAGGCAAGGCAGCCAGCTCAATCTCAATGACCACCTTGCTTGGCCACTCTCCAAGTTCACAGCTA
CAAGTGGGCCTGGCGGAGGCAGCCGGCACCGACAGGCCAGCCCCCTGGTGCACCGGCGGGACAGCAACCCCTTCA
CGGAGATCGCCATGAGCTCCTGCAAGTATAGCGGTGGGGTCAAGAGCCCCCTCAGCCGCTCAGCGCCTCCCGGA
GGAACCTCATCGAGGCCGAGACTGAGGGCCAACCCCTCCAGCTTTTCAGCCCTAGCAACCCCCCGGAGATCGTCA
TCTCCTCCCGGGAGGACAACCATGCCCACCAGACCCTGCTCCATCACCCTAATGCCACCCACAACCACCAGCATG
CCGGCACCAACCGCCAGCAGCACCACCTTCCCCAAAGCCAACAAGCGGAAAAACCAAAACATTGGCTATAAGCTGG
GACACAGGAGGGCCCTGTTTGAAGAGAAAGCGACTGAGTGACTATGCTCTGATTTTGGGATGTTTGAATTG
TTGTTATGGTGATAGAGACCGAGCTCTCTTGGGGTTTGTACTCAAAGGACTCCATGTTTTCGTTGGCCCTGAAAT
GCCTTATCAGTCTGTCCACCATCATCTTTTGGGCTTGATCATCGCCTACCACACAGTGAAGTCCAGCTCTTCG
TGATCGACAATGGCGCGGATGACTGGCGGATAGCCATGACCTACGAGCGCATCCTGTACATCAGCCTGGAGATGC
TGGTGTGCGCCATCCACCCCATTCCTGGCGAGTACAAGTTCTTCTGGACGGCAGCCTGGCCTTCTCTACACAC
CCTCCCGGGCGGAGGCCGATGTGGACATCATCTGTCTATCCCCATGTTCTTGGCCTGTACCTGATCGCCCCGAG
TCATGCTGCTGCACAGCAAGCTCTTACCGATGCCTCGTCCCGCAGCATCGGGGCCCTCAACAAGATCAACTCA
ACACCCGCTTTGTCTATGAAGACGCTCATGACCATCTGCCCTGGCACTGTGCTGCTCGTGTTCAGCATCTCTGT
GGATCATTGCTGCCTGGACCGTCCGTGTCTGTGAAAGGTACCATGACCAGCAGGACGTAACATAGTAACCTTCTGG
GTGCCATGTGGCTCATCTCCATCACATTCCCTTTCCATTGGTTATGGGGACATGGTGGCCCGTGGTGGCCCGAAAGC
AAGGTGTCTGTCTCCTCACTGGCATCATGGGTGCAGGCTGCACTGCCCTTGTGGTGGCCGTGGTGGCCCGAAAGC
TGGAACCTACCAAAGCGGAGAAGCACGTTTCACTAATTCATGATGGACACTCAGCTACCAAGCGGATCAAGAATG
CTGCAGCCAATGTCTTCGGGAAACATGGTTAATCTATAAACACACAAAGCTGCTAAAGAAGATTGACCATGCCA
AAGTGAGGAAACACCAGAGGAAGTTCCCTCCAAGCTATCCACGATTGAGGAGCGTCAAGATGGAACAGAGGAAGC
TGAGTGACCAAGCCAACACTCTGGTGGACCTTTCCAAGATGCAGAATGTCATGTATGACTTAATCACAGAACTCA
ATGACCGGAGCGAAGACCTGGAGAAGCAGATTGGCAGCCTGGAGTCAAGCTGGAGCATCTCACCAGCCAGCTTCA
ACTCCCTGCCGCTGCTCATCGCCGACACCCTGCGCCAGCAGCAGCAGCAGCTCCTGTCTGCCATCATCGAGGCC
GGGGTGTGAGCGTGGCAGTGGGCACCAACCCACACCCCAATCTCCGATAGCCCCATTGGGGTCAGCTCCACCTCCT
TCCCGACCCCGTACACAAGTTCAAGCAGTTGCTAAATAAATCTCCCCACTCCAGAAGCATTACCCATAGGTCTTA
AGATGCAAATCAACTCTCTCCTGGTGCCTTTGCCATCAAGAAACATTAGACCAGGGAACGGAAAGAAGAGAGAC
CGAGCTAATTAATAACTCATGTTTATTAGCGTGCTTGGTCCGACATGCCTTGAAACCAGAAATCTAATCTCTG
TTAGGTGCCTCTACTTGGGAGCGGGAAGAGGAGATGACAGGAAGCGACGCCTCTGGCAGGGCCCTTGCTGCAGA
GTTGGTGGAGAACAGAAATCCACGCTCAATCTCAGGTCTTACGCGGGGGGTGGGGGTGAGATGCACTGAAGTAG
CCAACAGCGAAGCCAGTCCAGAAGAGGGGTCCGCTGGGAGGGAGGGTTGTGTAGGCTTGGGGGATGGGCTCTTC
GCCATGGGGGTCTTTGAACACACCTCTCTCCTTTTCTTTGTCTACGGAAGCCTCTGGGTGACAAAAGTAAAGA
GAGCTGCCCAACTTGCCAAAACAGATATACTCGAATCAGACTGAAAAAAA

WO 2004/030615

PCT/US2003/028547

484/6881
FIGURE 452

GAAGGTTCTGGGCGGGGCTGGACTGTTCTAAGTGAGTTTCGGGTGGGGGAGCTTCACGAGGGGAGGCTGCTCTGTG
AAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCCTTTTCTCCCATATCTGTTTGGACATGAGCTGAGGGCACGGT
CGCGGGCGGTTCAGCCCTGTTTCGCAGCTACGGCGAGGAGGGGCGCGATTGTTTCCTTGTTGCCGCTCCGCTTAGTGG
CCGCGTCCATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGC
GGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTTCAGCGGCAAGAGGAAATCCGGGAAGGAC
TTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAG
GAACAGTATGCTCAGGAGCATGGCTTGAACCTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTTCGG
AAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGC
ATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGG
GCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTACGCCAGGG
GTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACCTTCGGGGACTTTGACTGGGTTCATCGAGAACCATGGAGTT
GAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGG
AGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCGATCCTGGCCGAGG
TGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGAC
CTCATTCTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTG
TGCTTGAAGGCGAAACCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGATCCTGACTGGA
TGTTCTCAGCCCCCTTGTCTGGGCAAGAACCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGAGCACAC
TCTCAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCTCGGG

WO 2004/030615

PCT/US2003/028547

485/6881
FIGURE 453

MAPLGGAPRLVLLFSGKRKSGKDFVTEALQSRLGADVCAVLRLSGPLKEQYAEHGLNFQRLLDSTYKEAFRKD
MIRWGEEKRQADPGFFCRKIVEGISQPIWLVSDTRRVSDIQWFREAYGAVTQTVRVVALEQSRQQRGWVFTPGVD
DAESECGLDNFGDFDWVIENHGVEQRLEEQLLENLIEFIRSRL

WO 2004/030615

PCT/US2003/028547

486/6881
FIGURE 454

ATGGGGCCTGAAACTGTCTGGGTCTGAGCTGGGGAGCGGAAGCCACTTGTCCCTCTCCCTCCCCAGGACTTCTGT
GACTCCTGGGCCACAGAGGTCCAACCAGGCTAAGGGCCTGGGGATACCCCCCTGCCTGGCCCCCTTGCCCAAAGTGA
GCAGGGGGGGCCAGGCTGGGCAGCAGCCCCCTTTTCACTCAACTATGGATCTCCTGCCCCCAAGCCCAAGTACA
ATCCACTCCGGAATGAGTCTCTGTATCGCTGGAGGAAGGGGCTTCTGGGTCCACCCCCCGGAGGAGCTGCCTT
CCCCATCAGCTTCATCCCTGGGGCCCATCCTGCCTCCTCTGCCTGGGGACGATAGTCCCACTACCCTGTGCTCCT
TCTTCCCCCGGATGAGCAACCTGAGGCTGGCCAACCCGGCTGGGGGGCGCCAGGGTCTAAGGGGGAGCCAGGAA
GGGCAGCTGATGATGGGGAGGGGATCGTAGGGGCAGCCATGCCAGACTCAGGCCCCCTACCCTCCTCCAGGACA
TGAACAAGCTGAGTGGAGGCGGCGGGCGCAGGACTCGGGTGGAGGGGGCCAGCTTGGGGGCGAGGAGTGGACCC
GCCACGGGAGCTTTGTCAATAAGCCACGCGGGGCTGGGTGCATCCCAACGACAAAGTCATGGGACCCGGGGTTT
CCTACTTGGTTCGGTACATGGGTGTGTGGAGGTCTCCAGTCAATGCGTGCCTTGGACTTCAACACCCGGACTC
AGGTCAACAGGGAGGCCATCAGTCTGGTGTGTGAGGCTGTGCCGGGTGCTAAGGGGGCGACAAGGAGGAGAAAGC
CCTGTAGCCGCCGCTCAGCTCTATCCTGGGGAGGAGTAACCTGAAATTTGCTGGAATGCCAATCACTCTCACCG
TCTCCACCAGCAGCCTCAACCTCATGGCCGACAGCTGCAACAGATCATCGCCAACCACCACATGCAATCTATCT
CATTTCATCCGGCGGGGATCCGGACACAGCCGAGTATGTCGCCTATGTTGCCAAAGACCCTGTGAATCAGAGAG
CCTGCCACATTCTGGAGTGTCCCGAAGGGCTTGCCAGGATGTCATCAGCACCATTGGCCAGGCCTTCGAGTTGC
GCTTCAAACAATACCTCAGGAACCCACCCAACTGGTCACCCCTCATGACAGGATGGCTGGCTTTGATGGCTCAG
CATGGGATGAGGAGGAGGAAGAGCCACCTGACCATCAGTACTATAATGACTTCCCGGGGAAGGAACCCCTTGG
GGGGGGTGGTAGACATGAGGCTTCGGGAAGGAGCCGCTCCAGGGGCTGCTCGACCCACTGCACCCAATGCCCAGA
CCCCCAGCCACTTGGGAGCTACATTGCCTGTAGGACAGCCTGTTGGGGGAGATCCAGAAGTCCGCAAACAGATGC
CACCTCCACCACCCTGTCCAGGCAGAGAGCTTTTGATGATCCCTCCTATGTCAACGTCCAGAACCTAGACAAGG
CCCGGCAAGCAGTGGGTGGTGTGGGCCCCCCAATCCTGCTATCAATGGCAGTGCACCCCGGGACCTGTTTGACA
TGAAGCCCTTCGAAGATGCTCTTCGCGTGCCTCCACCTCCCGAGTCGGTGTCCATGGCTGAGCAGCTCCGAGGGG
AGCCCTGGTTCATGGGAAGCTGAGCCGGCGGGAGGCTGAGGCACTGTGCGAGTCAATGGGGACTTCCTGGTAC
GGGAGAGCACGACCACACCTGGCCAGTATGTGCTCACTGGCTTGCAGAGTGGGCAGCCTAAGCATTGTACTTGG
TGGACCCTGAGGGTGTGGTTCGGACTAAGGATCACCCTTTGAAAGTGTGAGTCACTCACCTTATCAGCTACCACATGG
ACAATCACTTGGCCATCATCTCTGCGGGCAGCGAACTGTGTCTACAGCAACCTGTGGAGCGGAACTGTGATCTG
CCCTAGCGCTCTCTTCCAGAAGATGCCCTCCAATCCTTTCCACCCTATTCCTTAACCTCTCGGGACCTCGTTTGGG
AGTGTCTGTGGGCTTGGCCTTGTGTGAGAGTGGGAGTACGACTCTGGGTTTCATATCCAGCTGAGTGAG
AGGGTTTGAGTCAAAAGCCTGGGTGAGAATCCTGCCTCTCCCCAAACATTAATCACCAAAGTATTAATGTACAGA
GTGGCCCCCTCACCTGGGCCTTTCTGTGCCAACCTGATGCCCTTCCCCAAGAAGGTGAGTGCTTGTATGGAAA
ATGTCTGTGGTGACAGGCCAGTGGAACAGTCAACCTTCTGGGCAAGGGGGAACAAATCACACCTCTGGGCTTC
AGGGTATCCAGACCCCTCTCAACACCCGCCCCCCCATGTTTAACTTTGTGCCTTTGACCATCTCTTAGGTCT
AATGATATTTTATGCAAAACAGTTCTTGACCCCTGAATTCAATGACAGGGATGCCAACACCTTCTTGGCTTCTGG
GACCTGTGTTCTTGTGAGCACCCTCTCCGGTTTGGGTGGGATAACAGAGGCAGGAGTGGCAGCTGTCCCCCTCT
CCCTGGGGATATGCAACCCTTAGAGATTGCCCCAGAGCCCCACTCCCGGCCAGGCGGGAGATGGACCCCTCCCTT
GCTCAGTGCCTCCTGGCCGGGGCCCCCTCACCCCAAGGGGTCTGTATATACATTTTCATAAGGCCTGCCCTCCCATG
TTGCATGCCTATGTACTCTACGCCAAAGTGACGCCCTTCTCCTGAAGCCTCTGCCCTGCCTCCCTTTCTGGGAG
GGCGGGGTGGGGGTGACTGAATTTGGGCCTCTTGTACAGTTAACTCTCCAGGTGGATTTTGTGGAGGTGAGAAA
AGGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCCTGTAGAGTTGGAAGTGCATTCTTTTAAAG
TTTTATATGCATATATTTTAGGGCTGTAGACTTACTTTTCTATTTTCTTTTCCATTGCTTATTCTTGAGCACAAA
ATGATAATCAATTATTACATTTTATACATCACCTTTTGTACTTTTCCAAGCCCTTTTACAGCTCTTGGCATTTTCC
TCGCCTAGGCCTGTGAGGTAACCTGGGATCGCACCTTTTATACCAGAGACCTGAGGCAGATGAAATTTATTTCCAT
CTAGGACTAGAAAACTTGGGTCTCTTACCGCGAGACTGAGAGGCAGAAGTCAGCCCGAATGCCTGTGAGTTTCA
TGGAGGGGAAACGCAAAACCTGCAGTTCTGAGTACCTTCTACAGGCCCGGCCAGCCTAGGCCCGGGGTGGCCA
CACCACAGCAAGCCGGCCCCCCTCTTTTGGCCTTGTGGATAAGGGAGAGTTGACCGTTTTCATCTGGCCTCCT
TTTGCTGTTTGATGTTTCCACGGGTCTCACTTATACCAAGGGGAAACTCTTCATTAAAGTCCGTATTTCTTCT

WO 2004/030615

PCT/US2003/028547

487/6881
FIGURE 455

GAAAGAGCCGGTGAAGGGGCAGAACAGGÇAGGTTCCCTCGACCCAGGACCCCCCTGTTCCCAGGCTATGGCCCCCA
GTGCCCTGTAGACCTGGCAGGCCCCCGTGCTTGCGACCCCTATTTGGGGGTCTGGGTGGCTACTGGAGGGCCTT
GCAGAGGGGCAGAGAAGGCAGGACCATGACATCTAGGGCCTCTGAACTTTCTCCGGGGCGCAGCGTGACGGCTGG
CATCATCATTGTTGGAGATGAGATCCTTAAGTTGGAAACAACAAATGGCTTTTGAGTCCAAGAGTGATGCAATCA
CAGTGACGCATTAAACGGTTACTCCGGAGACATCAGAGCACTGTGGCTGGAGGCTGGGAGCCTGGCCAGGAAGC
TGTCGCCATTGTCCAGGTGAAAGGTGCTAAGGACCTGCTTGGTGGCAGTGGGGACAGAAAGAAGAAAGCAGGCCA
GGCGTGGTGGCTCACACCTATAATTCCAGCACTTTGGGAGGCTGAGGCAGGAGGATCACTTGAGACCAGGAATTC
AACACCAGCCTGGGCAACATGGCAAGACCCCATTTCTACAAAAAAATTTAAATGAGCTGAATGTGGTGGCAGC
CGCCTGTAGTCCCAGCTACTCGGAAGGCTGGGGTGGCCCTTGAAGCCAGGAGGTTGAGGCTGCAGTGAACCTGTGA
CTGAGCCACTATACTCCAGCCTGGGTGACAGAGACCCAGCTTTAAACCAAACAAATGGATTTTCCCACTCTTGT
GTCCAGTCCAGGCCCCCTCAGCAGCCTGAGGTGGTGTCTTCAAAGAGCAGAGCACTGCATCATCAGGTGGATGCA
GCCATCATCTTCAACCCCTCCCTTCATCCCTACAGTACTGATGGCCTCATCTTCCCTTCAACCCCCAGGGACA
CACTCAGGACACCAACACCTTCTTTCTGTGCCGGACACTGCGCTCCCTAGGGGTCCAGGTTTGCCGAGTCTCAGT
TGTAACCTGATGAGGTAGCCACCATTGCAGCTGAGGTCACTTCTTTCTCCAACCGCTTACCCATGTCTCTACAGC
AGGGGGCATCGGCCCCACTCATGATGATGTGACCTTTGAGGCAGTGGCACAGGCCTTTGGAGATGAGCTGAAGCC
ACACCCCAAGTTGGAAGCAGCCACCAAGCCCTAGGAGGGGAAGGCTGGGAGAAGCTATCATTGGTGGCCTCCTC
TGCCCGCTGCATTATGGCACAGATCCTTGCACTGGTCAACCTTTAGATTCCCTCTGGTCTCCGTCCGAAACGT
CTACCTCTTCCCAGGCATTCCAGAGCTGCTGCGGCGGGTGTGGAGGGGATGAAGGGACTATTCCAAAACCCAGC
TGTTCAAGTTCCACTCAAAGGAGCTATATGTGGCTGCTGATGAAGCCTCCATCGCCCCCATTCTGGCTGAGGCCCA
GGCCCACTTTGGACGTAGGCTTGGCCTGGGTTCCTACCCTGACTGGGGCAGCAACTACTATCAGGTGAAGCTGAC
TCTAGACTCAGAGGAAGAAGGACCCCTGGAGGAATGCTTGGCCTACCTGACTGCCCCGTTTGCCCCAGGGATCGCT
GGTCCCCACATGCCCAACGCTGTGGAGCAGGCCAGTGAGGCTGTATACAACTCGCTGAATCAGGTAGGGACCT
TATGGAGGAGGGGCATTATGCCCAAAGCCATTGGTGGCACCCAGATCTCAGTAATGCAGGGGCTGTTGGGTGCT
TCCTGCAAAATCCCTGAGAGGGCAGAAGATAGCTTCTGTTAATTCATTATTCTTCCAATAAATGTTGATTGAGTAC
CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

488/6881
FIGURE 456

MQPSSSTPPLHPYSTDGLIFPFNPQGHTQDTNTFFLCRTLRLSLGVQVCRVSVVPDEVATIAAEVTSFSNRFTVL
TAGGIGPTHDDVTFEAVAQAFGDELKPHPKLEAATKALGGEGWEKLSLVPSSARLHYGTDPCGTGQPFRLVSVR
NVYLFPGIPELLRRVLEGMKGLFQNPVQFHSKELYVADEASIAPILAEQAQAHFGRRGLGSDWGSNYYQVK
LTLDSEEEGPLEECLAYLTARLPQGS LVPYMPNAVEQASEAVYKLAESGRDLMEEGHYAQSHWWHPRSQ

WO 2004/030615

PCT/US2003/028547

489/6881
FIGURE 457

CGCTGCCATGCGGCTGGCGCTGCTCTGGGCCCTGGGGCTCCTGGGCGCGGGCAGCCCTCTGCCTTCCTGGCCGCT
CCCAAATATAGGTGGCACTGAGGAGCAGCAGGCAGAGTCAGAGAAGGCCCGAGGGAGCCCTTGAGCCCCAGGT
CCTTCAGGACGATCTCCCAATTAGCCTCAAAAAGGTGCTTCAGACCAGTCTGCCTGAGCCCCTGAGGATCAAGTT
GGAGCTGGACGGTGACAGTCATATCCTGGAGCTGCTACAGAATAGGGAGTTGGTCCCAGGCCGCCAACCCCTGGT
GTGGTACCAGCCCCGATGGCACTCGGGTGGTCAGTGAGGGACACACTTTGGAGAAGTCTGCTACCAGGGAAGAGT
GCGGGGATATGCAGGCTCCTGGGTGTCCATCTGCACCTGCTCTGGGCTCAGAGGCTTGGTGGTCTGACCCCA
GAGAAGCTATACCCTGGAGCAGGGGCTGGGGACCTTCAGGGTCTCCATTATTTGCGGAATCCAAGATCTCCA
CCTGCCAGGCCACACCTGTGCCCTGAGCTGGCGGGAATCTGTACACACTCAGACGCCACCCAGAGCACCCCTGGG
ACAGCGCCACATTGCGCGGAGGCGGGATGTGGTAACAGAGACCAAGACTGTGGAGTTGGTGATTGTGGCTGATCA
CTCGGAGGCCCAGAAATACCGGGACTTCCAGCACCTGCTAAACCGCACACTGGAAGTGGCCCTCTTGCTGGACAC
ATTCTTCCGGCCCCCTGAATGTACGAGTGGCACTAGTGGGCCTGGAGGCCTGGACCCAGCGTGACCTGGTGGAGAT
CAGCCCCAACCCAGCTGTCAACCTCGAAAACCTTCTCCACTGGCGCAGGGCACATTGCTGCCTCGATTGCCCA
TGACAGTGCCCACTGGTACTTCACTCTCTGGGCCTACGGTGGGCATGGCCATTGAGAACTCCATCTG
TTCTCCTGACTTCTCAGGAGGTGTGAACATGGACCACTCCACAGCATCCTGGGAGTCGCTCCTCCATAGCCCA
TGAGTTGGGGCCACAGCCTGGGCCTGGACCATGATTTGCCTGGGAATAGCTGCCCTGTCCAGGTCCAGCCCCAGC
CAAGACCTGCATCATGGAGGCCTCCACAGACTTCTACCAGGCCTGAACCTCAGCAACTGCAGCCGACGGGCCCT
GGAGAAAGCCCTCCTGGATGGAATGGGCAGCTGCCTCTTCGAACGGCTGCCTAGCCTACCCCTATGGCTGCTTT
CTGCGGAAATATGTTTGTGGAGCCGGGCGAGCAGTGTGACTGTGGCTTCTGGATGACTGCGTCGATCCCTGCTG
TGATTCTTTGACCTGCCAGCTGAGGCCAGGTGCACAGTGTGCATCTGACGGACCCTGTTGTCAAATTGCCAGCT
GCGCCCGTCTGGCTGGCAGTGTGCTCTACCAGAGGGGATTGTGACTTGCCTGAATCTGCCAGGAGACAGCTC
CCAGTGTCCCCCTGATGTGACCTAGGGGATGGCGAGCCCTGCGCTGGCGGGCAAGCTGTGTGCATGCACGGGCG
TTGTGCCTCCTATGCCAGCAGTGCCAGTCACTTTGGGGACCTGGAGCCCAGCCCGCTGCGCCACTTTGCCTCCA
GACAGCTAATACTCGGGGAAATGCTTTTGGGAGCTGTGGGCGCAACCCAGTGGCAGTTATGTGTCCTGCACCCC
TAGAGATGCCATTTGTGGGCAGCTCCAGTGCCAGACAGGTAGGACCCAGCCTCTGCTGGGCTCCATCCGGGATCT
ACTCTGGGAGACAATAGATGTGAATGGGACTGAGCTGAACCTGCAGCTGGGTGCACCTGGACCTGGGCAGTGATGT
GGCCCAGCCCCCTCCTGACTCTGCCTGGCACAGCCTGTGGCCCTGGCCTGGTGTGTATAGACCATCGATGCCAGCG
TGTGGATCTCCTGGGGGCACAGGAATGTGGAAGCAAATGCCATGGACATGGGGTCTGTGACAGCAACAGGCACTG
CTACTGTGAGGAGGGCTGGGCACCCCTGACTGCACCACTCAGCTCAAAGCAACCAGCTCCCTGACCACAGGGCT
GCTCCTCAGCCTCCTGGTCTTATTGGTCTTGGTGTGCTTGGTGGCGGCTACTGGTACCCTGCCCGCTGCACCA
GCGACTCTGCCAGCTCAAGGGACCCACCTGCCAGTACAGGGCAGCCCAATCTGGTCCCTCTGAACGGCCAGGACC
TCCGCAGAGGGCCCTGCTGGCACGAGGCACTAAGTCTCAGGGGCCAGCCAAGCCCCCAGGGGCTGGAATCCCGCCCCCTAGTGGT
ACCTTCCAGACCAAGCGCCACCGCCTCCGACAGTGTCTCGCTCTACCTCTGACCTCTCCGGAGGTCCCGCTGCCT
CCAAGCGGACTTAGGGCTTCAAGAGGCGGGCGTGCCCTCTGGAGTCCCCTACCATGACTGAAGGCGCCAGAGAC
TGGCGGTGTCTTAAGACTCCGGGCACCGCCACGCGCTGTCAAGCAACACTCTGCGGACCTGCCGGCGTAGTTGCA
GCGGGGGCTTGGGGAGGGGCTGGGGTTGGACGGGATTGAGGAAGGTCCGCACAGCCTGTCTCTGCTCAGTTGCA
ATAAACGTGACATCTTGGGAGCGTTAAAAA

WO 2004/030615

PCT/US2003/028547

490/6881
FIGURE 458

MRLALLWALGLLGAGSPLPSWPLPNIGGTEEQQAEESEKAPREPLEPQVLQDDLPISLKKVLQTSLEPELRIKLEL
DGD SHILELLQNRELVPGRPTLVWYQPDGTRVVSEGHTLENCYQGRVGRGYAGSWVSICTCSGLRGLVVLTPERS
YTLEQGPDLQGPPIISRIQDLHLPGHTCALSWRESVHTQTPPEHPLGQRHIRRRRDVVTETKTVELVIVADHSE
AQKYRDFQHLLNRTLEVALLLDTFFRPLNVRVALVGLEAWTQRDLVEISPNPAVTLENFLHWRRALLPRLPHDS
AQLVTGTSFSGPTVGMAIQNSICSPDFSGGVNMDHSTSILGVASSIAHELGHSLGLDHDLPGNSCPCPGPAPAKT
CIMEASTDFLPGLNFSNCSRRALEKALLDGMGSCLFERLP SLPPMAAFCGNMFVEPGEQDCGFLDDCVDPCCD S
LTCQLRPGAQCADGPPCQNCQLRPSGWQCRPTRGDCDLPEFCPGDSSQCPPDVSLGDGEPCAGGQAVCMHGRCA
SYAQQCQSLWGPGAQPAAPLCLQTANTRGNAFGSCGRNPSGSYVSCTPRDAICGQLQCQTGRTQPLLSIRDLLW
ETIDVNGTELNC SWVHLDLGSDVAQPLLTLPGTACGPGLV CIDHRCQRVDLLGAQECSRKCHGHGVCD SNRHCYC
EEGWAPPDCTTQLKATSSLTTGLLLSLLVLLVLM LGAGYWYRARLHQR L CQLKGPTCQYRAAQSGP SERPGPPQ
RALLARGTKSQGPAKPPPRKPLPADPQGRCPSGDLPGPGAGIPPLVVP SRPAPPPTVSSLYL

WO 2004/030615

PCT/US2003/028547

491/6881
FIGURE 459

CGACTTTCCCGATCGCCAGGCAGGAGTTTCTCTCGGTGACTACTATCGCTGTCAATGTCTGGTCGTGGCAAGCAAG
GAGGCAAGGCCCGCGCCAAGGCCAAGTCGCGCTCGTCCCGCGCTGGCCTTCAGTTCCCGGTAGGGCGAGTGCATC
GCTTGCTGCGCAAAGGCAACTACGCGGAGCGAGTGGGGGCCGGCGCGCCCGTCTACATGGCTGCGGTCCCTCGAGT
ATCTGACCGCCGAGATCCTGGAGCTGGCGGGCAACGCGGCTCGGGACAACAAGAAGACGCGCATCATCCCTCGTC
ACCTCCAGCTGGCCATCCGCAACGACGAGGAAGTGAACAAGCTGCTGGGCAAAGTCACCATCGCCAGGGCGGGCG
TCTTGCCTAACATCCAGGCCGTACTGCTCCCTAAGAAGACGGAGAGTCACCACAAGGCAAAGGGCAAGTGAAGGCT
GACGTCCGGCCCAAGTGGGCCCAGCCCGGCCCGCGTCTCGAAGGGGCACCTGTGAACTCAAAGGCTCTTTTCAG
AGCCACCCA

WO 2004/030615

PCT/US2003/028547

492/6881
FIGURE 460

MSGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNK
KTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTESHHKAKGK

WO 2004/030615

PCT/US2003/028547

493/6881
FIGURE 461

CTTTTCGCCATGGCTGCCGGGCCGATCTCCGAGCGGAATCAGGATGCCACTGTGTACGTGGGGGGCCTGGATGAGA
AGGTTAGTGAACCGCTGCTGTGGGAACGTGTTTCTCCAGGCTGGACCAGTAGTCAACACCCACATGCCAAAGGATA
GAGTCACTGGCCAGCACCAAGGCTATGGCTTTGTGGAATTCTTGAGTGAGGAAGATGCTGACTATGCCATTAAGA
TCATGAACATGATCAAACCTCTATGGGAAGCCAATACGGGTGAACAAAGCATCAGCTCACAACAAAAACCTGGATG
TAGGGGCCAACATTTTTCATTGGGAACCTGGACCCTGAGATTGATGAGAAGTTGCTTTATGATACTTTCAGCGCCT
TTGGGGTCACTTTACAAACCCCCAAAATTATGCGGGACCCTGACACAGGCAACTCCAAAGGTTATGCCTTTTATTA
ATTTTGCTTTCATTTGATGCTTCGGATGCAGCAATTGAAGCCATGAATGGGCAGTACCTCTGTAAACCGTCCTATCA
CCGTATCTTATGCCTTCAAGAAGGACTCCAAGGGTGAGCGCCATGGCTCAGCAGCCGAACGACTTCTGGCAGCTC
AGAACCCGCTCTCCCAGGCTGATCGCCCTCATCAGCTGTTTGCAGATGCACCTCCTCCACCCTCTGCTCCCAATC
CTGTGGTATCATCATTGGGGTCTGGGGCTTCCTCCACCAGGCATGCCTCCTCTGGCTCCTTCCCACCCCCAGTGC
CACCTCCTGGAGCCCTCCCACCTGGGATACCCCCAGCCATGCCCCCACCACCTATGCCTCCTGGGGCTGCAGGAC
ATGGCCCCCATCGGCAGGAACCCAGGGGCAGGACATCCTGGTCATGGACACTCACATCCTCACCCATTCCCAC
CGGGTGGGATGCCCCATCCAGGGATGTCTCAGATGCAGCTTGACACCATGGCCCTCATGGCTTAGGACATCCCC
ACGCTGGACCCCCAGGCTCTGGGGGCCAGCCACCGCCCCGACCACCACCTGGAATGCCTCATCCTGGACCTCCTC
CAATGGGCATGCCCCCGAGGGCCTCCATTCCGATCTCCCATGGGTCAACCAGGTCTATGCCTCCGCATGGTA
TGCGTGGACCTCCTCCACTGATGCCCCCATGGATACACTGGCCCTCCACGACCCCCACCCTATGGCTACCAGC
GGGGGCCTCTCCCTCCACCCAGACCCACTCCCCGGCCACCAGTTCCCCCTCGAGGGCCCACTTCGAGGGCCCTCTCC
CTCAGTAAATTACATTTTCTTCTCCTGTTACATTTTCCCAATATCTTTTCTATTCTTGGACCAATCAGAGA
TGCTGTAGCTCCTTGGGGCAAAGGTACTAATCCCTTTCAGCACCCCCACTCCATTCCCCTTTTTAATGTAACCTTT
TTCCACAGGAGGTATTTCTTTTTTATGTTGGTCCTGAGTATTTTGCAAATGCACAGAGAAAATAAACTAAACTC
CTTGTTAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

494/6881
FIGURE 462

MAAGPISERNQDATVYVGGGLDEKVSEPLLWELFLQAGPVVNTHMPKDRVTGQHQGYGFVEFLSEEDADYAIKIMN
MIKLYGKPIRVNKASAHNKNLDVGANIFIGNLDPEIDEKLLYDTFSAFGVILQTPKIMRDPDTGNSKGYAFINFA
SFDASDAAIEAMNGQYLCNRPITVSYAFKKDSKGERHGSAAERLLAAQNPLSQADRPHQLFADAPPPPSAPNPVV
SSLGSGLPFPGMPPPGSFPPFVPPPGALPPGIPPAMPPPPMPPGAAGHGPPSAGTPGAGHPGHGHSHPHPFPPGG
MPHPGMSQMQLAHHGPHGLGHPHAGPPGSGGQPPRPPPGMPHPGPPPMGMPPRGPPFGSPMGHPGPMPPHGMRG
PPPLMPPHGYTGPPRPPPYGYQRGFLPPPRPTPRPPVPPRGFLRGFLPQ

PCT/US2003/028547

49378881
FIGURE 463A

GCCGGGAGCAGTCGCCGCTGCCGCCCTCCGCCCGCGGGCCGGGACCCCGCTCCTCGCCGGGACTCCTTACCCGGGG
AACCTAGACCAGGTCTCCAGAGGCTTGTGGAAGAGAAGCAGGCCACCCCTTCTGAGTTATCCTGGCTTAGCCTCC
CAATCTGGCTCCCCCTCCCCCTCCCATTCGCCCTGCTCCCCCTGTCCCTTCCCCATCCACCCAAGTGAAGTGGGT
TAGGTCAAAGCTCCTCTCCTTCCCTTCTTCCCTTAGGCACCTCATTTGGCTAGGACCTGTTTGCTCTTTTTTTTGTG
CCCAGAGATACTGGAACACGCTTTCATCTAAGTAAGTGTGGGGAGGGGTCTTTTTGACTCTACAAGTCCTTGAGCA
AAAAGCTGAAAAAGAAGCAGGAGGTGGAGAAGACCCAGTGAAGTGCCCCAAGCCCCATCATGGAAGAGGGCTTCC
GAGACCGGGCAGCTTTTCACTCCGTGGGGGCCAAAGACATTGCTAAGGAAGTCAAAAAGCATGCGGCCAAGAAGGTGG
TGAAGGGCTGGACAGAGTCCAGGACGAATATTCCCGAAGATCGTACTCCCGCTTTGAGGAGGAGGATGATGATG
ATGACTTCCCTGCTCCCAGTGTATGGTTATTACCGAGGAGAAGGGACCCAGGATGAGGAGGAAGGTGGTGCATCC
GTGATGCTACTGAGGGCCATGACGAGGATGATGAGATCTATGAAGGGGAATATCAGGGCATTCCCCGGGCAGAGT
CTGGGGGGCAAAGGCGAGCGGATGGCAGATGGGGCGCCCCCTGGCTGGAGTAAGGGGGGGCTTGAGTGATGGGGAGG
GTCCCCCTGGGGGGCCGGGGGGAGGCACAACGACGGAAAGAACGAGAAGAACTGGCCCAACAGTATGAAGCCATCC
TACGGGAGTGTGGCCACGGCCGCTTCCAGTGGACACTGTATTTTGTGCTTGGTCTGGCGCTGATGGCTGACGGTG
TGGAGGTCTTTGTGGTGGGCTTCGTGCTGCCAGCGCTGAGAAAGACATGTGCCTGTCCGACTCCAACAAAGGCA
TGCTAGGCCTCATCGTCTACCTGGGCATGATGGTGGGAGCCTTCTCTGGGGAGGTCTGGCTGACCGGCTGGGT
GGAGGCAGTGTCTGCTCATCTCGCTCTCAGTCAACAGCGTCTTCGCCCTTCTTCTCATCTTTTGTCCAGGGTTACG
GCACCTTCTCTTCTGCGCGCTACTTTCTGGGGTTGGGATTGGAGGGTCCATCCCCATTGTCTTCTCCTATTTCT
CCGAGTTTCTGGCCCAGGAGAAACGAGGGGAGCATTGTAGCTGGCTCTGCATGTTTTGGATGATTGGTGGCGTGT
ACGCAGCTGCTATGGCCTGGGGCCATCATCCCCACTATGGGTGGAGTTTTAGATGGGTCTGCCTACCAGTTCC
ACAGCTGGAGGGTCTTCTGCTCCTGCTCTGCGCCTTTCTTCTGTGTTTGCCATTGGGGCTCTGACCACGCAGCCTG
AGAGCCCCCGTTTCTTCTTAGAGAATGGAAAGCATGATGAGGCCTGGATGGTGTGTAAGCAGGTCCATGATACCA
ACATGCGAGCCAAAGGACATCCTGAGCGAGTGTCTCAGTAACCCACATTAAGACGATTTCATCAGGAGGATGAAT
TGATTGAGATCCAGTCGGACACAGGGACCTGGTACCAGCGCTGGGGGGTCCGGGCCTTGAGCCTAGGGGGGGCAGG
TTTGGGGGAATTTTCTCTCCTGTTTTGGTCCCGAATATCGGCGCATCACTCTGATGATGATGGGTGTGTGGTTCA
CCATGTCATTACGCTACTATGGCCTGACCGTCTGGTTTTCTGACATGATCCGCCATCTCCAGGCAGTGGACTACG
CATCCCGCACCAAAGTGTTCGCCGGGGAGCGCGTAGAGCATGTAACTTTTAACTTACGTTGGAGAATCAGATCC
ACCGAGGCGGGCAGTACTTCAATGACAAGTTCATTGGGCTGCGGCTCAAGTCAGTGTCTTTGAGGATTCCCTGT
TTGAAGAGTGTTATTTGAGGATGTACATCCAGCAACACGTTTTTCCGCAACTGCACATTCATCAACACTGTGT
TCTATAACACTGACCTGTTTCGAGTACAAGTTTGTGAACAGCCGTCTGATAAACAGTACATTCTGCACAACAAG
AGGGCTGCCCGCTAGACGTGACAGGGACGGGCGAAGGTGCCTACATGGTATACTTTGTGAGCTTCTGGGGACAC
TGGCAGTGCTTCTTGGGAATATCGTGTCTGCCCTGCTCATGGACAAGATCGGCAGGCTCAGAATGCTTGTGGCT
CCAGCGTGATGTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
GCCTTTTTGGCGGGGTGAGCATTGCATCCTGGAATGCGCTGGACGTGTTGACTGTTGAACTCTACCCCTCAGACA
AGAGGACCACAGCTTTTGGCTTCTGAAATGCCCTGTGTAAGCTGGCAGCTGTGCTGGGGATCAGCATCTTCACAT
CCTTCGTGGGAATCACCAGGGCTGCACCATCCTCTTTGCCCTCAGCTGCCCTTGCCCTTGGCAGCTCTCTGGCC
TGAAGCTGCCCTGAGACCCGGGGGCAGGTGCTGCAGTGAAGGGGTCTCTAGGGCTTTGGGATTTGGCAGGCACATG
TGAGACCAACAACCTCCTTCCCTTCCCTGCCCTGCCATCCTGACCTCCAGAGCCCTCACTCCCCACTCCCCG
TGTTTGGTGTCTTAGCTGTGTGTGCGTGTGCGTGTGCATGTGTGTAACCCCGTGGGCAGGACTACAGGGAAGG
CTCCTTCATCCCAGTTTTGAGATGAAGCTGTACTCCCCATTTCCCACTGCCCTTGACTTTGCACAAGAGAAGGCT
GAGCCCCATCCTTCTCCCCCTGTAGAGAGGGGCCCTTGCTTCCCTGTTCAGGGGTTCCAGAATAGGCTTCTCTG
CCTTCCCCATCATCCTCTGCCTAGGCCCTGGTGAACCACAGGTATGCAATTATGCTAGGGGCTGGGGCTCTG
GTGTAGACCCATGGACCAAAAGAACCTTCTTAGAGTCTGAAGAGTGGGCCTCGGGTGCCCTCTCACATCTCCTGTTG
GATGCTGGGGGAGAAGCAATAAACCTCAGCCCTCTGGCCTCCACTTCTCTCAATTTGGGCTGCAAATATGAAG
CCTGAATTTTATGAAATTAGCTTCTGATTCTTATTTATTAATAGATTAAAGTCTGAGGCAGCTCCGCAGGACTG
TGTGTGAATGTGTATGTATACTTACATATGTGTGTGCATGTGCCATGGGGCGGGGGGTATCACTATACTGTCTC
AAATATAAGCCAAGGGTAATTTAGCGGATGCACACACAACCCTGCCTCCACAGTTCTCTCCCTAATCTGGTTT
CTGTGTTGAGCCTGGGATGGAGGAGCCCTAGGCCAGCCTGGGATAAGAGTCCCACAGTCTAGGGAGATCTGAGGG
CATCCGACAAGGCCCATCTCCTTCCCTCCTCAAGAAGCAGAGGCCTCCTCTGGAGTGAGAGGCTCCACCCACTAC

WO 2004/030615

PCT/US2003/028547

496/6881
FIGURE 463B

AGCACAGGCGGGAATAGCACAGCTGCCCTCCCATGCTCCCTACCTGTCCCTCACAGGGAGGGGAGCAGGGGAGG
GAAAGAAACCAGGCATCTGGTCAAACCAGCAGATCAAAAAGCACAAAGAGCTGGGGCAGAGGCAGGAAGCAGGGG
CCCTCCTGGCAGCTCCTCTGAGTGGGGAGAGGTTGGGCAGTGAGTGAGGGACCCCTAATGCAGGGACTAGAAGCC
TCAGTTTCCCCATTTTACCCTTCCACACAATAGCCTCTGTAGGTTAGGCTGCCCCATCCCACCCTACTCTGTGTG
GCTGCTTTCTTTGGTGCCCTCCCTCACCCCACTGTAGCTGTGACGTGTTGTAGTTTTTAGATGTTTGTAATG
TTTAAAAAATGTTAAAAGGAAAAAGTGAAAAATACAAAAAGAAAAATCAAAATTCACCTTCGTCATGCTGCGT
CCAGTGCCCCAACCTGTGGTCACTCTCCCATTTTGTAACACTGTACCAGGTGGTGACTGTTTAACTCTTTGGT
GTCTGTGCTCAAAGACTGCCTTCTCCAGTGCCCACTGTATGAGTGTGTGCCCTGTGCCCTTGTCCTCACTCCC
CACATGCTGGACGTAGCCCTCTTCTCGCACCCCTGGGAGGGACCCATCCATCTCCCTTGCTCTCCTGGGGAACC
CTAAACCAACTCTGTTGATGTGAAAAATGCAGTGAAAAATATTGACGAAAAATAAAACGGAAACAAATCCTCAA
AAT

WO 2004/030615

PCT/US2003/028547

497/6881
FIGURE 464

MEEGFRDRAAFIRGAKDIAKEVKKHAAKKVVKGLDRVQDEYSRRSYSRFEEEDDDDDFFPAPSDGYRGEQTQDEE
EGGASSDATEGHDEDEIYEGEYQGIPRAESGGKGERMADGAPLAGVRGGLSDGEGPPGGRGEAQRKEREELAQ
QYEAAILRECGHGRFQWTLYFVLGLALMADGVEVFVVGFLPSAEKDMCLSDSNKGMLGLIVYLGMMVGAFLWGGL
ADRLGRRQCLLISLSVNSVFAFFSSFVQGYGTFLFCRLLSGVGIGGSIPIVFSYFSEFLAQEKRGHLSWLCMFW
MIGGVYAAAMAWAIIIPHYGWSFQMGSAIQFHSWRVFLVCAFPVFAIGALTTPESPFRFFLENGKHDEAWMLK
QVHDTNMRAKGHPERFVSVTHIKTIHQEDELIEIQSDTGTWYQRWGVRLSLGGQVWGNFLSCFGPEYRRITLMM
MGVWFTMSFSYYGLTVWFPMIRHLQAVDYASRTKVFPGERVEHVTFNFTLENQIHRGGQYFNDKFIGLRLKSVS
FEDSLFEECYFEDVTSSNTFFRNCTFINTVFYNTDLFEYKFVNSRLINSTFLHNKEGCPDVTGTGEGAYMVYFV
SFLGTLAVLPGNIVSALLMDKIGRLRMLAGSSVMSCVSCFFLSFGNSESAMIALLCFLGGVSIASWNALDVLTV
LYPSDKRTTAFGFLNALCKLAAVLGISIFTSFVGITKAAPILFASAALALGSSLALKLPETRGQVLQ

WO 2004/030615

PCT/US2003/028547

498/6881
FIGURE 465

GGCAGGAAAAGCGGAAGAGGGAGCGAAAACCAACGTGTTCGGTGACAGACCCCAGCGCCGACTGAGCCTCTAAAG
CGACTTCAGCTCTGCCCCACCAACACCACCGCGCGCCCGGGAACAGCCGCTCCGGGAAGAAACCTGAGGGGACTG
CGGGGGGCACGAGGGACAGCTGAGGGAAGGAGGACGCGAGAGAAACAGCGCGAGCACGCTGAGGGCCGGGGGTT
GCCAGGAGAGGGGGCCCGCGGACCCGACAGCGGAGGAAGGTCCGGGAGAAAAGGGGCGGGACGGAGGAGAATCCG
GGATCGCCTGGCAGAAAAGAGAAGGGAGTTTCTGAATCCTGGGAAGAGGAGGCGTGGGTAGGGACGCTTAGCCC
GAGATCCGACAGCAGGGAACCGGAGCGCTCCGGGGGAGGGGCTTAATGCTGGGGAAGGGATGTCTTAAAAGAGGA
GAAGCTTTAAATTAGACGATCGGAGAAGGCTGAGGGAATTGCTATGAAGGGGCGGGAGCTGAAGTGTAGAGGACT
CCTTTAGACAGCAGAAAAGGGAAGCCGTTGAGAAGTTCCCTTCAAACCTCCACCTGCCTCCTCTCCAATTCAAACT
CCACTCCCTTCTCCTAAAAGTTAAAAGGAAAGCCAAGTTTACCACGCTCCCTGTTCCTACTCAATAAATACTTCT
TCTACTCCGCCACCGGGAACAGAAAAAACTAATTTCCCTTCCCAATATTAGGACTTAGAAAAGCTCTAGGT
CCCGCAATTTGAATTTTAGCCTAGGGGAATCAAAATAGTAGGAGCATTACTCTTTGTTTTCTTTTTCAAATCCCA
CACCTCATCTTCTCGCAGCCATGTCCACCAACATTTGTAGTTTCAAGGACAGGTGCGTGTCCATCCTGTGTT
GCAAATTCTGTAAACAAGTGCTCAGCTCTAGGGGAATGAAGGCTGTTTTGCTGGCTGATACTGAAATAGACCTTT
TCTCTACAGACATCCCTCCTACCAACGCAGTGGACTTCACTGGAAGATGCTATTTACCAAAAATCTGCAAATGTA
AACTGAAGGACATCGCATGTTTTAAATGTGGGAACATTGTAGGTTATCATGTGATTGTTCCATGTAGTTCCTGTC
TTCTTTCTGCAACAACAGACACTTCTGGATGTTTTACAGCCAGGCAGTTTATGATATTAACAGACTAGACTCCA
CAGGTGTAAACGTCCTACTTCGGGGCAACTTGCCAGAGATAGAAGAGAGTACAGATGAAGATGTGTTAAATATCT
CAGCAGAGGAGTGTATTAGATAAATGGAATTATGATATATATGATATACAACTTTTTTCTATTTAAAAATATAT
TAATGGATCAACTTTAAAATTGTTAGTTGCCAGTGATCTTTTTTGAAAAACAAAAATGGGGCATTTGTTGATTTA
TTTATTTTCTGTCTCTAATTAGTTACCTCAGTTTGATTGAAGCCAGTGGAGTTGTGCTTTTCTCTACTTCTACT
TCCTCTCCCCACCTTTTTCTGCCAGTGTAGGTGTATTCTTAAATTCAGACGGGAAGATTCTTTACATATCAC
TCAGTTACCTCCCAATCTGGGGGAGTTTTCTTACAACCTTGATACCAGATACCATTAATTTTACATTCTGAATA
AAGGCCTAGTACCCACGCATATTTCAACCATGCATATATCAAGTTCAACCGAGTTTAAATAGGGGATTAAAAAA
CAAGCTGTTAGGTTTCCATGGGCACCTGGTTCTCATAGGTTCTATTGGTGATAACTGCTTTAACATGGAGCAAGAG
TTTGTGAATCAGGAAATAGAATAAATTAAAAATTAATAATATATAGAGGAATCCTCTTGATTGCTCAGCATGATGT
TAGATAAATGAGTTTGTGAGAAAATATCAGTATACGCTGTTTACCAATGTTATTTATTTACATTCTTCTAAAGCC
ATTATGGATATTGTATTATGAGAGCTAAACCTAAATAAGTTATCCTGTTCCCTAGGACCTTCTCTGTAAATAGTG
AATTTTAGACGAGTGGTCTGTCTAAATCTTAAATAGAAAAAACTAAAGCGATTGCTTAAGCCATTGTACA
TTATAAAGAGCTGTTTTGTTTTGCTTTGCTTTGCTTTGTTTTGTTTTTAAAGCTGCATTACAGACTACAAAGG
AATAGGAAAGTAGGGTAGTGTGGATTCTGGTTTTATGTAACCTCTAAATAAATGTATCTCTTTAATATCTCAGT
TGTAGGGATTTGTCAATACCAAGCAGACTGAGTTGTGGTTTTGTAAATAAAGTTTTTCTAAAAATGACCATT
CTTCCTTAATTTTTGTTATGCCACATATTGTATGTAAAAATATAAATAAATAGTACTTAAAGTAT

WO 2004/030615

PCT/US2003/028547

499/6881
FIGURE 466

CAGCAGTGCTGTTTTACTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCA
AGAAGAGGAAGAAGACCAAGGCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGT
CTTGCAAGGACTCACTGGATAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTA
TGGAAGTTCCTTTTATGCATTGGAGGAAAAGCATGTTGGCTTTTCTCTTGACGTGGGAGAAAATTGAAAAAGAAGGG
GAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAGAAGGAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCA
AAACCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGATGAGAAAAGGGCCTGAAGTCTTGCAGGACTCACTGGA
TAGATGTTATTCAACTCCTTCAGGTTGTCTTGAACAGTACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACAT
ATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAAGTACCAAGAAGTGGAAGAAGACCA
AGACCCATCATGCCCCAGGCTCAGCGGGAGCTGTTGGATGAGAAAAGAGCCTGAAGTCTTGCAGGAGTCACTGGA
TAGATGCTATTCAACTCCTTCAGGTTGTCTTGAACAGTACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACAT
ATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAAGTACCAAGAAGTGGAAGAAGACCA
AGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGCTGGATGAGAAAAGAGCCTGAAGTCTTGCAGGACTCACTGGG
TAGATGTTATTGCACTCCTTCAGGTTATCTTGAACAGCTGCTGACTTAGGCCAGCCCTACAGCAGTGCTGTTTTACTC
ATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGACCA
AGGCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACTGGA
TAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTATGGAAGTTCCTTTTATGC
ATTGGAGGAAAAACATGTTGGCTTTTCTCTTGACGTGGGAGAAAATTGAAAAAGAAGGGGAAGGGGAAGAAAAGAAG
GGGAAGAAGATCAAAGAAGGAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAACCCACCATGCCCCAG
GCTCAACAGCATGCTGATGGAAGTGGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATATATGTTATTGCACTCC
GTCAATGTACTTTGAACTACCTGACTCATTCCAGCACTACAGAAGTGTTTACTCATTTGAGGAAGAGCATAT
CAGCTTCGCCCTTTACGTGGACAATAGGTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTGTTCCAGATGGG
AGTCATATTCCACAATAAGCAGCCCTTACTAAGCCGAGAGGTGTCAATCCTGCAGGCAGGACCTATAGGCACGT
GAAGATTTGAATGAAAGTACAGTTCCATTGGAAGCCAGACATAGGATGGGTCAGTGGGCATGGCTCTATTCTT
ATTCTCAAACCATGCCAGTGGCAACCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTTTAC
ATAACTGTGCAGCACATGCCGGGAGTGATCAGTCAGACATTTAATTGAAACACGTATCTCTGGGTAGCTACAA
AATTCCTCAGGGATGTCATTTTGCAGGCATGTCTCTGAGCTTCTATACCTGCTCAAGGTCAATTGTCATCTTTGTG
TTTAGCTCATCCAAAGGTGTTACCCTGGTTTCAATGAACCTAACCTCATTCTTTGTGTCTTCAGTGTGGCTTGT
TTTAGCTGATCCATCTGTAACACAGGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCTTGA
CAATTGTTAACCCTAGGCTCCTTTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGGTGTCAGTACTTAG
GAAGACCACAGCTAGATGGACAAACAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGAGAA
CAGGAGTCAGGAGCCGCTGGCAGGAGACAGCATGTACCCAGGACTCTGCCGGTGCAGAATATGAGCAATGCCAT
GTTCTTGCAAAAACGCTTAACCTGAGTTTCATAGGAGGTAATCACCAGACAACCTGCAGAATGTAGAACACTGAG
CAGGACAACCTGACCTGTCTCCTTCACATAGTCCATATCACCACAAATCACACAACAAAAGGAGAAGAGATATTT
TCGGTTGAAAAAAGTAAAAAGATA

WO 2004/030615

PCT/US2003/028547

500/6881
FIGURE 467

MDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEEQYLGLALD
VDRIKKDQEEEEEDQGPPCPRLSRELLEVAEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLD
VGEIEKKKGKGGKRRGRRSKKERRRGRKEGEEDQNPPCPRLNGVLMEVEEPEVLQDSLDCYSTPSMYFELPDSFQ
HYRSVFYSFEEEHISFALYVDNRFFTLTVTSLHLVFMGVIFTQ

WO 2004/030615

PCT/US2003/028547

501/6881
FIGURE 468

ATGACGCGAGACCCCGCCCCGCGAGCGCCCGCTTCCAAGATGGCGGCAGCGATGCCTGCCCGGCTGTTGGGGTGG
CGGTGACGACAGGCAGCAAAAGACCAGCTGGTCCCAGATTGCTGCTGGAGTGCTGGATGGAGCCTTTCTCTGCC
CTCTGTGACATTTCCAATTTTAGATAATGCCTCACATCTCTGTCCCCCGGGACCCCTGGAGCCCCATGATCC
CTAAGAAGACAGCTTGAACCTAGATCTCACCCCCAGGATGTTGCGGAGGCTGCTGGAGCGGCCTTGACAGCTGGC
CCTGCTTGTGGGCTCCCAGCTGGCTGTCATGATGTACCTGTCACTGGGGGGCTTCCGAAGTCTCAGTGCCCTATT
TGGCCGAGATCAGGGACCGACATTTGACTATTCTCACCCCTCGTGATGTCTACAGTAACTCAGTCACTGCTGG
GGCCCCAGGGGGTCTCCAGCTCCTCAAGGTCTGCCCTACTGTCCAGAACGATCTCCTCTCTTAGTGGGTCTGT
GTCGGTGTCTTTAGCCCAGTGCCATCACTGGCAGAGATTGTGGAGCGGAATCCCCGGGTAGAACCAGGGGGCCG
GTACCGCCCTGCAGGTTGTGAGCCCCGCTCCCGAACAGCCATCATTTGTCCTCATCGTGCCCGGGAGCACCACT
GCGCCTGCTGCTCTACCACCTGCACCCCTTCTTGACGCGCCAGCAGCTTGCTTATGGCATCTATGTATCCACCA
GGCTGGAAATGGAACATTTAACAGGGCAAACTGTTGAACGTTGGGGTGCGAGAGGCCCTGCGTGATGAAGAGTG
GGACTGCCTGTTCTTGACGATGTGGACCTCTTGCCAGAAAATGACCACAATCTGTATGTGTGTGACCCCCGGG
ACCCCGCCATGTTGCCGTTGCTATGAACAAGTTTGGATACAGCCTCCCGTACCCCCAGTACTTCGGAGGAGTCTC
AGCACTTACTCCTGACCAGTACCTGAAGATGAATGGCTTCCCCAATGAATACTGGGGCTGGGGTGGTGAGGATGA
CGACATTGCTACCAGGGTGCGCCTGGCTGGGATGAAGATCTCTCGGCCCCCACATCTGTAGGACACTATAAGAT
GGTGAAGCACCGAGGAGATAAGGGCAATGAGGAAAATCCCCACAGATTTGACCTCCTGGTCCGTACCCAGAATTC
CTGGACGCAAGATGGGATGAACCTCACTGACATACCAGTTGCTGGCTCGAGAGCTGGGGCCTCTTTATACCAACAT
CACAGCAGACATTGGGACTGACCCTCGGGGTCTCTCGGGCTCCTTCTGGGCCACGTTACCCACCTGGTTCTCTCCA
AGCCTTCCGTCAAGAGATGCTGCAACGCCGGCCCCCAGCCAGGCCTGGGCCTCTATCTACTGCCAACCACACAGC
CCTCCGAGGTTACACTGACTCCTCCTTCTGTCTACCTTAATCATGAAACCGAATTCATGGGGTTGTATTCTCC
CCACCCTCAGCTCCTCACTGTTCTCAGAGGGATGTGAGGGAACCTGAACCTCTGGTGCCGTGCTAGGGGGTAGGGG
CTCTCCCTCACTGCTGGACTGGAGCTGGGCTCCTGTAGACCTGAGGGGTCCCTCTCTCTAGGGTCTCCTGTAGGG
CTTATGACTGTGAATCCTTGATGTCATGATTTTATGTGACGATTCTAGGAGTCCCTGCCCTAGAGTAGGAGCA
GGGCTGGACCCCAAGCCCCCTCCTTCCATGGAGAGAAGAGTGATCTGGCTTCTCCTCGGACCTCTGTGAATAT
TTATTCTATTTATGTTCCCGGAAGTTGTTGGTGAAGGAAGCCCCCTCCCTGGGCATTTTCTGCCTATGCTGGA
ATAGCTCCCTCTTCTGGTCTGGCTCAGGGGGCTGGGATTTTGATATATTTCTAATAAAGGACTTTGTCTCGC

WO 2004/030615

PCT/US2003/028547

502/6881
FIGURE 469

MLRRLLERPCTLALLVGSQAVMMYLSLGGFRSLALFGRDQGPTFDYSHPRDVYSNLSHLPGAPGGPPAPQGLP
YCPERSPLLVGPSVSFSFSPVPSLAEIVERNPRVEPGGRYRPAGCEPRSRTAIIVPHRAREHHLRLLLYHLHPFLQ
RQQLAYGIYVIHQAGNGTFNRAKLLNVGVREALRDEEWDCLFLHDVDLLPENDHNLYVCDPRGPRHVAVAMNKFG
YSLPYYPQYFGGVSAITPDQYLKMNGFPNEYWGWGGEDDDIATRVRLAGMKISRPTSVGHYKMKVHRGDKGNEEN
PHRFDLLVRTQNSWTQDGMNSLTYQLLARELGPLYTNITADIGTDPRGPRAPSGPRYPFGSSQAFRQEMLQRRPP
ARPGPLSTANHTALRGSH

WO 2004/030615

PCT/US2003/028547

503/6881
FIGURE 470

GGCACGAGGGCCCCAGGAGAGGCAGAGAGTGAGGGAAAGGGCCTGGCCGGCATGCACAGATAGGATCACGGTCCT
GGGAGAAATTCCTGCTCTTATAGTCTAACCTACCATGGCTTCTCTTTTCTCAAGGCTCCCTCATGCTGCCCTTTGG
CCCTAGTGGCTGGTTTCCAGGGCTGAGGGGACTGAGTGAGCTGCCTGAGAAAAGAGGGTAGGGAACAGAAAAGCC
AGCCAGGAGCTGTGGGAGGAAACGCCCTCAGTAAAGATGACCGCGGTCACTGTTATCTAAACGCAAGTGAAGCCG
AGTCACAGGACCCGGATGTTGTGTCAGTTCGACGGTAAACGACCCTGCCAGCTTCCAAGAGGGCGGCTTCACTGTGC
GAATAGGTGAGAAGCCAAGAAGGAGGCGCGCTGGAGTTACTTCCGCCCGGTTCTCCTTCCCGCAGTCTGCAGCCG
GAGTAAGATGGCGGCGCTGAGGGCTTTGTGCGGCTTCCGGGGCGTTCGCGGCCAGGTGCTGCGGCCTGGGGCTGG
AGTCCGATTGCCGATTACGCCAGCAGAGGTGTTCCGGCAGTGGCAGCCAGATGTGGAATGGGCACAGCAGTTTGG
GGGAGCTGTTATGTACCCAAGCAAAGAAACAGCCCACTGGAAGCCTCCACCTTGGAAATGATGTGGACCCTCCAAA
GGACACAATTGTGAAGAACATTACCTTGAACCTTTGGGCCCCAACACCCAGCAGCGCATGGTGTCTGCGACTAGT
GATGGAATTGAGTGGGAGATGGTGCAGGAAGTGTGATCCTCACATCGGGCTCCTGCACCGAGGCACTGAGAAGCT
CATTGAATACAAGACCTATCTTCAGGCCCTTCCATACTTTGACCGGCTAGACTATGTGTCCATGATGTGTAACGA
ACAGGCCATTCTCTAGCTGTGGAGAAAGTTGCTAAACATCCGGCCTCCTCCTCGGGCACAGTGGATCCGAGTGTCT
GTTTGGAGAAATCACACGTTTGTGTAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGGCCATGAC
CCCTTTCTTCTGGCTGTTTGAAGAAAGGGAGAAGATGTTTGAAGTTCTACGAGCGAGTGTCTGGAGCCGAATGCA
TGCTGCTTATATCCGGCCAGGAGGAGTGACCCAGGACCTACCCCTTGGGCTTATGGATGACATTTATCAGTTTTT
TAAGAACTTCTCTCTTCGGCTTGATGAGTTGGAGGAGTTGCTGACCAACAATAGGATCTGGCGAAATCGGACAAT
TGACATTGGGGTTGTAAACAGCAGAAGAAGCACTTAAGTATGGTTTTAGTGGAGTGTGCTTCGGGGCTCAGGCAT
CCAGTGGGACCTGCGGAAGACCCAGCCCTATGATGTTTACGACCAGGTTGAGTTTGTGTTCTGTTGGTTCTCG
AGGGGACTGCTATGATAGGTACCTGTGCCGGGTGGAGGAGATGCGCCAGTCCCTGAGAATTATCGCACAGTGTCT
AAACAAGATGCCCTCCTGGGGAGATCAAGGTTGATGATGCCAAAGTGTCTCCACCTAAGCGAGCAGAGATGAAGAC
TTCCATGGAGTCACTGATTCACTTTAAGTTGTATACTGAGGGCTACCAAGTTCTCCAGGAGCCACATATAC
TGCCATTGAGGCTCCCAAGGGAGAGTTTGGGGTGTACCTGGTGTCTGATGGCAGCAGCCGCCCTTATCGATGCAA
GATCAAGGCTCCTGGTTTTGCCCATCTGGCTGGTTTGGACAAGATGTCTAAGGGACACATGTTGGCAGATGTCGT
TGCCATCATAGGTACCCAAGATATTGTATTGGAGAAGTAGATCGGTGAGCAGGGGAGCAGCGTTTGATCCCCC
TGCCATCAGCTTCTCTGTGGAGCCTGTTCTCTCACTGGAATTTGGCCTCTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTATGTTCTGTGTACACTGGCTGTCAGGCTTCTGTGTCATGTACTAAAAAAGGAGAAATTATAATAAAT
TAGCCGCTCTGCGGCCCTAGGCCTAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

504/6881
FIGURE 471

MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYPSEKTAHWKPPPWNDVDPEPKDT
IVKNITLNFQHPAAHGVRLRLVMEISGEMVRKCDPHIGLLHRGTEKLEIKTYLQALPYFDRLDYVSMMCNEQA
YSLAVEKLLNIRPPPPRAQWIRVLFGEITRLNHIMAVTTHALDLGAMTPFFWLFEEREKMFIFYERVSGARMHAA
YIRPGGVHQDLPLGLMDDIYQFSKNFSLRLDELEELLTNNRIWRNRITIDIGVVTAEALNYGFSVMLRGSGIQW
DLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLCRVEEMRQSLRIIAQCLNKMPPGEIKVDDAKVSPKRAEMKTSM
ESLIHHFKLYTEGYQVPPGATYTAIEAPKGEFGVYLVSDGSSRPYRCKIKAPGFAHLAGLDKMSKGHMLADVVAI
IGTQDIVFGEVDR

WO 2004/030615

PCT/US2003/028547

505/6881
FIGURE 472

CCGGAACCCAAGATGGCTGCGCTGTTGCTGAGACACGTTGGTCGTCATTGCCTCCGAGCCCACCTTTAGCCCTCAG
CTCTGTATCAGAAATTGGTCTCTTCCCATGGCGATGTCCATCTGCCACCGTGGCACTGGTATTGCTTTGAGTGCA
GGGGTCTCTCTTTTTTGGCATGTGCGCCCTGTTACTCCCTGGGAACCTTTGAGTCTTATTTGGAACCTTGGAAGTCC
CTGTGTCTGGGGCCAGCACTGATCCACACAGCTAAGTTTGCACCTTGTCTTCCCTCTCATGTATCATACCTGGAAT
GGGATCCGACACTTGATGTGGGACCTAGGAAAAGGCCCTGAAGATTCCCCAGCTATACCAGTCTGGAGTGGTTGTC
CTGGTTCTTACTGTGTTGTCCTCTATGGGGCTGGCAGCCATGTGAAGAAAGGAGGCTCCCAGCATCATCTTCCTA
CACATTATTACATTACCCATCTTTCTGTTTGTCACTTCTTATCTCCAGCCTGGGAAAAGTTCTCCTTATTTGTTT
AGATCCTTTTGTATTTTCAGATCTCCTTGGAGCAGTAGAGTACCTGGTAGACCATAATAGTGGAAGGGTCTAG
TTTTCCCTTGTTTCTAAAGATGAGGTGGCTGCATCTCTCTCCATATTGGGCTTT

WO 2004/030615

PCT/US2003/028547

506/6881
FIGURE 473

AATCATAGTGAAAGATTTCGTTTTTCATTGCAGAGTGGTATGATCCAAATGCTTCACCTTCTTCGACGTTATGAGCTT
TTATTTTACCCAGGGGATGGATCTGTTGAAATGCATGATGTAAAGAATCATCGCACCTTTTAAAGCGGACCAAA
TATGATAACCTGCACCTTGAAGATTTATTTATAGGCAACAAAGTGAATGTCTTTTCTCGACAACCTGGTATTAATT
GACTATGGGGATCAATATACAGCTCGCCAGCTGGGCAGTAGGAAAGAAAAACGCTAGCCCTAATTAAACCAGAT
GCAATATCAAAGGCTGGAGAAATAATTGAAATAATAAACAAAGCTGGATTTACTATAACCAAACCTCAAAATGATG
ATGCTTTCAAGGAAAGAAGCATTGGATTTTCATGTAGATCACCAGTCAAGACCCTTTTCAATGAGCTGATCCAG
TTTATTACAACCTGGTCCTATTATTGCCATGGAGATTTTAAAGAGATGATGCTATATGTGAATGGAAAAGACTGCTG
GGACCTGCAAACCTCTGGAGTGGCACGCACAGATGCTTCTGAAAGCATTAGAGCCCTCTTTGGAACAGATGGCATA
AGAAATGCAGCGCATGGCCCTGATTCTTTTGCTTCTGCGGCCAGAGAAATGGAGTTGTTTTTTCCTTCAAGTGGA
GGTTGTGGGCCGGCAAACACTGCTAAATTTACTAATTGTACCTGTTGCATTGTTAAACCCCATGCTGTCAGTGAA
GGACTGTTGGGAAAGATCCTGATGGCTATCCGAGATGCAGTTTTGAAATCTCAGCTATGCAGATGTTCAATATG
GATCGGGTTAATGTTGAGGAATTCTATGAAGTTTATAAAGGAGTAGTGACCGAATATCATAGGACATGGTGACAG
AAATGTATTCTGGCCCTTGTGTAGCAATGGAGATTCAACAGAATAATGCTACAAAGACATTTTCGAGAATTTTGTG
GACCTGCTGATCCTG

WO 2004/030615

PCT/US2003/028547

507/6881
FIGURE 474

GCCCTTGCCTTGAGTCAGTGCCTGCTCTCCAGCCCGCTTGAACGCTCCCCGCAGCCACCGCCACCCATTGGAAT
GGCCAACAGGGGACCTGCATATGGCCTGAGCCGGGAGGTGCAGCAGAAGATTGAGAAACAATATGATGCAGATCT
GGAGCAGATCCTGATCCAGTGGATCACCACCCAGTGCCGAAAGGATGTGGGCCGGCCCCAGCCTGGACGCGAGAA
CTTCCAGAACTGGCTCAAGGATGGCACGGTGCTATGTGAGCTCATTAAATGCACTGTACCCCCAGGGGGCAGGCCCC
AGTAAAGAAGATCCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGATCTCTCAGTTCTGCAAGCAGCTGA
GCGCTATGGCATTAAACACCACTGACATCTTCCAAACTGTGGACCTCTGGGAAGGAAAGAACATGGCCTGTGTGCA
GCGGACGCTGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCCAACTGGTT
CCCTAAGAAATCCAAGGAGAATCCTCGGAACTTCTCAGATAACCAGCTGCAAGAGGGGCAAGAACGTGATCGGGTT
ACAGATGGGCACCAACCGCGGGGCGTCTCAGGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATC
CCACCCAGGCCTTGCCCCCTGCCCTCCCACGAATGGTTAATATATATGTAGATATATATTTTAGCAGTGACATTC
CCAGAGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTCAGGGTGGGGGGTTCAGCCTGTCTGTACCTCTGAGGTG
CCTGCTGGCATCCTCTCCCCCATGCTTACTAATACATTCCCTTCCCCATAGCCATCAAACTGGACCAACTGGCC
TCTTCCCTTTCCCTGGGACCAAAATTTAGGGGCTCAGTCCCTCACCGCCATGCCCTGGCCTATTCTGTCTCTCC
TTCTTCCCCCTGGCCTGTTCTGTCTCTGAGCTCTGTGTCCTCCGTTCAATCCATGGCTGGGAGTCACTGATGCTG
CCTCTGCCTTCTGATGCTGGACTGGCCTTGCTTCTACAAGTATGCTTCTCCACAGCTGTGGCTGCAGGAACCTTA
ATTTATAGGGAGGAGCCTGTGGCAGCTGCTGCCCCAGCCACAGCTGCACTGACTGTGCTCACCACACATCTGGGG
CAGCCTTCCCTGGCAGGGGCCCTCGTGGCTTCTCATTTTCCATTCCCTTCACTGTGGCTAAGGGGTGGGGTGAGG
GGATGGAGAGGGAGGGCTGCCTACCATGGTCTGGGGCTTGAGGAAGATGAGTTTGTGATTTAAATAAAGAATTT
GTCATTTTTG

WO 2004/030615

PCT/US2003/028547

508/6881
FIGURE 475

MANRGPAYGLSREVQQKIEKQYDADLEQILIQWITTQCRKDVGRPQPGRENFQNLKDGTVLCELINALYPEGQA
PVKKIQASTMAFKQMEQISQFLQAAERYGINTTDFQTVDLWEGKNMACVQRTLMNLGGLAVARDDGLFSGDPNW
FPKKSKEPRNFSDNQLQEGKNVIGLQMGNTNRGASQAGMTGYGMPRQIL

WO 2004/030615

PCT/US2003/028547

509/6881
FIGURE 476A

GTGGAGCCGAGCGGTGCGGAGCAGATCTGGTGGTTCTCCGGAGAGCAGCTTCCTCGGGTGTTACATGAGCCAAGC
CCTCACTGTACAGAAGAGTGAGAGCTGAAACCTGTTCCCTGAGCTGATCAGAAGGACATCCCTTGGCCCCCTCCAT
CTGGGCTCCTGTGGATAGGAGGGGCTGGGTGAGCAGGCCAGCTGGGCTATGGTGTGGTGCCCTCGGCCCTGGCCGTC
CTCAGCCTGGTCATCAGCCAGGGGGCTGACGGTCGAGGGAAGCCTGAGGTGGTATCGGTGGTGGGCCGGGCTGGG
GAGAGTGTGGTGCTGGGCTGTGACCTGCTGCCCCCGGCCGGCCGGCCCCCCTGCATGTCTCAGTGGCTGCGC
TTTGGATTCTGCTTCCCATCTTCATCCAGTTTGGGCTCTACTCTCCCCGAATTGACCCTGATTACGTGGGACGA
GTCCGGCTGCAGAAGGGGGCTCTCTCCAGATTGAGGGTCTCCGGGTGGAAGACCAGGGCTGGTACGAGTGCCGC
GTGTTCTTCTGGACCAGCACATCCCTGAAGACGATTTTGCTAACGGCTCCTGGGTGCATCTGACAGTCAATTCA
CCCCCTCAATTCCAGGAGACACCTCCTGCTGTGTTGGAAGTGCAGGAAGTGGAGCCTGTGACCCTGCGTTGTGTG
GCCCGTGGCAGCCCCCTGCCTCATGTGACGTGGAAGCTCCGAGGAAAGGACCTTGGCCAGGGCCAGGGCCAGGTG
CAAGTGCAGAACGGGACGCTGCGGATCCGCCGGGTAGAGCGAGGCAGCTCTGGGGTCTACACCTGCCAAGCCTCC
AGCACTGAGGGCAGCGCCACCCACGCCACCCAGCTGCTAGTGCTAGGACCCCCAGTCATCGTGGTGCCCCCAAG
AACAGCACAGTCAATGCCTCCAGGATGTTTTATTGGCCTGCCATGCTGAGGCATACCCTGCTAACCTCACCTAC
AGCTGGTTCAGGACAACATCAATGTCTTCCACATTAGCCGCTGCAGCCCCGGGTGCGGATCCTGGTGGACGGG
AGCCTGCGGCTGCTGGCCACCCAGCCTGATGATGCCGGCTGCTACACCTGTGTGCCAGCAATGGCCTCCTGCAT
CCACCTCAGCCTCTGCCTACCTCACTGTGCTCTACCCAGCCCAGGTGACAGCTATGCCTCCTGAGACACCCCTG
CCCATAGGCATGCCGGGGGTGATCCGCTGCCCGGTTCTGTGCCAACCCCCCACTGCTCTTTGTGAGCTGGACCAAG
GATGGAAGGCCCTGCAGCTGGACAAGTTCCCTGGCTGGTCCCAGGGCACAGAAGGCTCACTGATCATGCCCTG
GGGAACGAGGATGCCCTGGGAGAATACTCCTGCACCCCTACAACAGTCTTGGTACCGCCGGGGCCCTCTCCTGTG
ACCCGCGTGCTGCTCAAGGCTCCCCAGCTTTTATAGAGCGGGCCCAAGGAAGAATATTTCCAAGAAGTAGGGGCTG
GAGCTGCTCATCCCCCTGCTCCGCCCAAGGGGACCCCTCCTCCTGTTGTCTCTTGGACCAAGGTGGGCGGGGCTG
CAAGGCCAGGCCAGGTGGACAGCAACAGCAGCCTCATCCTGCGACCAATTGACCAAGGAGGGCCAGGGCACTGG
GAATGCAGTGCCAGCAATGCTGTGGCCGAGTGGCCACCTCCACGAACGTCTACGTGCTGGGCACTAGCCCTCAT
GTTGTACCAATGTGTCCGTGGTGGCTTTGCCCAAGGGTGCCAATGTCTCCTGGGAGCCTGGCTTTGATGGTGGT
TATCTGCAGAGATTAGTGTCTGGTACACCCCACTGGCCAAGCGTCTTGACCGAATGCACCATGACTGGGTGTCC
TTGGCAGTGCTGTGGGGGCTGCTCACCTCCTAGTGCCAGGGCTGCAGCCCCACACCCAGTACCAGTTACGCGTG
CTAGCTCAGAACAGCTGGGGAGTGGTCCCTTCAGCGAAATCGTCTTGTCTGCTCCGGAAGGGCTTCTACCACG
CCAGCTGCACCCGGGCTTCCCCAACAGAGATACCGCCTCCCTGTCCCTCCGCGGGGTCTGGTGGCAGTGAGG
ACACCCCGGGGGGTACTCCTGCATTGGGATCCCCAGAGCTGGTCCCTAAGAGACTGGATGGCTACGTCTTGGA
GGCCGGCAAGGCTCCAGGGCTGGGAGGTGCTGGACCCGGCTGTGGCAGGCACAGAAACAGAGCTGCTGGTGCCA
GGCCTCATCAAGGTATGTTCTCTACGAGTTCGCGCTCGTGCCCTTCGCGGGCAGCTTCGTGACGACCCAGCAA
CACGGCCAACGTCTCCACTTCCGGTCTGGAGTCTACCTTCGCGCACGCAGCTGCCGGGCTCCTGCCTCAGCC
CGTGCTGGCCGGCTGGTGGGCGGAGTCTGCTTTCTGGGAGTGGCCGCTCCTTGTGAGCATCCTGGCCGGCTGCCT
CCTGAACCGGCGCAGGGCTGCCCGCCGCCGCAAGCGCTCCGCCAAGATCCACCTCTTATCTTCTCTCCGAC
CGGGAAGTCAGCTGCACCTCTGCTCTGGGCTCAGGCAGTCTGACAGCGTGGCGAAGCTGAAGCTCCAGGGATC
CCAGTCCCCAGCTGCGCCAGAGTCTGCTCTGGGGGATCCTGCCGGAAGTCCAGCCCCACCCGGATCCTCC
ATCTAGCCGGGGACCTTACCTCTGGAGCCCCATTTGCCGGGGCCAGACGGGCGCTTTGTGATGGGGCCACTGT
GGCGGCCCCCAGGAAAGGTGAGGCCGGGAGCAGGCAGAACCTCGGACTCCAGCCAGCGTCTGGCCCGGTCTTT
TGACTGTAGCAGCAGCAGCCCCAGTGGGGCACCCAGCCCCCTCTGCATTGAAGACATCAGCCCTGTGGCACCCCC
TCCAGCAGCCCCACCCAGTCCCTTGCCAGGTCTGGACCCCTGCTCCAGTACCTGAGCCTGCCCTTCTTCCGAGA
GATGAATGTGGATGGGGACTGGCCCCCGCTTGAGGAGCCAGCCCTGCTGCACCCCAAGATTACATGGATACCCG
GCGCTGTCCACCTCATCTTTCTTCTCCAGAAACCCCTCCTGTATCCCCAGGGAATCACTTCTGGGGC
TGTGGTAGGGGCTGGGGCCACTGCAGAGCCCCCTTACACAGCCCTGGCTGACTGGACACTGAGGGAGCGGCTGCT
GCCAGGCCTTCTCCCTGCTGCCCCCTCGAGGCAGCCTCACCAGCCAGAGCAGTGGGCGAGGCAGCGCTTCGTTCT
GCGGCCCCCTCCACAGCCCCCTCTGCAGGAGGCAGCTACCTCAGCCCTGCTCCAGGAGACACCAGCAGCTGGGC
CAGTGGCCCTGAGAGATGGCCCCGAAGGGAGCATGTGGTGACAGTCAGCAAGAGGAGGAACACATCTGTGGACGA
GAACTATGAGTGGGACTCAGAATCCCTGGGGACATGGAATTGCTGGAGACTTTGCACCTGGGCTTGGCCAGCTC
CCGGCTCAGACCTGAAGCTGAGCCAGAGCTAGGTGTGAAGACTCCAGAGGAGGGCTGCCTCCTGAACACTGCCCA

WO 2004/030615

PCT/US2003/028547

510/6881
FIGURE 476B

TGTTACTGGCCCTGAGGCCCGCTGTGCTGCCCTTCGGGAGGAATTCCTGGCCTTCCGCCGCCGCCGAGATGCTAC
TAGGGCTCGGCTACCAGCCTATCGACAGCCAGTCCCCACCCCGAACAGGCCACTCTGCTGTGAACATCCCTGAT
GTGAGGCTGTGAAAAGGCATATGGACCTGCAAAGGAGGCCCCCAACCAGACAGACCTAGTTTCAAACGAGGGCAC
TCCCCCTGCCTGCCCTTTGGTGCCAGGCACAGACCCTGATAGTGGGTTTGGGTCACCTTGGTATGGAATGTAT
GTGCTGACCCCTAGGTGAGTCTGGGGATTGGAACAGGGATCTTAGGTCTGCCTCTCTCTCTCTCTCTCTCTCTC
TCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGAAGTTTTTACAGGTGAATAAACAAGTTTGAAAGATG

WO 2004/030615

PCT/US2003/028547

511/6881
FIGURE 477

TTTCCGTGCTACCTACAGAGGGGTCCATATGGCGTTGTTCTGGATTCCCGTCGTAACTCAAAGGGAAACTTTCA
CAATGTCGGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACT
TAGGTGGCACC AATCTTGACTTACAGATGGAACAGTATATCTATAAAAGGAAAAGTGATGGCATCTACATCATAA
ATCTGAAGGGAACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCTATTGTTGCCATTGAAAACCCCTGCTGATGTCA
GTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTG
CTGGCCACTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCTGGGAGCCATGGCTTCTTATGGTTA
CTGACCCCAGGGGCTGAACCATCAGCCTCTCACAGAGGCATCTTATGTTAATCTACCTACCATCGCTCTGTGTAA
ACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCGTGCAACAACAAGGGAGCTCACTGAGTGGGTTTGATG
TGGTGGATGCTGGCTCGGGAAGTACTGTGCATGCGTGGCACCATTTCCTGTAACACCCATGGGAGGTCATGCCT
GATCTCTGCTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAAAAGGCAGTGACCAAG
GAGGAATTCAGGGTGAATGGTCTGCTCCAGCTCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAGACTGGTTT
GAAGGTATACAGGTGCCCTCTGTGCCATTTCAGCAGTTCTACTGAACAATGGAGCACTCAGCCTGCCACGGAAT
ACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGAATGGTCTTAAGCTGTTCTTG
CATGGGCTCTTAAGCAACATGGAAAAATGGTTGATGGAAAATAAACATCAGTTTCT

WO 2004/030615

PCT/US2003/028547

512/6881
FIGURE 478

MSGALDVLQMKEEDVLKFLAAGTHLGGTNLDLQMEQYIYKRKSDGIYIINLKGTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAVLKFAAATGATPIAGHFTPGTFTNQIQAAFWEPWLLMVTDPGR

WO 2004/030615

PCT/US2003/028547

513/6881

FIGURE 479

AAAGGGAAACTTTTACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTG
CAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTACAGATGGAACAGTATATCTATAAAAGGAAAAGTGATG
GCATCTACATCATAAATCTGAAGGGAACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCTATTGTTGCCATTGAAA
ACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTG
GAGCCACTCCAATTGCTGGCCACTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCATCTTATGTTAATCTAC
CTACCATCGCTCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCGTGCAACAACAAGGGAG
CTCACTGAGTGGGTTTGAIGTGGTGGATGCTGGCTCGGGAAGTACTGTGCATGCGTGGCACCATTTCCTGTAAC
ACCCATGGGAGGTGATGCCTGATCTCTGCTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTG
CTGA

WO 2004/030615

PCT/US2003/028547

514/6881
FIGURE 480

MSGALDVLQMKEEDVLKFLTAGTHLGGTNLDFQMEQYIYKRRSDGIYIINLKRTWEKLLLAARAIVAIENPAVVS
VISSRNTGQRAVLKFAAVTGATPIAGRFTPGNFTNQIQEASYVNLPTIALCNTDSPLHFVDIAIPCNNKGAH

WO 2004/030615

PCT/US2003/028547

515/6881
FIGURE 481A

AGGTAGCAAGATGCGCCGCCGCTGAGGAAGGCTGTAGTGTGCGGGCCGAAGCGGACAGGGAATTGGAGGAGCTTCT
GGAAAGTGCTCTTGATGATTTTCGATAAAGCCAAACCTCCCCAGCACCCCTTCTACCACCACGGCCCTGATGC
TTCGGGGCCCCAGAAGAGATCGCCAGGAGACTGCCAAAGATGCCCTCTTCGCTTCCCAAGAGAAGTTTTTCCA
GGAAGTATTCGACAGTGAAGTGGCTTCCCAAGCCACTGCGGAGTTCGAGAAGGCAATGAAGGAGTTGGCTGAGGA
AGAACCCACCTGGTGGAGCAGTTCCAAAAGCTCTCAGAGGCTGCAGGGAGAGTGGGCAGTGATATGACCTCCCA
ACAAGAATTCAGTCTTGCCTAAAGGAAACACTAAGTGGATTAGCCAAAAATGCCACTGACCTTCAGAACTCCAG
CATGTCGGAAGAAGAGCTGACCAAGGCCATGGAGGGGCTAGGCATGGACGAAGGGGATGGGGAAGGGAACATCCT
CCCCATCATGCAGAGTATTATGCAGAACCTACTCTCCAAGGATGTGCTGTACCCATCACTGAAGGAGATCACAGA
AAAGTATCCAGAATGGTTGCAGAGTCATCGGGAATCTCTACCTCCAGAGCAGTTTGAAAAATATCAGGAGCAGCA
CAGCGTCATGTGCAAAATATGTGAGCAGTTTGAGGCAGAGACCCCCACAGACAGTGAAACCACTCAAAAGGCTCG
TTTTGAGATGGTGTGGATCTTATGCAGCAGCTACAAGATTTAGGCCATCCTCCAAAAGAGCTGGCTGGAGAGAT
GCCTCCTGGCCTCAACTTTGACCTGGATGCCCTCAATCTTTTCGGGGCCACCAGGTGCCAGTGGTGAACAGTGTCT
GATCATGTGAAACACAACACGTTTTCTCTCTGAGTCCCAGCTATGGGGAACATCTGGAGTCAGCAGAACCATTG
GGACCTGAGGCAGGAGTGTACCTGCGGGAGAACTGTGCCCGCTGCCCTCTGTCTATCCCATTCAGATTGTGCCA
TACCAGCTGAGGTTTTCTCTCTCTAGGAATAGGGTCTGTTTCACAGGCCATTTCTGTGAACCCTACTCC
ATTGTGGTTTTCTGCCACTATCAAAGTTCAGCTACCTGCAAGGTGAAGGAAGGCATCCCTTTTGGGGCATGCACT
TTCTTTCTTTCTCAAAATAATGTTATATGTGGCCACACTGATGTTACCTTTACGTCCAGGGTCTTTGTGCCTT
GTCTCTACTCCCTCTCTTGGATCTGGGGAGGAGGGGCAGAGACCTGGGACTCTGTATTTCTATAGTTCTCTTGGC
AGAGCCTTTGAGAATGGGGAGAAACAGCCTGGGCTGGGGCTACAGGTCTGTCACTATGCTCTCTTGCCTTCAGAC
AGACCATTCTGAATTTCTTAAAGGGAAAGGGCTTTTGCATCTAATCACAATAGAGTTGAAAGAGAGGCCCTTAGGA
TTCTCCTCTCTCTAGGTGCTGAGCCCTCACCTCCCTGTTCCAGGCTGAGAACTCAAATGGTTACCTGCTTCTTC
CTACAATGCTGTGTGATATGGGTGAACCCAGCCCTGACCTTCCTCTATCCCTGCCCATCCTCCCTTTTACCTC
CTCTCTTTTTTAAACACCTGTTTATCCCAACCTTTTGTAGCTCAAGCTGTGATAAAGAAGGGCCCATCCTATTTT
CCCTCATCTAGTCCATTTACGATTCTCACTGACTCCCCGCTTCTCTGGCAGACACAAATAAACCAGTGTCAGGT
CTAGGAAATTAATGGCTATTCTTCCCCAGATACATTCTGGCTTATTTGAGATACATGATTCTCTTAGAATCCTGT
CCCTTGGTTTCAGGAAAGTAGCTTGGAAAAGGAGTAGGGGTATAGCTTGGGTCCCTTTTCTGCAAGGCCCATGG
GGCAGAATATAATAAATATTCTGAGTGAGGAGTGTGGTCTTTTTCTGATCTTCTCAGCTTCCGTAAGTTGCAGA
GTGAGGTATATTAGGAGACTAGTTCTACACAATATTGTAATGCTGGGTCCATCAACACCCACCTTCCACAACCTC
AGTCTGCACCTCAGTTGGCAAAGGAGACTGGATGGCCATCTTTCCTCATGTTCCCTTGAGTATTTCAATGTAGAA
AGCCCTTCAAGTGGTATTATATTTTAACTTTTACATTATTGTTATTAATGTTAGTAATATATTGTTATGTTTTT
TAAATTATTTTTCTTAAAGCTGACGTGGCTTTTTTCTGTGGCTCCCAGTGGGTCTACGGACCTTGGCTGACATA
TGTTGGTAGGTACTCTGGTCAGCTCAGCTGGCTGTCTGTTCACTCAGAAGATAAGTCTCTCCAAAGCAAATTC
ACATGCATTATGAGTCGCTTTGAGCTTCTGACATGTCACTTGCCCCGAGGTTAAAACTTTTTACCCCTTGAAGAC
CTTACATGTTTTATGGTATTGGTGAGGAAGGAAATGTTCTCAAGGTCTCAGGCTATTTGGGAAATTCCAACCTCT
ATACCTTACCAGAGCATGGAAGAGCCCAGATCTGAATGTAAACGTCCTCTGTTCTGCCAGAGATGGAAAAATAC
AGGTATACTTGTGATATAGTCAATGGGGCTTCAGTGTCACTATTTTCTCCTTAAAGCTCCAGCCAAAACTGGACA
AGGATAGAGAGGAGGAGGGAAGAACAAGAGCCCTTCTCTATGAACCTTGTGCCTTCTGTCTACCAGTTTTCT
TTTACAGATTTCTCACTTCTGCTAGCCTAGCCAGGGCTTACTCCAGGAATCTAAATAGATGCCCTAGTCCACTTTA
TCTTTGTTCCCAAGGCACTCATTTTTATTTTGAATTTGATTGAATGTGAGCAGGTTGACCTCAGGTACACTTTG
TTCCAAAACTTTTGAATATTTCAGGACTTGTGGTGGAGTTATGGTACTCTAGGGCAGTCTTTCTCAAACCTAT
GTATGGTAAAGGACCAGGTTTTTTGTTTTCCAGTCTTCACTTATCAATATGCATTCTATTGCCGATGACAGGT
ATGGAGTTTCACACTGTGTGCTGCCGACCCGGCAAGTTTGACAGCACCCAACTGGCCAGACTGTTCTGTAGGTTA
AGTCCATTGATCATGTACTTGGATATCACAGCAACATTGAAATGCTAAAAAGTTTTTAAACACTCTCAATTTCTA
ATTCACCATGTACAGACTGGTGAAAAAAGGTTGTTCACTGACCAGCACAAGTCTGCAGATCATCTTTG
AGTAGCACTGTTTTGGGGCCCTCGGTCTCTCTGAAGACCCTAGCAGAACTGATACCTACCTGTATCTCTTGTCT
CTCCTATTTGAGTTTCACTTCCAGAGAACTTGTCTTCAAGAAATGTGTCACTAGTAAGGACATCTCTAGCAT
TTCTCTAGCCTTCTTTTCTGCTGCTCAAAAATAATCGTTACAAAGCTTAGGTTTAAAGCTGTATATGAAATATTT
ATGCGACTCTCAAACCTTAAAGGAGTTGCTCCTTTGTTCCAAAATTAATGTGTTAGATAAATTTGTGATTGTAT

WO 2004/030615

PCT/US2003/028547

516/6881
FIGURE 481B

GGGTGGCTTCATGAATTAAGAATTGAATTAATACAGACTTTTTGATAATAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

517/6881
FIGURE 482

MAAAEEGCSVGAEADRELEELLESALDDFDKAKPSPAPPSTTTAPDASGPQKRSPGDTAKDALFASQEKFFQELF
DSELASQATAEFEKAMKELAE EEPHLVEQFQKLSEAAGRVS DMTSQQEFTSCLKETLSGLAKNATDLQNSSMSE
EELTKAMEGLGMDEGDGEGNLPIMQSIMQNLLSKDVLVPSLKEITEKYPEWLQSHRESLPPEQFEKYQEHSVM
CKICEQFEAETPTDSETTQKARFEMVLDLMQQLQDLGHPPKELAGEMPPGLNFDLDALNLSGPPGASGEQCLIM

WO 2004/030615

PCT/US2003/028547

518/6881
FIGURE 483A

GAGAAGGGACCTTCAGGTCCAGGCCAAAGGGGGAACTTCTGTCTGTTGGGAACGAAAAAGAAAGAGGATTTACAGGGT
GGGGGGACAGAGGGGCGAGCAGGAACCAGAAGGGAGACAGTGGCGGTTCGCGGCGGGGCCGATCCGAGAGTTCCCTT
TAGAGAACGGAGCTCACGGGCGGGGAGGCCTCACCTGCTAGTAGGACGCAGAAAGACAGAAGGCCGAAGGAGACCC
CGACTTCCCGGGTCAGCCCCAGAGCCACCCCTGCCGTAGCCATCTTGCCCTCTCTGCTGAGCGGAAGCCCCCGTT
CGGCTCCTGTCTGTAGCGGCCTCTCTAGGCTACCACTGACACCGTCTCTGTGGCCCGGAGCCTAAGAGACCGGA
AGTTCGTGTTTTCCAGGCGCTTCCGGAAACCGCGGGAGAGGGTTCGTGACGTGGAGGCGTCCGAAGGGCAGCAGGG
TGTGTCTGGGGCTCGGATTAAGACATCGGAGTCGGAGACCTGAGAGATGTTAACCAAATTCGAGACCAAGAGCGCG
CGGGTCAAAGGGCTCAGCTTTACCCCCAAAGACCTTGGATCCTGACTAGTTTACATAATGGGGTCATCCAGTTA
TGGGACTATCGGATGTGCACTCTCATTGACAAGTTTGATGAACATGATGGTCCAGTGGCAGGGCATTGACTTCCAT
AAGCAGCAGCCACTGTTTCGTCTCTGGAGGAGATGACTATAAGATTAAGGTTTGGAAATTACAAGCTTCGGCGCTGT
CTTTTACATTGCTTGGGCACTTAGATTATATTCGCACCACGTTTTTTCATCATGAATATCCCTGGATTCTGAGT
GCCTCCGATGATCAGACCATCCGAGTGTGGAACCTGGAATCTAGAACCTGTGTTTGTGTGTTAACAGGGCACAAAC
CATTATGTGATGTGTGCTCAGTTCCACCCACAGAAGACTTGGTAGTATCAGCCAGCCTGGACCAGACTGTGCGC
GTTTGGGATATTTCTGGTCTGAGGAAAAAAACCTGTCCCTGGTGGCGGTGGAATCGGATGTGAGAGGAATAACT
GGGGTTGATCTATTTGGAACCTACAGATGCAGTGGTGAAGCATGTACTAGAGGGTCACGATCGTGGAGTAACTGG
GCTGCTTCCACCCCACTATGCCCTTATTGTATCTGGGGCAGATGATCGTCAAGTGAAGATCTGGCGCATGAAT
GAATCAAAGGCATGGGAGGTTGATACCTGCCGGGGCCATTACAACAATGTATCTTGTGCCGTCTTCCACCTCGC
CAAGAGTTGATCCTCAGCAATTCTGAGGACAAGAGTATTGAGTCTGGGATATGTCTAAGCGGACTGGGGTTCAG
ACTTTCGCAGAGACCATGATCGTTTCTGGGTCTAGCTGCTCACCCTAACCTTAACCTCTTTGCAGCAGGCCAT
GATGGTGGTATGATTGTGTTTAAAGCTGGAACGGGAACGGCCAGCCTATGCTGTTTATGGCAATATGCTACACTAT
GTCAAGGACCGATTCTTACGACAGCTGGATTTCAACAGCTCCAAGATGTAGCTGTGATGCAGTTGCGGAGTGGT
TCCAAGTTTCCAGTATTCAATATGTACATAAATCCAGCAGAAAAATGCAGTCTGCTTTGTACAAGAGCTAGCAAT
CTAGAGAATAGTACCTATGACCTGTACACCATCCCTAAAGATGCTGACTCCAGAATCCTGATGCGCCTGAAGGG
AAACGATCCTCAGGCCTGACAGCCGTTTGGGTGCTCGAAATCGGTTTGTCTGTCTAGATCGGATGCATTGCTGCTT
CTGATCAAGAATCTGAAGAATGAGATCACAAAAAGGTACAGGTGCCCACTGTGATGAGATCTTCTATGCTGGC
ACAGGCAATCTCCTGCTTCGAGATGCGGACTCTATCACACTCTTTGACGTACAGCAGAAGCGGACTCTGGCATCT
GTGAAGATTTCTAAAGTGAAATACGTTATCTGGTCAGCAGACATGTACATGTAGCACTACTAGCCAAACACGCC
ATTGTGATCTGTAACCGCAAACCTGGATGCTTTATGTAACATTCATGAGAACATTTCGTGTCAAGAGTGGGGCTGG
GATGAGAGTGGGGTATTTATCTATACCACAACACATCAAAATATGCTGTACCACTGGGGACCACGGGATC
ATTGCAACTCTGGATTTACCCATCTATGTCACACGGGTGAAGGGCAACAATGTATACTGCCTAGACAGGGAGTGT
CGTCCCCGGGTACTCACCAATTGATCCCCTGAGTTCAAAATCAAGCTGGCCCTGATCAACAGAAAAATATGATGAG
GTACTGCACATGGTGAGGAATGCCAACTAGTTGGCCAGTCTATTATTGCTTATCTCCAGAAGAAGGGCTATCCT
GAAGTGGCACTGCATTTTGTCAAGGATGAGAAAACCTCGCTTTAGTCTGGCACTGGAGTGTGGAACATTGAGATT
GCTCTGGAAGCAGCCAAAGCACTGGATGACAAGAAGCTGCTGGGAAAAGCTGGGAGAAGTGGCCCTGCTGCAGGGG
AACCACCAGATTGTGGAATGTGCTATCAGCGTACCAAAAACCTTTGACAAAACCTTCTCCTGTATCTTATCACT
GGCAACTTAGAAAAACCTTCGCAAGATGATGAAGATTGCTGAGATCAGAAAGGACATGAGTGGCCACTATCAGAAT
GCCCTATACCTGGGTGATGTGTGTCAGAGCGTGTGCGGATCCTGAAGAAGTGTGGACAGAAGTCCCTGGCCTATCTC
ACAGCTGCTACCCATGGCTTAGATGAAGAAGCTGAGAGCCTAAAGGAGACATTTGACCCAGAGAAGGAGACAATC
CCAGACATTGACCCTAATGCCAAGCTGCTCCAGCCACCTGCACCTATCATGCCATTGGATACCAATTGGCCTTTA
TTGACTGTATCCAAAGGATTTTTTGAAGGCACCATTTGCCAGCAAAGGGAAGGGAGGAGCACTGGCTGCTGACATT
GACATTGACACTGTTGGTACAGAGGGCTGGGGAGAGGATGCAGAGCTGCAGTTGGATGAAGATGGGTTTGTGGAG
GCTACAGAAGGTTTGGGGGATGATGCTCTTGGCAAGGGACAGGAAGAAGGAGGTGGCTGGGATGTAGAAGAAGAT
CTGGAGCTCCCTCCTGAGCTGGATATATCCCCTGGGGCAGCTGGTGGGGCTGAAGATGGTTTCTTTGTGCCCCCA
ACCAAGGGAACAAGTCCAACCTCAGATCTGGTGTAACTCTCAGCTTCCAGTTGATCACATCCTGGCAGGCTCT
TTGAAACAGCCATGCGGCTCCTTCATGACCAAGTAGGGGTAATCCAGTTTGGCCCTACAAGCAACTGTTCTTA
CAGACATACGCCCAGGGCCGACAACTATCAGGCTCTGCCCTGCCTACCCTCCATGTATGGCTATCCTAATCGC
AACTGGAAGGATGCAGGGCTGAAGAATGGTGTACCAGCTGTGGGCTGAAGCTTAATGACCTCATCAACGGTTG
CAGCTGTGCTACCAGCTCACACAGTTGGCAAATTTGAGGAGGCTGTGGAAAAATCCGTTCCATCCTTCTCAGT

WO 2004/030615

PCT/US2003/028547

519/6881
FIGURE 483B

GTGCCACTTCTTGTGTGGACAATAAACAAGAGATTGCAGAGGCCAGCAGCTCATCACCATTGCGGTGAGTAC
ATTGTGGGTTTGTCCGTGGAGACAGAAAGGAAGAAGCTGCCCAAAGAGACTCTAGAACAGCAGAAGCGCATCTGT
GAGATGGCAGCCTATTTACCCACTCAAACCTGCAGCCTGTGCACATGATCCTGGTGCTGCGTACAGCCCTCAAT
CTGTTCTTCAAGCTCAAGAAGCTTCAAGACAGCTGCCACCTTTGCTCGGCGCCTACTAGAACTCGGGCCCAAGCCT
GAGGTGGCCCAACAGACCCGAAAAATCCTGTCTGCCTGTGAGAAGAATCCCACAGATGCCTACCAGCTCAATTAT
GACATGCACAACCCCTTTGACATTTGTGCTGCATCATATCGGCCCATCTACCGTGGAAGCCAGTAGAAAAGTGT
CCACTCAGTGGGGCCTGCTATTCCCCTGAGTTCAAAGGTCAAATCTGCAGGGTCACCACAGTGACAGAGATTGGC
AAAGATGTGATTGGTTTAAAGGATCAGTCCTCTGCAGTTTCGCTAAGGCCCCCTTTGTGTGCATGGGTCAGTCACC
ATATGTTCCCCCAGAGAATGTGTCTATATCCTCCTTCTAACAGCACCTTCCCCCTGCAGCTACTCTTCAGATCT
GGCTCTCTGTACCCTAAACCTAGTATCTTTTTCTCTTCTATGGAAAATCCGAAGGTCTAAACTTGACTTTTTTG
AGGTCTTCTCAACTTGACTACAGTTGTGCTCATAATTGTCCTTGCCTTTCCAGCTTAATTATTTTAAGGAACAAA
TGAAAACCTCTGGGCTGGGTGGAGTGGCTCATACTGTAATCCCAGCACTTTGGGAGGCTACGGTGGGCAGATCAT
CTGAGGCCAGGAGTTCGAGACCTGCCTGGCCAACATGGCAACACCCGCTCTCTAATAAAAAATATAAAAAATTAGCC
TGGCATGGTAGCATGCGCCTATAGTCCCAGCTGCTCAGGAGGCTGAGGCATGAGAATCGCTTGAACCTAGGAGGT
GGAGGTTGCATTCAACTGAGATCATACCACTTCATTCCAGCCTGGGTGACAGAGCAAGACTCTGTCTCAAAAAA
AAAAAAGGAAAACTCTGTGATGGACATTTGTTTAGTAAATCCCTTCAGTATTTATCCCTCCTTTCCCCACAGCA
GCTTTCCTTCTGTCAACTAGAAAGGAGCAGGATGTAATAAATACATTTTGGTGTGACTAGGCCACACCAACTCT
TAATCATCTCCCATTTTCTTAGACATTTAAATTTCAAGGCAGGTACCCTCTGTGTACTCAGAAATTTGAAGAAG
TTATTTGGTTTTCCAAAATGCACACTGCGGGTTATTGATTTGTTCTTTACAACCTATTGTTCTCATATTTCTCACA
CTAAATAAATCTCTATGAGAGCTTCTTG

WO 2004/030615

PCT/US2003/028547

520/6881
FIGURE 484

AGCTGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTTGTAAACCCCGAGTGAGGTTCTGCTTACCCGAGGCCG
CTGCTGTGCGGAGACCCCGGGTGAAGCCACTGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACT
TGGGGGATAAGAAGGAAGGTGAATATATTAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAG
TGGTTCCAATGAATTCATTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCC

WO 2004/030615

PCT/US2003/028547

521/6881
FIGURE 485

GAAGGATTTGTAAACCCCGGAGTGAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCGGGTGAAGCC
ACTGTCATCATGTCTGACCAGGAGGCAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGGTGAATATATT
AAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAGTGAAAATGACAACACATCTCAAGAACTC
AAAGAATCATACTGTCAAAGACAGGGCGTTCCAATGAATTCATTCAAGTTTCTCTTTGAGGGTCAGAGAATTGCT
GATAATCATACTCCAAAAGAACTGGGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAATGGGGGGT
CATTCAACAGTTTAGATATTCTTTTTATTTTTTTTTCTTTCCCTCAATCCTTTCTCATTTTAAAAATAGTTCTT
TTGTAATGTGGTGTTAAAAACGGAATTGAAAACCTGGCACCCCATCTCTTTGAAACATCTGGTAATCTGAATTCTA
GTGCTCATTATTTCATTATTGTTTATTTTCATTGTGCTGATTTTTGGTGATCAAGCCTCAGTCCCCTTCATATTAC
CCTCTCCTTTTTTATTGTGGTGATAAATAAGATTGACCAATGCAAGCGTTCATAATAACTTGCGAATTGGCCCTGA
TGTTCTAGCATGTGATTACTTCACT

WO 2004/030615

PCT/US2003/028547

522/6881
FIGURE 486

GTTTGCCAAAATCCCAGGCAGCATGGACCTCAGTCTTCTCTGGGTACTTCTGCCCCTAGTCACCATGGCCTGGGG
CCAGTATGGCGATTATGGATAACCCATACCAGCAGTATCATGACTACAGCGATGATGGGTGGGTGAATTTGAACCG
GCAAGGCTTCAGCTACCAAGTGTCCCCAGGGGCGAGGTGATAGTGGCCGTGAGGAGCATCTTCAGCAAGAAGGAAGG
TTCTGACAGACAATGGAACCTACGCCTGCATGCCCACGCCACAGAGCCTCGGGGAACCCACGGAGTGCTGGTGGGA
GGAGATCAACAGGGCTGGCATGGAATGGTACCAGACGTGCTCCAACAATGGGCTGGTGGCAGGATTCCAGAGCCG
CTACTTCGAGTCAGTGCTGGATCGGGAGTGGCAGTTTTACTGTTGTCGCTACAGCAAGAGGTGCCCATATTCTTG
CTGGCTAACAACAGAATATCCAGGTCACTATGGTGAGGAAATGGACATGATTTCTTACAATTATGATTACTATAT
CCGAGGAGCAACAACCACTTTCTCTGCAGTGGAAAGGGATCGCCAGTGGAAAGTTCATAATGTGCCGGATGACTGA
ATACGACTGTGAATTTGCAAATGTTTAGATTTGCCACATACCAAATCTGGGTGAAAGGAAAGGGGCCGGGGACAG
GAGGGTGTCCACATATGTTAACATCAGTTGGATCTCCTATAGAAGTTTCTGCTGCTCTCTTTCTTCTCCCTGAG
CTGGTAACCTGCAATGCCAACTTCTGGGCCTTTCTGACTAGTATCACACTTCTAATAAAATCCACAATTAACCA
TGTTTTCTCACTTTTACATGTTTTCATAGCAACTGCTTTATATGACTGATGATGGCTTCCTTGCACACCACATATA
CAGTGCGCATGCTTACAGCCGGGCTTCTGGAGCACCAGCTGCAGCCTGGCTACTGCTTTTTTACTGCAGAATGAAC
TGCAAGTTCAGCATAGTGGAGGGGAGAGGCAGAACTGGAGGAGAGGTGCAGTGAAGGTTCTCTACAGCTAAGCCT
GTTTGAATGATACGTAGGTTCCCCACCAAAGCAGGCTTTCTGCCCTGAGGGACATCTTCCCACTCCCCTGCTCC
ACATGAGCCATGCATGCTTAGCAATCCAAGTGCAGAGCTCTTTGCTCCAGGAGTGAGGAGACTGGGAGGTGAAAT
GGGGAAATGGAAGGGTTTGGAGGCAGAGCTGAAAACAGGGTTGGAAGGATTTCTGAATTAGAAGACAAACGTTA
GCATACCCAGTAAGGAAAATGAGTGCAGGGGCCAGGGGAACCGTGAGGATCACTCTCAAATGAGATTAAAAACA
AGGAAGCAGAGAATGGTCAGAGAATGGGATTGAGATTGGGAACCTTGTGGGGATGAGAGTGACCAGGTTGAACTGG
GAAGTGGAAAAAGGAGTTTGAAGTCACTGGCACCTAGAAGCCTGCCACGATTCTTAGGAAGGCTGGCAGACACCC
TGGAACCTTGGGGAGCTACTGGCAAACCTCTCCTGGATTGGGCCTGATTTTTTTGGTGGGAAAGGCTGCCCTGGGG
ATCAACTTTCTTCTGTGTGTGGCTCAGGAGTTCTTCTGCAGAGATGGCGCTATCTTTCTCCTCCTGTGATGTC
CTGCTCCCAACCATTTGTACTCTTCATTACAAAAGAAATAAAAATATTAACGTTT

WO 2004/030615

PCT/US2003/028547

523/6881
FIGURE 487

MDLSLLWVLLPLVTMAWGQYGDYGYPYQQYHDYSDDGWVNLNRQGF SYQCPQGQVIVAVRSIFS KKEGSDRQWNY
ACMPTPQSLGEPTECWEEINRAGMEWYQTCSNNGLVAGFQSR YFESVLDREWQFYCCRYSKRCPYSCWLTTEYP
GHYGEEMDMISYNDYYIRGATTTTFAVERDRQWKFIMCRMTEYDCEFANV

WO 2004/030615

PCT/US2003/028547

524/6881
FIGURE 488

AGAGGAAGCCAAGAACGGTGAAAAGGCCAGGCGGAGTTCAGAGGAGGTGGACGGCCAGCACCCGGCCCAAGAGGA
GGTCCCGGAATCGCCCCAGACCTCTGGCCCAGAGGCAGAAAATAGGTGTGGGAGCCCCAGGGAGGAAAAGCCAGC
TGGAGAGGAAGCAGAGATGGAAGGCTACAGAGGTGAAGGGGGAGAGGGTGCAAAATGAAGAGGTGGGACCTGA
ACATGACAGCCAAGAAACAAAGAAGCTGGAGGAGGGAGCTGCAGTGAAGGAGACCCCCACAGTCCCCCTGGAGG
AGTGAAGGGCGGAGATGTCCCCAAGCAGGAAAAAGGCAAGGAAAAACAACAGGAGGGGGCAGTGCTCGAGCCAGG
CTGCAGCCCCCAGACCGGCCCTGCCAGCTGGAGACCAGCAGTGAGGTCCAGAGCGAGCCAGCAGTCCCCAAGCC
GGAGGATGACACTCCTGTCCAGGACACTAAAATGTGAAGAACAGCTCATTGTGCCCCAGTGATGAAGTTGCTGGA
CACATCTCTTTGCAGGTAGCAGCAACAGTTGTAGCAGCAGCAGACGAAGCCATTGCAGAGGCAGAATATGCTGAG
TGTCTGGAGTCAGCCTGAAGACACAGGGTGGATTATTTCTGGCCTCCACACCAAACGTTCCCTTGCAGATGGAG
ACTGAATCTGAGGGCAGCAGACTTTTATCAGCTTGAGTTTATGTCAATTTGATGGACTTGTTCAACAACAAGAAC
TTACTTAAAACAATGTACTGTGGTGATGAGTCCCAGGGGCAGTGGTCAGCCTGTGGAGCCCTGGATGCTATCCAC
ACCCACCTATCCCTGCAGCTAATTTAGCTGATCTCTAATTTAACTGAGCTCTAATTTAGCTGATCAGATTTTGCT
TGGGTAAAGTTCCTTTTTAATGTTCTAAAGTGTTTACGGTTCTCAAATATCAGTTAAAACTAATTTTAGGTGGC
CATAAACATAAAATAGAAACCCTGTAAGTTACAGAAGACCCTAAATTTGTATCAAAACCCTAGAGACAACTTTTCA
ATTTGATCCAAATTTGAAGTGGCCAACCAGTCTTTAAACACTGGACTAGAAGAGATAATGATTGAAACATTTAA
AAAAAAAAAGTGCTCCATTTCGCAGGAGCTTTTCTGTCTGTGGTTTTCCAGTTGGTGACCACCATGGGAGGTGCG
CTGGCTCGGCTCACTCCCTTCTCCACCCCTTGAGAATGTGGAGAACTCCCATGGAGAGGCAGAATGGCAGGAGGT
TTCATGTCCCGCGTTGCATCTCCTCCTGAAAGAAAAGCAGTGATACCTGAATAATGCTGGCTCTCCGATTGATCC
TGTGAGGATGAATTTGCATTTCCAGAATCCTTGAGCATGGATTAGATGTTTCTGGGAGGTGCCTTGAGTACCAT
TATGTGCAAGCTACATAATTAACATTTTTCTTAGTTTCCCTGGGAAGCTTTTCTTGACTCACAGCCCAGGTTT
TTCTGCCCAACACAAAAGGAGTGAGTTGGGGTCTTTAGTCTCTTCTTATTGGGTAGCTCTTGCTTTAATATTCTG
TTTGGTGAGTGTAAGGGATTCTGCAAGGGACAGGGGGCTGACTACCCAGTCTTTGACTTGATCCTCTCCCCTC
TTCATACACTCCTGCTGAAAAATGTTAATCCAAATACACATTTAACTTAGGGTCGGTCTTATTCTGATTTGAG
TATTTAATGTCTCAGTGTGCTGATTTGGTAGTTGGAAGAATTATTCTTCTGGAGGTCTGTTAGACTACATCCTA
CACTGACTTCAGAAAACAGTCTGTGCAGACAAAAGGCCTTATGTCACCACTGGTACCTCAGTTTCCTCATCCCAT
TTACAGTTTTTCTAACTCCAGGGTAGTGTTTAGTGTTAATATTTGGGATATATTTTTTTTCAAACTGTTTTTAA
GTAGTTTGTAAATTTGTAACAACTTGTAACCTGGTTGGGACTGATATTGTCATAGCTATGATAAACTTTGGATAT
TAGCAGAATTTGGGAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

525/6881
FIGURE 489

MEKATEVKGGERVQNEEVGPEHDSQETKKLEEGA AVKETPHSPPGGVKGGDVPKQEKGKEKQQEGAVLEPGCSPQT
GPAQLETSSEVQSEPAVPKPEDDTPVQDTKM

WO 2004/030615

PCT/US2003/028547

526/6881
FIGURE 490

GGACGTTGAGAGAACGAGGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCG
CAGCAGGGCTACAGTGCTTACAACACCCAGCCCCTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAA
AGCTATGGAACCTATGGACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACC
GCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAAC TGCCCCCAGGCATACAGCCAGCCT
GTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCT
CAATCTGCATATGGCACTCAGCCTGCTTATCCAGCTTATGGG CAGCAGCCAGTAGCCACTGCACCTACAAGACTG
CAGAATGGAAACAAGCCCCTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGA
TATGGACAGAGTAACTGCAGTTATCCCCAGGTACCTGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCC
TACCCTCCTACCAGCTATTCTCTACACAGCCAAGTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTAT
GGGAAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAACAAAGCAGCTATGGGCAGCTGCCTCCCCTAGT
TACCCACCCCAAACCTTGATCCTACAGCCAAGCTCCAAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCAGCAG
AGTTTCATTCTGACAGGACCACCCAGTAGC **ATCG**GGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACTAGGA
GAGAACC GGAGCATGAGTGGCCCTGATAACTGGGGCAGGGGAAGAGGGGGATTGATCGTGAGGCATGAGCAGA
GGTGGGGGGGAGGAGGATGCGGTGGAATGGGCAGCGCTGGAGAGCAAGTTGGCTTCAATAAGCCTGGTGGACCC
ATGGATGAAGGACCAGATCTTGATCTAGGCCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTAT
GTACAAGGATTAAATGACAATGTGACTCTAGATGATCTGGTAGACTTCTTTAAGCAGTGTGGGGTTGTTAAGATG
AACAAGAGAACTGAGCAACCCATGATCCACACCTACCTGGACAAGGAAACAAGAAAGCCCAAAGGTGATGCCACA
GTGTCTGTGAAGACTCACCTACTGCCAAAGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAA
CTTAAAGTCTCTCTTGCTCGGAAGAGGCCTCCAGTGAACAGTATGCAGGGTGGTATGCCACCCCATGAGGGCAGA
GGGATGCCACCACCACTCTGCGGAGGTCCAGGAGGCCCAGGAAGTCTGGGGGACCCATGGGTACATGGGAGGC
CGTGGAGGAGATAGAGGAGGCCTCCCTCCAAGAGGACCCAGGGTCCCGAGGGGAACACCTCTGGAGGAGGAAAC
GTCCAGCACCAAGCTGGAGACAGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAG
AGCAACAAGTGTAAGGCTCCAAAGCCTGAAGGCTTCTCCCGCCACCCTTCCACCCCGGGTGGTGATCATGGC
AGAGGTGGCCCTGGTGGCATGTGGGGAGGAAGAGGTGGCCTCATGGATCATGGTGGTCCCGGTGGAATGTTTCAGA
GGTGGCTGTGGTAGAGACAGAAGTGGCTTCTGTGGTGGCTGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGAC
AAGGTGGCCCTGGGGGGCCCCCGGACCTTTGATGTAACCAATGGGAGGAAGAAGAGGAGGACGT **GAA**AGGACCTGG
AAAAACGGATAAAGGCGAGCACTGTCAGGAGCGCAGAGATCAGCCCTACTAGATGCAGAGAACCCGCAGAGCTGC
ATTGACTACCAGATTTATTTTTTAAACCAGAAAATGTTTTAAATTTATAATTCCATATTTATAATGTTGGCCACA
ACATTATGATTATTCTTTCTCTGTACTTTAGTATTTTTACCATTGTGTAAGAAACATTAAACAAGTTAAATGG
TA

WO 2004/030615

PCT/US2003/028547

527/6881
FIGURE 491

MGVYGQESGGFSGLGENRSMSPDNWGRGRGGFDRGGMSRGGRRGGCGGMSGAGEQVGFNKPGGPMDEGPDLDLG
PPVDPDESDNSAIYVQGLNDNVTLDDLVDFFKQCGVVKMNRTEQPMIHTYLDKETRKPKGDATVSCEDSPTAK
AAVEWFDGKDFQGSKLKVS LARKRPPVNSMQGGMPPEHGRGMPPPLCGGPGGPGSPGGPMGHMGGRRGGDRGGLPP
RGPQGSRGNTSGGGNVQHQAQDRQCPNPGCGNQNFARWTESNKCKAPKPEGFLPPFFPPPGGDHGRGGPGGMWGG
RGGLMDHGGPGGMFRGGCGRDRSGFCGGWAWTEVALVEEDKVALGGPRTFDVTNGRKKRRT

WO 2004/030615

PCT/US2003/028547

528/6881
FIGURE 492

AACGAGGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTAC
AGTGCTTACAACACCCAGCCCACTCAAGGATATGCACAGCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGG
TTATACTACTCCAAGTCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCAC
CACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATATGGCACTCAGCCTGCTTATCCAGC
TTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAAATGGAAACAAGCCCACTGAGACTAGTCAACC
TCAATCTAGCACAGGGGGTTACAACCAGCCAGCCTAGGATATGGACAGAGTAACTGCAGTTATCCCCAGGTACC
TGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCCTACCCCTCCTACCAGCTATTCTCTACACAGCCAAC
TAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGAAACCGAGCAGCTATGGACAGCAGAGTAGCTA
TGGTCAACAAAGCAGCTATGGGCAGCTGCCTCCCACTAGTTACCCACCCCAAACCTTGATCCTACAGCCAAGCTCC
AAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCTGACAGGACCACCCCAGTAGCATGGG
TGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACTAGGAGAGAACCGGAGCATGAGTGGCCCTGATAACTGGGG
CAGGGGAAGAGGGGGATTG

WO 2004/030615

PCT/US2003/028547

529/6881
FIGURE 493

AACGAGGAGGAAGGAGAGAAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTAC
AGTGCTTACAACACCCAGCCCCTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACC
TATGGACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACT
TCTTATGGACAGCCTCCCACTGGTTATACTACTCCAAGTGCACCCAGGCATACAGCCAGCCTGTCCAGGGGTAT
GGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATAT
GGCACTCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAC
AAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCACCAAGCTGGAGACAGGCAGTGT
CCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGAGCAACAAGTGTAAGGCTCCAAAGCCTGAA
GGCTTCCTCCCGCCACCCTTCCCACCCCGGGTGGTGATCATGGCAGAGGTGGCCCTGGTGGCATGTGGGGAGGA
AGAGGTGGC

WO 2004/030615

PCT/US2003/028547

530/6881
FIGURE 494

GGAGGAAGGAGAGAAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGGCTACAGTGC
TTACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGG
ACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACTTCTTA
TGGACAGCCTCCCACTGGTTATACTACTCCAAGTGGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCAC
TGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATATGGCAC
TCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAACAAGCC
CACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAACTG
CAGTTATCCCCAGGTACCTGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCCTACCCCTCCTACCAGCTA
TTCCTCTACACAGCCAACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAGCTGCCTCCAC
TAGTTACCCACCCCAAACCTTGATCCTACAGCCAAGCTCCAAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCA
GCAGAGTTTATTCTGACAGGACCACCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACT
AGGAGAGAACCGGAGCATGAGTGGCCCTGAT

WO 2004/030615

PCT/US2003/028547

531/6881
FIGURE 495

TTTCCGGTGCTATGCCCCGGAAGCGGAAGTGCATCTTCGGGCTGTCAGAGTTGGTCTGTTACTCGGTGGTGGCG
GAGTCTACGGAAGCCGTTTTTCGCTTCACTTTTCCTGGCTGTAGAGCGCTTTCCCCCTGGCGGGTGAGAGTGCAGA
GACGAAGGTGCGAGATGAGCACTATGTTTCGCGGACACTCTCCTCATCGTTTTTATCTCTGTGTGCACGGCTCTGC
TCGCAGAGGGCATAACCTGGGTCCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGGAAAAAC
AGAGTAAAAAATTGGAAGAAGAAGGAAACAATAACAGAGTCAGCTGGTCTCTATCAATGGTTCGAATGAAAT
CCATGTTTGCTATTGGCTTTTGTCTTACTGCCCTAATGGGAATGTTCAATTCCATATTTGATGGTAGAGTGGTGG
CAAAGCTTCCTTTTACCCCTCTTTCTTACATCCAAGGACTGTCTCATCGAAATCTGCTGGGAGATGACACCACAG
ACTGTTCCCTTCATTTTCTGTATATTCTCTGTACTATGTCTGATTTCGACAGAACATTCAGAAGATTCTCGGCCTTG
CCCCCTTCACGAGCCGCCACCAAGCAGGCAGGTGGATTTCTTGGCCACCACCTCCTTCTGGGAAGTTCTCTTGAA
CTCAAGAACTCTTTATTTTCTATCATTCTTTCTAGACACACACACATCAGACTGGCAACTGTTTTGTAGCAAGAG
CCATAGGTAGCCTTACTACTTGGGCCTCTTTCTAGTTTTGAATTATTTCTAAGCCTTTTGGGTATGATTAGAGTG
AAAATGGCAGCCAGCAAACCTTGATAGTGCTTTTGGTCTAGATGATTTTTATCAAATAAGTGGATTGATTAGTTA
AGTTCAGGTAATGTTTATGTAATGAAAAACAAATAGCATCCTTCTTGTCTTCAATTTACATAAGTATTTTCTGTGGG
ACCGACTCTCAAGGCACTGTGTATGCCCTGCAAGTTGGCTGTCTATGAGCATTTAGAGATTTAGAAGAAAAATTT
ACAAGCCAAATACATGACATAAGATCAATAAAGAGGCCAAATTTTTAGCTGTTTTATGTACAAGGAGAGATCTGT
TTCATTTTGTCTTGGCGTATTTCTAGATATAAGTTTTAGCATGGGCCAGGAAGGACTAAAATAAAAGTTTTTAAG
GTACTG

WO 2004/030615

PCT/US2003/028547

532/6881
FIGURE 496

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGRQKKKKIERQEEK
LKNNNRDLMSVRMKSMFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQGLSHRNLLGDDTTDCSFIFLYILC
TMSIRQNIQKILGLAPSRATKQAGGFLGPPPPSGKFS

WO 2004/030615

PCT/US2003/028547

533/6881
FIGURE 497

AGACAGTTTTGAAGTTTTCAAAGACTGGCTCTGCTGTTAAGAAGTTGTACTTAAAGCGGAGGAGCTAAGCCACCT
GCCAAAATGTGCAAAGGACTTGCAGCTTTGCCCCACTCATGCCTGGAAAGGGCCAAGGAGATTAAGATCAAGTTG
GGAATTCCTCCTCCAGAAGCCAGACTCAGTTGGTGACCTTGTCATTCCGTACAATGAGAAGCCAGAGAAACCAGCC
AAGACCCAGAAAACCTCGCTGGACGAGGCCCTGCAGTGGCGTGATTCCCTGGACAAACTCCTGCAGAACAACTAT
GGACTTGCCAGTTTCAAAGTTTTCTGAAGTCTGAATTCAGTGAGGAAAACCTTGAGTTCTGGATTGCCTGTGAG
GATTACAAGAAGATCAAGTCCCCTGCCAAGATGGCTGAGAAGGCCAAAGCAAATTTATGAAGAATTCATTCAAACG
GAGGCTCCTAAAGAGGTGAATATTGACCACTTCACTAAGGACATCACAAATGAAGAACCTGGTGGAACCTTCCCTG
AGCAGCTTTGACATGGCCCAGAAAAGAATCCATGCCCTGATGGAAAAGGATTCTCTGCCTCGCTTTGTGCGCTCT
GAGTTTTATCAGGAGTTAATCAAGTAGTAATTTAGCCAGGCTATGAAATCATCCTGTGAGTTATTTCCCTCCATAA
TAACCCTGCATTTCCCATTAATCTACATATCTTCCACAGCAGCTTTGCTCAGTGATACCCACATGGGAAAAATC
CCAGGGGATGTTGCTTACTCTTTTTGCCCACACTGCTTTGGATACTTATCTACTGTCCGAAGGCCTTCTTTCCCC
ACTCAATTCCTTCCCTGCCCTGTTATTAATTAAGATATCTTCAGCTTGTAGTCAGACCCAATCAGAATCACAGAAAA
ATCCTGCCTAAGGCAAAGAAATATAAGACAAGACTATGATATCAATGAATGTGGGTAAAGTAATAGATTTCCAGC
TAAATTGGTCTAAAAAAGAATATTAAGTGTGGACAGACCTATTTCAAAGGAGCTTAATTGATCTCACTTGTTTTA
GTTCTGATCCAGGGAGATCACCCCTCTAATTATTTCTGAACCTTGGTTAATAAAAGTTTATAAGATTTTATGAAG
CAGCCACTGTATGATATTTTAAGCAAATATGTTATTTAAATATTTGATCCTTCCCTTGGACCACCTTCATGTTAG
TTGGGTATTATAAATAAGAGATACAACCATGAATATATTATGTTTATACAAAATCAATCTGAACACAATTCATAA
AGATTTCTCTTTTATACCTTCCCTCACTGGCCCCCTCCACCTGCCCATAGTCACCAAATTCTGTTTTAAATCAATG
ACCTAAGATCAACAATGAAGTATTTTATAAATGTATTTATGCTGCTAGACTGTGGGTCAAATGTTTCCATTTTCA
AATTATTTAGAATTCTTATGAGTTTAAATTTGTAAATTTCTAAATCCAATCATGTAAATGAAACTGTTGCTCC
ATTGGAGTAGTCTCCACCTAAATATCAAGATGGCTATATGCTAAAAAGAGAAAATATGGTCAAGTCTAAATGG
CTAATTGTCCTATGATGCTATTATCATAGACTAATGACATTTATCTTCAAAACACCAAATTGTCTTTAGAAAAAT
TAATGTGATTACAGGTAGAGGCCTTCTAGGTGAGACACTTTTAAGGTACACTGCATTTTGCAGAAAAAATAA
AAAAGTAATCTTTTAGCAACCCAGTATTCCTTCACTATTTTCGCTTCCCTGCATTAGCAAATTTTACTTACAGTCA
AAAGTGCAGATTTATACTCCTGACGTGTCTCATTACAGCTAAATAATAGGCCATAGGACTTTTGGTAGGTTTAA
ACTTTTAATTCTGTATTTTATGATTATAAGTCTTGCTAGAATTTTTCTAATCTTTAGTAGATTTGATTAAATAA
TGATTCACAGAATTTAGTAACAGAATCAAATAAGCCATGTATGAGGGTAATCGAGATGAGGATATTAACCTCAA
AGAAATAGGGTGATTTTTAAAGGATTAATAAAATCTGAAATGTTAAGTAG

WO 2004/030615

PCT/US2003/028547

534/6881
FIGURE 498

MCKGLAALPHSCLERAKEIKIKLGILLQKPD SVGDLVIPYNEKPEKPAKTQKTS LDEALQWRDSL DKLLQNNYGL
ASFKSFLKSEFSEENLEFWIACEDYKKIKSPAKMAEKAKQIYEEFIQTEAPKEVNIDHFTKDITMKNLVEPSLSS
FDMAQKRIHALMEKDSLPRFVRSEFYQELIK

WO 2004/030615

PCT/US2003/028547

535/6881
FIGURE 499

GACACCTTTTAAAATGCAGAACTAACTGAGGCATTTTCAGTAACTTTGCTTTCAAATCAATAAAGTCAAATGTATG
GAAACATTTTGTGCCCTACTCTCCATACCCTGTGTACTCAAATTTCTCTACTGTATGAATTATGCTTTAAGTAGAA
TTCAGTGCCAAGGAGAACTTGGTGAAATAAATTATTTTAAATTTTTTTTTTATCCTTTACAAAGCCATGGATTTTA
TTTGGTTGATGTGTGCTCTGTACACAAGCCATTTCAATAGGATGGAGCTGTTAATTATTTTCCAAAGAGTAATAG
ACATGCAAAAGTTTCAATATAAACTGGGCCATTAACAAATAAATTAATAAACTAATAAGCATTCCCTTCTAGGTT
TTTGCCAACTGCCTATCCAATAACAAATTTGAGAATCGTTGAAAAAGCTAGTTATATTTTCCAGAGAAATGATTTT
CATTATTGAACTGTTCTCCCTAGCAGGCCATTTTCCCTTTTTCTGGGAGTTTAGCAAGTTTAGGAGAGAATAG
TCATGAAAAGAAAGGGAAGAAAGGGGAGAAGGGAAGAGGTTAAAAAGTAAGTGCTCAGACCTATGAACGTAATCC
CTTTGCTAGAAATATTTAAGAGCAGCTCAGCTTGGTTGAACTGAGTTTTGTCTCTCCATATTTGCAGGAAGG
TATTTTCTGACTTGCAATGCAGCTAGATGTAAATTTTATTTTATCATCCTAGAAAGCCTTGACTAGAAAAATGA
ATAAATATTGAGGTTTCTGTCCATATCTGGCTTGCATGTGCCAGAAAGCAGAGAATAGAAAATGTAATCTCCA
ACATCCAAGCATCGAAACCAAGGGGTAGGCAATTCTATGTAGGTTTTGGACATGAAGTTTGGTGCATCTTGGTT
TATGCTGGCTCAACTGCTATTAAACCTCTCTGGCTTATAGTCTCTTCATTCTATTAGACAAGCACGTATCGAACA
CTTGCTTCGCACAAGGCTCTTTAGTTAACAATTTAGCAGCTACTGTTTGTGTTAAACACACTTTTCACCAAATAG
GTTCTGAGGCAACGAGAGCAATGACTATTTAAAGAAAGGCTTTCCCAGCATCACTTACACATCCCAAACTAAA
AAGATCAACTCTTCCAAGTGAAGAAAGACTCCTGGCTTTGAATGGAACTTACAGCAGAGAGTCACAGGCCACGG
CAACAACAACGACAACAACAACATTTGGAATATTATTCTCAACTCACGTTTTAATAATACATCTTAATTATTTT
TCTAGTAGAGAACTACAAATCAGCCTCTTCAACATTTATATACAGTTTAATAAGCCTCTTGCAAGTTACTTGTT
CTCTCACCTGAGGTATTTTTTCTCCCACTTGCCCTGTTCTCCCTTCTCTCTCCCTTTGCAAGAGGAA
ATATTTAACATATTTGGGTCCAATTCATAATGTAATAATTAATACATTAAAAGCATTTAACCTCCTTTCTAGA
AAAATGCACAGGCTAAGGCATAGACAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGGAGACAAGCAATCTGA
ATAAATATTTGCCAAAAGTTCTTTTATGTCATATAGTGTGAGGATTTGAAGGAGCTATTTTTTTTAAATGTTGCA
ACTAGCAACTCATCTTCGGAAGACACAGCCAGGAGAATGAAGTAGAAGTGAAAGGTTTATAAATCCATTTGTAAG
CATTTATCCCATATATTTTAAATTCAAGAAAAATTGTGTTTATCTTTAGAATTTTGATTCAATACITTTATGTAC
TATGTGACTCATGCTTCTGGATAAATAAAGCACCAAAATATGTATCTGTAACCACAATCACACATATTATATTA
TATATATCTATATAACAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

536/6881
FIGURE 500

MYGNILCPTLHTLCTQILYCMNYALSRIQCQGEINYNFNFFILYKAMDFIWLMCALYTSHFNRMELLIIFQR
VIDMQKFQ

WO 2004/030615

PCT/US2003/028547

537/6881
FIGURE 501

AGCGGGCCCTGCAGAGGCAGGTCCACCTGAGAGGCCGGCCGGCCCTCCCAGCCCCTGTTCATCCGGGGCATCACCT
ACTATAAAGCCAAGGTCTCTGAAGAAGAGAATGACATTGAAGAGCAGCAAGATGAGTTTTTCAGCGGTGACAATG
GAGTGGATTTTGCTGATTGAAGATCAGCTCCTGAGACACAACGGCCTGATGACCAGTGTACCCGGAGGCCTGCAG
CCACCCGTCAGGGACACAGCACTGCTGTGACAAGCGACCTGAACGCTCGGACCGCACCCCTGGTCCCTCAGCACTGC
CACAGCCCTCGACCTCAGATCCCAGCATCGCCAACCATGCCTCAGTGGGACCAACACTCCAAACAACCTCGGTGT
CTCCAGATCCCACAAGGGAGTCAGTCTGTCAGCCTTCTCCTCAGGTACCAGCCACCCTGTGGCCACACAGCCA
CCCAGCAACCAGCAGCCCCAGCTCCTCCGGCAGTGTCTCCAGGGAGGCATTGATGGAAGCTATGCACACAGTCC
CAGTGCCTCCCACCACAGTCAGAACAGACTCGCTGGGGAAGATGCTCCTGCTGGGTGGGGAACAACCCCTGCCA
GCCCCACGCTGAGCCCCGAAGAAGAAGATGACATCCGGAATGTCATAGGAAGGTGCAAGGACACTCTCTCCACAA
TCACGGGGCCGACCACCCAGAACACATATGGGCGGAATGAAGGGGCCTGGATGAAGGACCCCTGGCCAAGGATG
AGCGGATTTACGTAACCAACTATTACTACGGCAACACCCCTGGTAGAGTTCCGGAACCTGGAGAAGTTCAAAACAAG
GTCGCTGGAGCAATTCTTACAAGCTCCCGTACAGCTGGATCGGCACAGGCCACGTGGTATACAATGGCGCCTTCT
ACTACAATCGCGCCTTACCCGCAACATCATCAAGTACGACCTGAAGCAGCGCTACGTGGCTGCCTGGGCCATGC
TGCTATGACGTGGCCTACGAGGAGGCCACCCCTGGCGATGGCAGGGCCACTCAGACGTGGACTTTGCTGTGGACG
AGAATGGCCTATGGCTCATCTACCCGGCCCTGGACGATGAGGGCTTCAGCCAGGAGGTGATTGTCTGTAGCAAGC
TCAATGCCGCGGACCTGAGCACACAGAAGGAGACCACATGGCGCACGGGGCTCCGGAGGAATTTCTACGGCAACT
GCTTCGTATCTGTGGGGTGTGTATGCCGTGGATAGCTACAACCAGCGGAATGCCAACATCTCCTACGCTTTTCG
ACACCCACACCAACACACAGATCGTCCCCAGGCTGCTGTTTCGAGAATGAGTATTCCTATACGACCCAGATAGACT
ACAACCCCAAGGACCGCCTGCTCTATGCCTGGGACAATGGCCACCAGGTCACTTACCATGTCTCTTTGCCTACT
GACACCCCTTGTCCCCACAAGCAGAAGCACAGAGGGGTCACTAGCACCTTGTGTGTATGTGTGTGCGCGCACGTGT
GTGTAGGTGGGTATGTGTTGTTTAAAAATATATATATTTTGTATAATATTGCAAATGTAAATGACAATTTGGG
TCTATTTTTTTATATGGATTGTAGATCAATCCATACGTGTATGTGCTGGTCTCATCCTCCCCAGTTTATATTTT
GTGCAAAATGAACCTTCTCCTTTTGACCAGTAACCACTTCTTCAAGCCTTCAGCCCTCCAGCTCCAAGTCTCAG
ATCTCGACCATTGAAAAGGTTTCTTCTATCTGGGTCTTGCAGGAGGCAGGCAACACCAGGAGCAGAAATGAAAGAG
GCAAGAAAGAAGTGCTATGTGGCGAGAAAAAAGTTTTAATGTATTGGAGAAGTTTTAAAAAACCAGAAAAACG
CTTTTTTTTTTTAATAAAGAAGAAATTTAAAATC

WO 2004/030615

PCT/US2003/028547

538/6881
FIGURE 502

MTSVTRRPAATRQGHSTAVTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPDPTRESVLQPSPOV
PATTVAHTATQQPAAPAPPAVSPREALMEAMHTVPVPPTTVRTDSLKGKAPAGWGTPASPTLSPEEEDDIRNVI
GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYYGNTLVEFRNLENFKQGRWSNSYKLPYSWIGT
GHVVYNGAFYYNRAFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFAVDENGWLWIYPALDDEGF
SQEVIVLSKLNAADLSTQKETTWRITGLRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHNTQIVPRLLFEN
EYSYTTQIDYNPKDRLLYAWDNHGHQVITYHVIFAY

WO 2004/030615

PCT/US2003/028547

539/6881
FIGURE 503

GGCACGAGGGATGCAAGGAGATGAGACAGTTAGATTTACTTCCTCTTTCTAATCTGAGAGGTTTCATGTTGAAG
AAAATCAGTGTGGGGTTGCAGGAGACCTAAACACAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCC
CTCTACCTTTCCCTTGGTGTGCTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAG
GGACCTGTCTGCACTGAGGAGAGCAGTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCCAG
GTCAAGGCCTACACTTTTCAGTGAACCTTCCACCTGATTGTGTCTATGACTGGCTGATCCTCCAAGGTCCAGCC
AAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGCCCTGGCAAGACTGGCCACTGACTCAGGTGACC
TTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCA
GACAGCGGGCACTACCACTGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTG
GCTATCACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCTCAGCTGAACCCCAAGCAGGAAGC
CCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGCTCCTCTTCTCCTTCTACAAG
GATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATCCAGATCCCCACAGCTTCAGAAGATCACTCCGGG
TCATACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAG
GGTGCTTCCAGCTCTGCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCT
GAGGAGGCCCTGGGCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGG
ATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCTCCTCGGT
CACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAG
TAAACAGTTCATCCATGATCTCACTTAACACCCCAATAAATCTGATTCTTTATTTTCTTCTCCTGTCTGCACA
TATGCATAAGTACTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTTA
TATAAAGTGAGAAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCA
GGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATACAGCAG
TCTCAACTGGGGGCAATTTTGGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTTTGGTCATTATACCTGGG
GGGTGGGGGATGGTGGGATGTGTGTGCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTA
TAATGCACAGGGCAGTACCCCAACAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAACCC
CAGCCTAATGAAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCT
CATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGTATGGTCTGTTCTTTAGTTCTAGTTTGTATCCC
CTCAAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAGAAGTGGGCCTTTGGGAAGTGATTAG
ATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCTT
CCACCATATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAACACCGACTCTG
TCGTTGCCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGTTGTTTGTAAAAA
AAAAAA

WO 2004/030615

PCT/US2003/028547

540/6881
FIGURE 504

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQVKAYTFSEPFHLIV
SYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSP
GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEF
QIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSAAPP TLNPAFQKSAAPGTAPEEAPGPLPPPPTPS
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

WO 2004/030615

PCT/US2003/028547

541/6881
FIGURE 505

AAGCAGTGGTATCAACGCAGAGTGCCCATACGGCCGGGGGTGGCATCATGTGGCAGCTGCTCCTCCCAACTGCT
CTGCTACTTCTAGTTTCAGCTGGCATGCGGACTGAAGATCTCCCAAAGGCTGTGGTGTTCCTGGAGCCTCAATGG
TACAGGGTGCTCGAGAAGGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAGGACAATTCCACACAG
TGGTTTCACAATGAGAGCCTCATCTCAAGCCAGGCCTCGAGCTACTTCATTGACGCTGCCACAGTCGACGACAGT
GGAGAGTACAGGTGCCAGACAAACCTCTCCACCCTCAGTGACCCGGTGCAGCTAGAAGTCCATATCGGCTGGCTG
TTGCTCCAGGCCCCCTCGGTGGGTGTTCAAGGAGGAAGACCCTATTACCTGAGGTGTCACAGCTGGAAGAACACT
GCTCTGCATAAGGTACATATTTACAGAATGGCAAAGGCAGGAAGTATTTTCATCATAATTCTGACTTCTACATT
CCAAAAGCCACACTCAAAGACAGCGGCTCCTACTTCTGCAGGGGGCTTGTTGGGAGTAAAAATGTGTCTTCAGAG
ACTGTGAACATCACCATCACTCAAGGTTTGGCAGTGTCAACCATCTCATCATTCTTTCCACCTGGGTACCAAGTC
TCTTTCTGCTTGGTGATGGTACTCCTTTTTGTCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAACATTCTGA
AGCTCAACAAGAGACTGGAAGGACCATAAAATTTAAATGGAGAAAGGACCCTCAAGACAAATGACCCCCATCCCAT
GGGGGTAATAAGAGCAGTAGCAGCAGCATCTCTGAACATTTCTCTGGATTGCAACCCTATCATCCTCAGGCCTC
TCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCCTTATCCAACCTCTCGACTTTTCCTTGGTCTCCAGT
GGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGTAGCTGCATTCTAGAAATTGAAGTTTCAG
AGCTACACAAACACTTTTTCTGTCCCAACCGTTCCTCACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

542/6881
FIGURE 506

MWQLLLPTALLLLVSAGMRTE¹DLPKAVVFLEPQWYRVLEKDSVTLKCQGAYSPEDNSTQWFHNESLISSQASSYF
IDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKGRKY
FHHNSDFYIPKATLKDSGSYFCRGLVGSKNVSSETVNITITQGLAVSTISSFFPPGYQVSFCLVMVLLFAVDTGL
YFSVKTNIRSSTRDWKDHKFKWRKDPQDK

WO 2004/030615

PCT/US2003/028547

543/6881
FIGURE 507

ATGGCGGACGGGACCTGTCAGGACGTGGCCATCGTGGGCTACAAGGACTCGCCCTCCATCTGGGCCGCGTCCCC
GGGAAAACCTTCGCCAACATCGCGCCAGCTGAGGTTGGTGTCTCTGGCTGGCAAAGACAGGTCAAGATGGGGAATT
TTGCATGGATCTTCGTATACCAAGAGTACCGGTGGAGCCCCACCTTCAATGTCACTGTCACCAAGACTGACAAG
ACGCTAGTCCTGCTGATGGGCAAAGAAGGTGTCCACGGTGGTTTGATCAACAAGAAATGTTATGAAATGGCCTCC
CACCTTCGGCGTTCCCACTTGA

WO 2004/030615

PCT/US2003/028547

544/6881
FIGURE 508

MADGTCQDVAIVGYKDSPSIWAAVPGKTFANIAPAEVGVLGKDRSRWGILHGSSYTKSTGGAPTFFNVTVTKTDK
TLVLLMGKEGVHGGGLINKKCYEMASHLRRSQY

WO 2004/030615

PCT/US2003/028547

545/6881
FIGURE 509

ATGGTTGTAGGATTCACTGAGTTTGAATCCTTCCACCCAGGCCTTGCTGCTGCAGCCTCTGCCAGAGCCAGCTCC
TGGTGGACCCATGTGGAAATGGGACCTCCAGATCCCATCCTGGGAGTCACTGAAGCCTTTAAGAGGGACATCAAT
AGCAAAAAGATGAATCTGGGAGTTGGGATGATAATGGGAAGCCGCTTTGCCAGTGGTGATGGTGATAAGGATGCC
TGGGCTCTGCACCACTTCATCGAACAGGGCATTAAATGTTTGTCTCTGCCAATCATATGCCAAGAACATGGGCTTA
TATGGTGAGCATGTAGGAGCCTTCACTGTGGTCTGCAAAGATGCAGATGAAGCCAAAAGGGTAGAGTCACAGTTG
AAGATCTTGATTAGTCCCATGTATTCCAACCTCTCCCTCAATGGGGCCCAGATTGCTTCTACCATTCCAAACACC
CCAGTTGGTTTGAAGGTCTGGGTCTGAGGAGCCTACATGATCATCCTCAGGTTATGAGTGACGAGAAAGAGACA
ACACTGAGAGCAGTGGCTGTCAAGTACTGGATCAGAGTCCGGCTGTGCCACTTCCTTGAAACATTTCATGTCTCCG
GACCTTACTGGCTGGAAAAAACTGCAGCAGGAAGATGGCCTTACCTCACTTCTAGCTTCCAAGTCTCACAAGAGA
GCACAGGCAGAACCGAAGCCACATCCAGGACCTGGGCTGAGAACATCTGGCACATGGAGCCTGTAG

WO 2004/030615

PCT/US2003/028547

546/6881
FIGURE 510

MVVGFTFESFHPGLAAAASARASSWTHVEMGPPDPILGVTEAFKRDINSKKMNLGVGMIMGSRFASGDGDKDA
WALHHFIEQGINVCLCQSYAKNMGLYGEHVGAFTVVCKDADEAKRVESQLKILISPMYSNSPLNGAQIASTIPNT
PVGLKVWVMGGLHDHPQVMSDEKETTLRAVAVKYWIRVRLCHFLETFMSPDLTGWKKLQQEDGLTSLLASKSHKR
AQAEPKPHPGPGLRTSGTWSL

WO 2004/030615

PCT/US2003/028547

547/6881
FIGURE 511

CGGTTGCTTGCTGTCCCAGCGGCGCCCCCTCATCACCGTCGCCATGCCCCGAGGTCTGCTTCTCGGGGACGTGGC
TCCCAACTTTGAGGCCAATACCACCGTCGGCCGCATCCGTTTCCACGACTTCTGGGAGACTCATGGGGCATTCT
CTTCTCCCACCCTCGGGACTTTACCCAGTGTGCACCACAGAGCTTGGCAGAGCTGCAAAGCTGGCACCAGAATT
TGCCAAGAGGAATGTTAAGTTGATTGCCCTTTCAATAGACAGTGTGAGGACCATCTTGCCCTGGAGCAAGGATAT
CAATGCTTACAATTGTGAAGAGCCACAGAAAAGTTACCTTTTCCCATCATCGATGATAGGAATCGGGAGCTTGC
CATCCTGTTGGGCATGCTGGATCCAGCAGAGAAGGATGAAAAGGGCATGCCTGTGACAGCTCGTGTGGTGTGTTGT
TTTTGGTCTGTATAAGAAGCTGAAGCTGTCTATCCTCTACCCAGCTACCACTGGCAGGAACCTTTGATGAGATTCT
CAGGGTAGTCATCTCTCTCCAGCTGACAGCAGAAAAAGGGTTGCCACCCAGTTGATTGGAAGGATGGGGATAG
TGTGATGGTCCTTCCAACCATCCCTGAAGAAGAAGCCAAAAAAGCTTTTCCGAAAGGAGTCTTCACCAAAGAGCT
CCCATCTGGCAAGAAATACCTCCGCTACACACCCAGCCTTAAAGTCTCTTGGAGAAGTTGGTGTGTGAGCCAGA
GGATGTCAGCTGCCAATTGTGTTTTCTGCAGCAATTCCATAAACACATCCTGGTGTATCACAGCCAAGGTTTT
TAGGTTGCTATACCAATGGCTTATTAAATGAAAATGGCACTAAAAGTTTCTTGAGATTCTTTATACTCTCTGCCT
TCAGCAATCAATTCCATTACATACATCAGCACTCTGCTGGTTCTGTTTGAAATATGTTCTGTATTTAAACTCAA
TCTTGTTGGATCTCTGCAGGGCTTGTGACCAATGAAGTCATATTTGTTGATGGTTGACAAAGCTTGCTTCACTCC
ATCAGAGAATGACTATCAATTTTTTTTTAACTGTCCTATCACGTCCTCTCCTGTCACCCATTTTGAAGAGTGGCA
GAACTTGAAGTTCAACTTCCTCTGTAAATATCCAAGTATAAAGCCAGGAACCTCTAGAATAACCCAGATGCGCT
TTAATTTTTTTTTAATATGTTTTGATCACAGAACTTCTAGAATAACCCAGATGCTCTTTCATATTCTTTAATACA
TCTTGATCACAGCTGGGGGAAAAAAGCTTTTTAATTCTGTACCTTCCTAGTAGATAAGTGAAGAGCAGGGAAAG
AGACCTTTAAATATTTTGCTATAAAAAAATTTGTGATAAGTTTCTATCAAATGGGGAGATTGCAGAAAAGGCTT
CCCTTGGCTCCCAAGGAGGTGTAGCAGGTGTGAGCAATATTAGTGCCATGTGCCTTTCACACAGGGTTTGCATTT
ATCAGTCTGTTTTCCGATGATGTGTACATGAAAGAGTACACCATGTGAAGAGAAGAGAGAATGATTGAAAATGTT
TTAGTATAGAACTCTTCTTGCAAGTGGGTTGCTATTTTCTAGATTTTACTTTTTAGGGAACAAAATAAAATCCTTT
GTT

WO 2004/030615

PCT/US2003/028547

548/6881
FIGURE 512

MPGGLLLGDVAPNFEANTTVGRIRFHDFLGDSWGILFSHPRDFTPVCTTELGRAAKLAPEFAKRNVKLIALSIDS
VEDHLAWSKDINAYNCEEPTEKLPFFIIDDRNRELAILLGMLDPAEKDEKGMPTARVVFVFGPDKKLKLSILYP
ATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMVLPTIPEEEAKKLFPKGVTKELP SGKKYLRYTPQP

WO 2004/030615

PCT/US2003/028547

549/6881
FIGURE 513

AGAGACCGTCCGAGGTAATTGTCTGCCACGAGTGCACATTCTGAAAACAGGAGATTTTAGTTCCTAAAAATGGGA
AGAACCTACATTGTAGAAGAGACTGTTGGCCAGTATCTTTCAAACATAAATCTCCAAGGAAAGGCTTTTGTCTCT
GGCCTTTTAATAGGACAGTGTTCGTACAAAAGGATTATGTGATTCTTGCCACTAGAACGCCACCCAAAGAGGAG
CAAAGTGAGAACCTCAAACATCCCAAAGCTAAGTTGGATAACTTGGATGAAGAATGGGCCACAGAACATGCCTGC
CAGGTATCCAGAATGCTACCAGGGGGACTTTTAGTTCTTGGAGTATTTATTATTACTACTTTAGAAGTGGCAAAT
GATTTTCAAATGCCCTGCGTAGACTAATGTTTGTCTGTGGAAAAGTCTATAAATAGAAAGAGATTGTGGAATTTT
ACAGAGGAGGAAGTCTCAGAACGAGTGACACTTCACATTTGTGCTTCTACAAAAAAATATTTTGTGCAACTTAT
GATATCCATGATCCAAAGAGTTTACGCAAGACCAGCAGATTGGAAGTATCAAAGTGGATTATCATCCTCATGGCTT
TCTTTAGAGTGTACAGTTTACATTAATATTACATCCCACTTTCTGCTACTTCTGTGCTAGCTATACTCTGGAGAAA
AATACAAAGAATGGACTTACACGCTGGGCCAAGGAAATAGAAAATGGTGTATTTTATTGATTAAATGGACAAGTTAAA
GATGAAGATTGTGACCTATTAGAAGGACAGAAAAAATCTTCTAGAGGAAATACTCAAGCAACTAGTCATTCTTTT
GATGTCAGAGTGCTAACGCAGTTGCTCCTGAATTCAGACCACAGATCCACAGCCACAGTCCAGATATGTAGCGGT
TCTGTAAACCTTAAGGGTGCTGTGAAATGCAGAGCTTATATCCACAGCAGTAAACCCAAAGTTAAAGATGCTGTG
CAGGCAGTAAAGAGGGATATATTGAACACAGTTGCTGATCGTTGTGAAATGCTATTTGAGGATCTGCTTTTGAAT
GAAATTCAGAAAAAAGATTCTGAAAAAGAGTTCCACGTCCTCCCTTATCGAGTCTTTGTTCCCTTCTCTGGA
TCCACTGTAATGTTGTGTGATTATAAATTTGACGATGAGTCAGCTGAAGAAATCAGGGACCATTTTATGGAGATG
TTGGATCACACAATTCAAATAGAAGATTTGGAAATTGCAGAGGAAACAAACACAGCTTGTATGAGTTCTTCTATG
AATAGTCAAGCTTCATTGGACAACACAGATGATGAACAACCAAAACAACCAATTAAACTACAATGTTATTGAAA
ATTGAGCAAAACATAGGTGTGATTGCAGCATTTACAGTTGCAGTCCTTGCTGCGGGTATCTCCTTTTATTACTTC
AGTGATTAGGGTGAGGCACAAAGAGTTTCTTGATCATCCAGAGAACATTGACAGACAATTATGAATAATAAGAT
GTTAACAATCCATCTGTATTTAAACACTAGCAGCCAGATCTGCTGCCATGATGCCTATTTGGTGTGTTTCTGAT
TAAATGAAATCACAAGCTGCCTTGTTAGCCTGCTTTACATTGTAGGTGGCCCGCATTTCCAGAAATAACGTTA
TGCATCTAGATGGAAGCTGCATGTAACAAATCATTATTATCTATTTTAAAAGCTTCAAATGATGGGATATGAT
CATAGATTTTAGTCTTACTAATCTGAATCACATATTAATCAGGACATTAAAACTTTAACAGAGGCATGATGGCT
CACACGTATAATCCTAATGCTTTGAGAGGCTGAGGTAGGAGCATCACCTGGGGCTGGGAGGGAGTTGGAGACCAG
CCTGGATGACATAATGAGATTCTGTCTCTACTGGAAAAA

WO 2004/030615

PCT/US2003/028547

550/6881
FIGURE 514

MLPGGLLVLGVFIIITTELELANDFQNALRRLMFAVEKSINRKRLWNFTEEEVSERVTLHICASTKKIFCRTYDIHD
PKSSARPADWKYQSGLSLSSWLSLECTVHINIHIPLSATSVSYLEKNTKNGLTRWAKEIENG VYLINGQVKDEDC
DLLEGQKKSSRGNTQATSHSFDVRVLTQLLLNSDHRSTATVQICSGSVNLKGAVKCRAIYHSSKPKVKDAVQAVK
RDI LNTVADRCEMLFEDLLLNEIPEKKDSEKEFHVLPYRVFVPLPGSTVMLCDYKFDDSAEEIRDHFMEMLDHT
IQIEDLEIAEETNTACMSSSMNSQASLDNTDDEQPKQPIKTTMLLKIQQNIGVIAAFTVAVLAAGISFHYFSD

WO 2004/030615

PCT/US2003/028547

551/6881
FIGURE 515A

CGAGACGGAAGCGGGCTGGGAGGCGTCGGCGGCGGCAGCGCACGTGGTGACGTGCGAGGGGGTGC GGCGCGAGCG
GTCGGCGGCGGCGGAGGCAGTGTCTCCCGGTCGCGCGTGGAGGTGGTTCGCTCAGAGCTGCTGGGCGCAGTTTCT
CCGCTGCTGCTTCGGCGCGGCTGTATCGGCGAGCGAGCGAGTTCCCGCGAGTTCTCGGTGGCGCTCCCCCTTCC
TTTCAGTCTCCACGACTGGCCCCCTCGTCCTTCTACTTGACCGCTCCCGTCTTCCGCCGCTTCTGGCGCTTTCC
GTTGGGCGGATTCCCGCCCGCTTCTCTGCTTCCCATCGAAGCTCTAGAAATGAATGTTTCCATCTCTTCAGAG
ATGAACCAGATTATGATGCATCATTATCACAGAAGAAATTCGTGTCTATAGCTTTTAAGGACTTGATTACATCAT
TTTCAAGCCTGATAGTTTGAATCACCATTAGAGCTTAAGACACACCTGCCCTTCATTTCAACCACCTGTCTTCA
TACCTGACGAAGTGCACCTTTTAACACTCCTTTGTCTTGGATTACTTAAGAGTTCCAGAAATACATTGCCA
CCAACAGAGTAGCCAAATTTATAAGGAAAAATGATTCCCAATGGATATTTGATGTTTGAGGATGAAAATTTTATT
GAGTCTTCTGTTGCCAAATTAATGCCCTGAGGAAAAGTGGCCAGTTCTGTGATGTTGACTTCAGGTCTGTGGC
CATGAAATGTTAGCACACAGAGCAGTGCTAGCTTGCTGCAGTCCCTATTTATTTGAAATCTTTAATAGTGATAGT
GATCTCATGGAATTTCTCACGTTAAATTTGATGATCTCAATCCAGAAGCTGTTGAAGTCTTGTGTAATTATGCC
TACACTGCTCAGTTGAAAGCAGATAAGGAATTGGTAAAAGATGTTTATTCTGCAGCAAAAAGCTGAAGATGGAT
CGAGTAAAGCAGGTTTGTGGTGATTATTTACTGTCTAGAATGGATGTTACCAGCTGCATCTCTTACCGAAATTTT
GCAAGTTGTATGGGAGACTCCCGTTTGTGAATAAGGTTGATGCTTATATTCAGGAGCATTGTTACAAATTTCT
GAAGAGGAGGAGTTTCTTAAGCTTCCAAGGCTAAAGTTGGAGGTAATGCTTGAAGATAATGTTTGCTTGCCAGC
AATGGCAAAATTATATACAAAGGTAATCAACTGGGTGCAGCGTAGCATCTGGGAGAATGGAGACAGTCTGGAAGAG
CTGATGGAAGAGGTTCAAACCTTGTACTACTCAGCTGATCACAAGCTGCTTGATGGGAACCTACTAGATGGACAG
GCTGAGGTGTTTGGCAGTGATGATGACCACATTCAGTTTGTGCAGAAAAAGCCACCACGTGAGAATGGCCATAAG
CAGATAAGTAGCAGTTCAACTGGATGTCTCTCTTCTCAAATGCTACAGTACAAAGCCCTAAGCATGAGTGGAAA
ATCGTTGCTTCAGAAAAAGACTTCAAATAACACTTACTTGTGCCTGGCTGTGCTGGATGGTATATTCTGTGTCTATT
TTTCTTCATGGGAGAAAACAGCCACAGAGCTCACCAACAAGTACTCCAAAACCTAAGTAAGAGTTTAAGCTTTGAG
ATGCAACAAGATGAGCTAATCGAAAAGCCCATGTCTCCTATGCAGTACGCACGATCTGGTCTGGGAACAGCAGAG
ATGAATGGCAAACTCATAGCTGCAGGTGGCTATAACAGAGAGGAATGTCTTCGAACAGTCGAATGCTATAATCCA
CATAAGATCACTGGTCCCTTCTTGTCTCCCATGAGAACACCAAGAGCCCGATTTCAAATGGCTGTACTCATGGGC
CAGCTCTATGTGGTAGGTGGATCAAATGGCCACTCAGATGACCTGAGTTGTGGAGAGATGTATGATTCAAACATA
GATGACTGGATTCTGTTCAGAAATGAGAACTAACCGTTGTAATGCAGGAGTGTGTGCTCTGAATGGAAAGTTA
TACATCGTTGGTGGCTCTGATCCATATGGTCAAAAAGGACTGAAAAATTGTGATGTATTTGATCCTGTAAACAAAG
TTGTGGACAAGCTGTGCCCTCTTAACATTCGGAGACACCACTGCTGCAGTCTGTGAGCTTGGTGGTTATTGTAC
ATAATCGGAGGTGCAGAACTTTGGAATTGTCTGAACACAGTAGAACAATACTGAAAATAATACCTGGACT
TTAATTGCACCCATGAATGTGGCTAGGCGAGGAGCTGGAGTGGCTGTTCTTAATGGAAAACCTGTTTGTATGTGGT
GGCTTTGATGGTTCTCATGCCATCAGTTGTGTGGAATGTATGATCCAACCTAGAAATGAATGGAAGATGATGGGA
AATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACACCATTTATGCAGTGGGAGGATTCGAT
GGCAATGAATTTCTGAATACGGTGGAAGTCTATAACCTTGAGTCAAATGAATGGAGCCCCCTATACAAAGATTTTC
CAGTTTAAACAAATTTAAGACCCCTCTCAAACCTAACAGGCTTAGTGATGTAATTATGGTTAGTAGAGGTACACTTG
TGAATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCATACTATTAAC
ATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAGATGAAGGTCTGTTTTGTGTACTTTTAAGACT
TTGGTTATTTTACTTTTTGGAAAAGAATAAACCAAGAATTGATTGGGCACATCATTTCAAGAAGTCCCCCTCTCCT
CCACATTTGTTTTGCCAATTGTCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGG
TTTAAAGATGTAGACAGTTGGGTTTTTTAAGGGCCCTTTTTCAATAACTGGAACACTCTATAACAAAGGATACTT
ATTTAAATAGATGACATTGACTATTTTTGTTTTTATTAAGGAAGCTTACATGCCTACCAATATTTAATCTTTT
ATGATTGCCTTTTTATAACTTTTTATATTCTCAGCAGAGTGCTTTACCAATTGAAGTAAATGTGGCAGGCTGGA
GTTATTGAAGCAGAGTGGCAGTCTTCAGTTTGCAGAGTAGGGGTCTGTCTTTTAACTCTGAGTGCAAACTTCAG
AGTTCTTGCTTGGCTGCAGTTTTTTTCTTCAAGAATGCAGTACTAACATTTATTTGAGTGGAGTTACTGAACA
GTAACATAGCTGTGATTTTTGGTATTTGAAACACTGGTTTTAAATATTTTACTTGTGGAGGTATGTTTTATAT
AGCAAGACATTATATAGCAGTAAAAAATGGTGTTTTATCTCTATATAATTCCTGTTTTTATTATTAACAAAACA
GTCCTAAATAGCAGCCCTCAATTGTGAAAAAATTTACTTTAACTACATTAGGTTGTGAATGCAGGTTTTATCAG
AACTATGTTTTTGTTCAGTTTATCTGTTCATATGGATAAATATTGGTTGGGATGACTTGGTGTCTAATGTGTAGT

WO 2004/030615

PCT/US2003/028547

552/6881

FIGURE 515B

GCTACACACCTAACTTATGGGGCCAAAATAGCATGTCCTAATGCTTGCTGCTGATTAAACACATTAAAGGTACT
TTGCAGGAAATCCTTGCACCATGGGATTAATATCCAATTGCTGCTTGTACACTCATTCACTACTAAAAGTTTGA
GAAATTTTTTTTTTCCAGTAATGAGCTTAAGAAATTTGTGGAAAATAACTCACCTGGCATCTTACATCTGAAATAA
GGAATGATATAAGGTTTTTTTTTCTCACAGAAGATGAAGCACACAGGAACCTAATGGGCCAACTGGGATGAGGTG
ACTATTCTGAGATGACTATTCACTGGCTAACTTGGGTTAGGAAGAAAATAATTAGGTATTTTCTCCAAATGTTCA
CTGGTACTCTGCCACTTTATTTCTCTCATCTGTTACACAAAGAACCACCAGGAAAGCAAATCAGTTTGGTTGGTA
ACTCTGTAATTCCTAACTATCACTGGTTTGGTTCTGGACTAAAACCTACATTGACAGATTGAATTTGCCTAATATG
ATGACTGTTTTTAATATGGATCTGTATGTGTTCTATTTCAGCACAAAGGAAATAAAATTTTAGTTGAGGATTCAGC

WO 2004/030615

PCT/US2003/028547

553/6881
FIGURE 516

MIPNGYLMFEDENFIESSVAKLNALRKSGQFCDVRLQVCGHEMLAHRAVLACCSPYLFEIFNSDSDPHGISHVKF
DDLNPEAVEVLLNYAYTAQLKADKELVKDVYSAAKKLKMDRVKQVCGDYLLSRMDVTSCISYRNFASCMGDSRL
NKVDAYIQEHLQISEEEFLKLPRLKLEVMLEDNVCLPSNGKLYTKVINWVQRSIWENGDSLEELMEEVQTLYY
SADHKLLDGNLLDGQAEVFGSDDDDHIQFVQKKPPRENGHKQISSSTGCLSSPNATVQSPKHEWKIVASEKTSNN
TYLCLAVLDGIFCVIFLHGRNSPQSSPTSTPKLSKSLSFEMQQDELIKPMSPMQYARSGLGTAEEMNGKLIAGG
YNREECLRTVECYNPHTDHWSFLAPMRTPRARFQMAVLMGQLYVVGGSNHGSDDLSCGEMYDSNIDDWIPVPELR
TNRCNAGVCALNGKLYIVGGSDPYGQKGLKNCDFDPVTKLWTSCAPLNIRRHQSACVCELGGYLYIIGGAESWNC
LNTVERYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAISCVEMYDPTREWKMMGNMTSPRSNAG
IATVGNTIYAVGGFDGNEFLNTVEVYNLESNEWSPTYTKIFQF

WO 2004/030615

PCT/US2003/028547

554/6881
FIGURE 517

CCTTTGCCGCTGGTCGGGATTGGGATGTCGAAGAACACAGTGTCTCGGCCCCGCTTCCGGAAGGTGGACGTGGAT
GAATATGACGAGAACAAGTTTCGTGGACGAAGAAGATGGGGGCGACGGCCAGGCCGGGCCCCGACGAGGGCGAGGTG
GACTCCTGCCTGCGGCAAGGAAACATGACAGCTGCCCTACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAG
AGTCAGGCAGTGAAGGACCGGGCAGGCAGCATTGTCTTGAAGGTGCTCATCTCTTTTAAAGCTAATGATATAGAA
AAGGCAGTTCAATCTCTGGACAAGAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCCG
TCTGACAATAGCAGTGTCTATGTTACTGCAATGGCATGAAAAGGCACCTTGCTGCTGGAGGAGTAGGGTCCATTGTT
CGTGTCTTGACTGCAAGAAAACTGTGTAGTCTGGCAGGAAGTGGATTATCTGCCTCGGGAGTGGGAATTGCTGG
TACAAAGACCAAAACAACCAATGCCACCGCTGCCCTGTGGGTAGCATCTGTTTCTCTCAGCTTTGCCCTTCTTGC
TTTTTCATATCTGTAAAGAAAAAATTACATATCAGTTGTCTTTAATGAAAATTGGGATAATATAGAAGAAATT
GTGTTAAATAGAAAGTGTTCATCCTTTCAAACCATTTTCAGTGATGTTTATACCAATCTGTATATAGTATAATT
TACATTCAAGTTTAAATTGTGCAACTTTTAACCCCTGTTGGCTGGTTTTTTGTTCTGTTTTGTTTTGTATTATTTT
TAACTAATACTGAGAGATTTGGTCAGAATTTGAGGCCAGTTTCCTAGCTCATTGCTAGTCAGGAAATGATATTTA
TAAAAAATATGAGAGACTGGCAGCTATTAACATTGCAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATA
TGTTTTTTGGAATAAGTGGTGGGTGAATACCACTGCCAAGTTATAGCTTTGTTTTTGCTTGCCCTCCTGATTATCTG
TACTGTGGGTTTAAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCCCAATTTATTTGTGGTCACCCA
GGGTTTCAGAGCAAGAAGTCTTGCTTTATACAAATGTATCCATAAAATATCAGAGCTTGTTGGGCATGAACATCAA
ACTTTTGTTCCTACTAATATGGCTCTGTTTGGAAAAAAGTGCAAATCAGAAAGAAATGATTTGCAGAAAGAAAGAAA
AACTATGGTGTAATTTAACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTT
AGACATTATGAGGTATACAACCTAGTATTTAAGATACCATTTAATATGCCCCGTAAATGCTTCAGTGTTCTTCAG
GGTAGTTGGGATCTCAAAAGATTTGGTTTCAGATCCAACAAATACACATTCTGTGTTTTAGCTCAGTGTTTTCTA
AAAAAAGAACTGCCACACAGCAAAAAATTGTTTACTTTGTTGGACAAACCAATCAGTTCTCAAAAAATGACCG
GTGCTTATAAAAAAGTTATAAATATCGAGTAGCTCTAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCT
TAGTATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACTGGTGCAGAAATCTATAAACTCTT
TGCTGTTTTTTGATACCTGCTTTTTGTTTCATTTTGTGTTTTGTGTTTTGTAAAAATGATAAACTTCAGAAAAATAAAT
GTCAGTGTTGAATAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

555/6881
FIGURE 518

MSKNTVSSARFRKVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLRQGNMTAALQAALKNPPINTKSQAVKDRA
GSIVLKVLISFKANDIEKAVQSLDKNGVDLLMKYIYKGFESPSDNSSAMLLQWHEKALAAGGVGSIVRVLTARKT
V

WO 2004/030615

PCT/US2003/028547

556/6881
FIGURE 519A

GCCAGGCAGAGTCCTACTATAGGCATGCAGCTCAGCTTGTCCCCTCCAATGAAGCATTGCTGTGAAGTTCCCTTT
CCCAGCTGCCTCCACTAATCTGCAAAAAGCACTTTCTAAAGCACTGGAAGCCGAGATGAGGTGAAAACCAAGTG
GGGTGTTTCTGACTTCATCAAGGCCCTTTATTAAATTCCACGGTCATGTGTACCTGAGTAAGAGCTTGGAAAAGTT
GAGCCCTCTTCGAGAGAAATTGGAAGAACAGTTTAAAGAGGCTGCTATTCCAAAAGCTTTCAACTCTCAGCAGTT
AGTTCAITGTCAGTGTCAATTAACCTGTTTCAACTTCATCACCTTCGTGACTTTAGCAATGAAACCGAGCAGCACAC
TTATAGCCAAGATGAGCAGCTATGTTGGACACAGTTGCTGGCCCTCTTTATGCTCTTTCTTGGCATCCTGTGCAA
GTGTCTCTACAGAATGAGTCTCAGGAGGAGTCTTACAATGCCTATCCTCTTCCAGCAGTCAAGGTCTCCATGGA
CTGGCTAAGACTCAGACCCAGGGTCTTTCAGGAGGCAGTGGTGGATGAAAGACAGTACATTTGGCCCTGGTTGAT
TTCTCTTCTGAATAGTTTCCATCCCCATGAAGAGGACCTCTCAAGTATTAGTGCGACACCACTTCCAGAGGAGTT
TGAATTACAAGGATTTTTGGCATTGAGACCTTCTTTCAGGAACCTTGGATTTTTCCAAAGGTCACCAGGGTATTAC
AGGGGACAAAAGAGGCCAGCAACGACGAATACGACAGCAACGCTTGATCTCTATAGGCAAATGGATTGCTGATAA
TCAGCCAAGGCTGATTCAAGTGTGAAAATGAGGTAGGGAAATTGTTGTTTATCACAGAAATCCCAGAATTAATACT
GGAAGACCCAGTGAAGCCAAAGAGAACCTCATTCTGCAAGAAACATCTGTGATAGAGTCGTGGCTGCAGATGG
GAGCCAGGGCTAAAATCAGTGTCTATCTACAAGCCGAAATTTAAGCAACAACCTGTGACACAGGAGAGAAGCCAGT
GGTTACCTTCAAAGAAAACATTAAGACACGAGAAGTGAACAGAGACCAAGGAAGAAGTTTTCTCCCAAAGAGGT
GAGAAGGGACTATAGCAAAGGAATAACTGTAACATAAGATGGAAGAAGGACAACAACAAGAGGAAAACCTGA
AACCAAGAAATGCACCTTAGAAAAGTTACAGGAAACAGGAAAGCAGAATGTGGCAGTGCAGGTAAAATCCCAGAC
AGAATAAGAAAGACTCCAGTGTCTGAAGCCAGAAAAACACCTGTAACCTCAAACCCCAACTCAAGCAAGTAACCTC
CCAGTTCATCCCCATTATCACCTGGAGCCTTCCCTCTCTTCCAGCAGGCCAGGGTTCCGCCCCCAACATA
TGTTATCCCCCGCCTGTGGCATTCTTCTATGGGCTCAGGTTACACCTTCCAGCTGGTGTCTGTCTCCAGGAAC
CTTTCTTCAGCCTACAGCTCACTCTCCAGCAGGAAACCAGGTGCAAGCTGGGAAACAGTCCACATTCTTACAG
CCAGCAACGGCCCTCTGGACCAGGGCCAATGAACCAGGGACCTCAACAATCACAGCCACCTTCCAGCAACCCCT
TACATCTTTACCAGCTCAGCCAACAGCACAGTCTACAAGCCAGCTGCAGGTTCAAGCTCTAAGCTCAGCAACAACA
ATCCCTTACAAAAGCTGTGCCGGCTTTGGGAAAAGCCCGCCTCACCCTCTGGATTCCAGCAGTATCAACAGGC
AGATGCCTCCAAACAGCTGTGGAATCCCCCTCAGGTTCAAGGCCATTAGGGAATAATTATGCCTGTGAAACAGCC
CTACTACCTTCAGACCCAAGACCCCATAAAACGTTTTGAGCCGTCTATTGCAACCTCCTGTAATGCAGACGAGCC
TCTAGAAAAAAAATGAAGCCTTTTCCCATGGAGCCATATAACCATAATCCCTCAGAAGTCAAGGTCCCAGAATT
CTACTGGGATTCTTCTACAGCATGGCTGATAACAGATCTGTAATGGCACAGCAAGCAACATAGACCGCAGGGG
CAAACGGTCACCAGGAATCTTCCGTCCAGAGCAGATCTGTATCCCAAGATGCCGTTTGAGAAATCCTTATTGGA
GAAGCCCTCAGAGCTCATGTACATTCTCTTTCTGTCCCTCACCAGATTCTCTCTCAATCAGGAAAGATA
CCCAATAATAGTATGTTCAATGAGGTATATGGGAAAACCTGACATCCAGCTCCAAAGCAGAACTCAGTCCCTC
AATGGCCCCCAGGAAACATCTCTGTATTCCCTTTTGAAGGGACTCCGTGGTCTCCATCACTTCTGCCAGTTC
AGATCATTCAACACCAGCCAGCCAGTCTCCTCATTCTCTAACCACAGCAGCTACCCAGCTCTCTTCCACACA
CAACCATAATTCTGTTCCATTCTCCAATTTTGGACCCATTGGGACTCCAGATAACAGGGATAGAAGGACTGCAGA
TCGGTGGAAAACCTGATAAGCCAGCCATGGGTGGGTTTGGCATTGATTATCTCTCAGCAACGTCTCCTCTGAGAG
CAGTTGGCATCAGGCCAGCACTCCGAGTGGCACCTGGACAGGCCATGGCCCTTCCATGGAGGATTCTCTGCTGT
CCTCATGGAAAGCCTAAAGTCTATCTGGTCCAGTTCCATGATGCATCCTGGACCTTCTGCTCTGGAGCAGCTGTT
AATGCAGCAGAAGCAGAAACAGCAACGGGGACAAGGCACCATGAACCCTCCACACTGAGGCCAAAGTGGAACCT
GGGAATGAAGGCTCCATAAACCATGGCATGTTGGGTTTGCAGGACTGGCCACACAGTCCCTTGCAGGTGGCAGC
CCTCTTTTCTGTTTCTCGCTGTCAAGAGGGTGTAAAGTATCCACCAGCCCGCTGAGTGTGCACGAAATGTTTCGCA
GTGCAACAAAAAGAAAAATCCATCAGGAACCTCTCCGTCCCCCGGGGCCCTCCGGAGGGAGAGAGAGAGGAACTG
CTGTTTATCTCACTCAGTTACTTGGTATCACCGCTCTCACCTTCTCCATCGTGCATGTCCCCAGCCACATGGGA
AGTGAAAGCTGAGAAGGGAAGGCAGATGGGAGAAGCCAATGGGAACCTTCTCAGTCTTTTTTCTCTTTGGGGAA
TAAATAGGAATCCATTAATGATTGCTTGGCTGACTGAGAATGTAGTTGAAATTAAACATCTTTTATTATTATTA
CTCTCAGTAGTAAATATCACACTGAATCTTCCATACACAGGTGTGCTTCTAGTCAGTGTGTAGCAAGGAAAGC
CCGTTCACTGCTCTGTGAGAGGTTGGTGGTGACAGGATGGGGAACCGACCTCTTCAGCCAGTGGAAATGTTCC
ATAAGGGAGAGTTCAAGGCCTGTGAGAAGGCTCTGGTAGGCCTTCTCTGGCCAGGAGACTCCAGCAGGGAATGC
CCTTCACTCTGTAGGTGCTCGAGCCCCAATCGAGGATACAGTGTGGGTGGTGGTGGTGGGCTGGACTAGCAGGTA

WO 2004/030615

PCT/US2003/028547

557/6881
FIGURE 519B

GACTGCTGTAGGATTTCAAATTACGTTTTTGTATTCTGTACATTTTACAGTCGCACAGCAAGCAGTCTCACAGAA
GGCAGGCTAGTCCATTACAGCCTGACACGTTCTAATAGGTAGAAGCTTTCAGTGTGGTTATTTTTCTTTGGTT
GGTTTTTGTGCCCCCATTCTACTTCCCACCCTCCTGCCCCATCTCCATCCCTTCTTTTACCCAATGCTGTATGCT
AGTAATTGTTTTTATTCCTAATGTGTGCAACATCACATCTCCCCAAGAAGCAACAGCATGGGGTCCAGCAGTTGG
GGCCCAAAAGACAGTCTGAAGAGGAAGGAAGCAGCAGTATCTGCGTAGCCACAGAGGGCCAGGCCCTGCCCA
GCTGCAGTCTCCCAGCCTCCACTTTTCAGAGTGAAATTCAGGCAGCACGGACATGTGCCCATCAGGCACAGAAGA
AAACACGACGTCGTCCATTTTGGAGAGACGAAAGAAAGGAAAATAAACTCTTTGTATGATATTTATTAGGAGGA
AAGAGGACTGAAAATGTTCTTGTGTAGAAACAGAAGGACAGCATTCTGTAGTCATTTCTGGAAAAGTAATAT
TTTAAGGGGAAATTATGGAAACAATCTAATTGTTCAATTGCTGTGCTAGTGGTAGGGTTTATTTCTGGGAGGTC
TCTCCTTTGTGTGTCTGTATGTTTGTGTACACACACGTGCCCATCTGCTGTCCCAGAGGGGAGGGGTTGTGTGTG
CGAGTGTATGGAGTTAGTGTGGAACCTTAAGAGCTGGAAGACAGCTGTAGAGCAAAGCACATCCAGGAGCCCCAGT
TGTCAGTGCAGTCTGGGCAACCCAGCAATGAAAAGGGGTGAGATAACGCTCATTGCTCTTCAGAGAGAGTGGTT
GGAGCCCCCCCCCGCCCCGTATGCTTACATTATTGCTCTTTTAGTTTGACATGGTGTGTTGGGTTTTGTTTTTTGA
AAGGTCTGAAAAGGTGAAGCCCCCTACCCAATGGCAATATGAAACCTTTTGTGCTTCTCTTCAGCCCCCTCCCTG
TGTCCACCTTTCTCTCTCTTCCCAAGCCTTTTTCTACTACCTTTACCCAGTTTGTGTGTTTGAGCTCTGCATT
CAGGCAGCTGCAACATTCCAGTGTTTGAAGTGTACTGATTCTTGCGCCCTAGACAAGCTAACCCAGGTTTACCAT
CTCACTCCCAGTAATACCCAGCTCCTATCTAAAGCCCCATTCTGCATGAGAATTTGGTGTGTTGGAATGTTTTCTG
ACTCTTGGGGCGGGATTCTCGCCTTATCATCTCACTGTGGAGTAATGAGGGGGAGGAGAATCTTTATCAGAAA
CTGGTTTTGTGTAGTAACTTTCTTTTGTGGTTTTTTGTTTTGTTTTCTGGGTTTTGTTTTTGTCTGT
GCAAGACCTGCAGCTGCTGAAAATCAGCTTTGCCTTTAATTAAACCATGTTCTCTCC

WO 2004/030615

PCT/US2003/028547

558/6881
FIGURE 520

MSFLGILCKCPLQNESQEESYNAYPLPAVKVSMDWLRLRPRVFQEAVVDERQYIWPWLISLLNSFHPHEEDLSSI
SATPLPEEFELQGFLALRPSFRNLDFSKGHQGITGDKEGQRRIRQQRLISIGKWIADNQPRLIQCENEVGKLLF
ITEIPELILEDPSEAKENLILQETSVIESLAADGSPGLKSVLSTSRNLSNNCDTGEKPVVTFKENIKTREVNRDQ
GRSFPPKEVRRDYSKGITVTKNDGKKDNNKRKTETKKCTLEKLQETGKQNVAVQVKSQTELKTPVSEARKTPVT
QTPTQASNSQFIPIHHPGAFPPPLPSRPGFPPPTYVIPPVAFSMGSGYTFFAGVSVPGTFLQPTAHSPAGNQVQA
GKQSHIPYSQQRPSGPGPMNQGPQSQPPSQPLTSLPAQPTAQSTSQQLQVQALTQQQQSPTKAVPALGKSPPHH
SGFQQYQQADASKQLWNPPQVQGPLGKIMPVKQPYLQTDPIKLFEPQLQPPVMQQQPLEKKMKPFPMEPYNHN
PSEVKVPEFYWDSSYSMADNRSVMAQQANIDRRGKRSPGIFRPEQDPVPRMPFEKSILLEKPSSELMSSSSFLSLT
GFSLNQERYPNNSMFNEVYGKNLTSSSKAELSPSMAPQETSLYSLFEGTPWSPSLPASSDHSTPASQSPHSSNPS
SLPSSPPTHNNHNSVPFSNFGPIGTPDNRDRRTADRWKTDKPAMGGFGIDYLSATSSSESSWHQASTPSTGTWTHG
PSMEDSSAVLMESLKS IWSSSMHHPGPSALEQLLMQKQKQQRGQGTMNPPH

WO 2004/030615

PCT/US2003/028547

559/6881
FIGURE 521A

ACCACCTGATCAAGGAAAAGGAAGGCACAGCGGAGCGCAGAGTGAGAACCACCAACCGAGGCGCCGGGCAGCGAC
CCCTGCAGCGGAGACAGAGACTGAGCGGCCCGGCCCGCCATGCCTGCGCTCTGGCTGGGCTGCTGCCTCTGCTT
CTCGCTCCTCTGCCCCGAGCCCGGGCCACCTCCAGGAGGGAAGTCTGTGATTGCAATGGGAAGTCCAGGCAGTG
TATCTTTGATCGGGAACCTTCACAGACAACTGGTAATGGATTCCGCTGCCTCAACTGCAATGACAACACTGATGG
CATTCACTGCGAGAAGTGCAAGAATGGCTTTTACCGGCACAGAGAAAGGGACCGCTGTTTGCCCTGCAATTGTAA
CTCCAAAGGTTCTCTTAGTGCTCGATGTGACAACCTCCGGACGGTGACAGCTGTAAACCAGGTGTGACAGGAGCCAG
ATGCGACCGATGTCTGCCAGGCTTCCACATGCTCAGGATGCGGGGTGCACCCAAGACCAGAGACTGCTAGACTC
CAAGTGTGACTGTGACCCAGCTGGCATCGCAGGGCCCTGTGACGCGGGCCGCTGTGTCTGCAAGCCAGCTGTCAC
TGGAGAACGCTGTGATAGGTGTGATCAGGTTACTATAATCTGGATGGGGGGAACCTGAGGGCTGTACCCAGTG
TTTCTGCTATGGGCATTGACCCAGCTGCCGAGCTCTGCAGAATACAGTGTCCATAAGATCACCTCTACCTTTCA
TCAAGATGTTGATGGCTGGAAGGCTGTCCAACGAAATGGGTCTCCTGCAAAGCTCCAATGGTCACAGCGCCATCA
AGATGTGTTTAGCTCAGCCCAACGACTAGACCCTGTCTATTTTGTGGCTCCTGCCAAATTTCTTGGGAATCAACA
GGTGAGCTATGGTCAAAGCCTGTCTTTGACTACCGTGTGGACAGAGGAGGCAGACACCCATCTGCCCATGATGT
GATTCTGGAAGGTGCTGGTCTACGGATCAGAGCTCCCTTGATGCCACTTGGCAAGACACTGCCTTGTGGGCTCAC
CAAGACTTACACATTCAGGTTAAATGAGCATCCAAGCAATAATTGGAGCCCCCAGCTGAGTTACTTTGAGTATCG
AAGGTTACTGCGGAATCTCAGACCCCTCCGCATCCGAGCTACATATGGAGAATACAGTACTGGGTACATTGACAA
TGTGACCCTGATTTAGCCCCGCCCTGTCTCTGGAGCCCCAGCACCCCTGGGTTGAACAGTGTATATGTCCTGTTGG
GTACAAGGGGCAATTTCTGCCAGGATTGTGCTTCTGGGTACAAGAGAGATTGAGCGAGACTGGGGCCTTTTGGCAC
CTGTATTCTTTGTAACCTGTCAAGGGGGAGGGGCTGTGATCCAGACACAGGAGATTGTTATTAGGGGATGAGAA
TCCCTGACATTGAGTGTGCTGACTGCCCAATTGGTTTCTACAACGATCCGCACGACCCCCGAGCTGCAAGCCATG
TCCCTGTGATAACGGGTTTCACTGCTCAGTGATGCCGAGACGGAGGAGGTGGTGTGCAATAACTGCCCTCCCGG
GGTCAACCGGTGCCCGCTGTGAGCTCTGTGCTGATGGCTACTTTGGGGACCCCTTTGGTGAACATGGCCAGTGAG
GCCTTGTGACCCCTGTCAATGCAACAACAATGTGGACCCAGTGCCCTCTGGGAATTGTGACCGGCTGACAGGCAG
GTGTTTGAAGTGTATCCACAACACAGCCGGCATCTACTGCGACCAAGTGCAAAGCAGGCTACTTCGGGGACCCATT
GGCTCCCAACCCAGCAGACAAGTGTGAGCTTGCAACTGTAAACCCATGGGCTCAGAGCCTGTAGGATGTGGAAG
TGATGGCACCTGTGTTTGAAGCCAGGATTTGGTGGCCCCAACTGTGAGCATGGAGCATTGAGCTGTCCAGCTTG
CTATAATCAAGTGAAGATTGAGATGGATCAGTTTATGAGCAGCTTCAGAGAATGGAGGCCCTGATTTCAAAGGC
TCAGGGTGGTGATGGAGTAGTACCTGATACAGAGCTGGAAGGCAGGATGACAGAGGCTGAGCAGGCCCTTCAGGA
CATTCTGAGAGATGCCAGATTTGAAAGGTGCTAGCAGATCCCTTGGTCTCCAGTTGGCCAAGGTGAGGAGGCCA
AGAGAACAGCTACCAGAGCCGCTGGATGACCTCAAGATGACTGTGGAAGAGTTCGGGCTCAGGAAAGTCAAGTCTCCTT
GGGAAACACTAACATTCCTGCCTCAGACCACTACGTGGGGCCAAATGGCTTTAAAGTCTGGCTCAGGAGGCCAC
AAGATTAGCAGAAAGCCACGTTGAGTCAGCCAGTAACATGGAGCAACTGACAAGGGAAACTGAGGACTATTCCAA
ACAAGCCCTCTCACTGGTGCGCAAGGCCCTGCATGAAGGAGTCGGAAGCGGAAGCGGTAGCCCGGACGGTGCTGT
GGTGAAGGGCTTGTGGAAGAAATGGAGAAACCAAGTCCCTGGCCAGCAGTTGACAAGGGAGGCCACTCAAGC
GGAAATTGAAGCAGATAGGTCTTATCAGCACAGCTCCTCGCTCCTGGATTGAGTGTCTCGGCTTCAGGGAGTCAG
TGATCAGTCCCTTCAGGTGGAAGAAGCAAGAGGATCAAACAAAAGCGGATTCACTCTCAAGCCTGGTAACCAG
GCATATGGATGAGTTCAAGCGTACACAGAAGAATCTGGGAAACTGGAAAGAAGAAGCACAGCAGCTCTTACAGAA
TGGAAAAAGTGGGAGAGAGAAATCAGATCAGCTGCTTTCCCGTGCCAATCTTGCTAAAAGCAGAGCACAAGAAGC
ACTGAGTATGGGCAATGCCACTTTTATGAAGTTGAGAGCATCCTTAAAAACCTCAGAGAGTTTGACCTGCAGGT
GGACAACAGAAAAGCAGAAGCTGAAGAAGCCATGAAGAGACTCTCCTACATCAGCCAGAAGGTTTCAGATGCCAG
TGACAAGACCCAGCAAGCAGAAAAGAGCCCTGGGGAGCGCTGCTGCTGATGCACAGAGGGCAAAGAATGGGGCCGG
GGAGGCCCTGGAATCTCCAGTGAGATTGAACAGGAGATTGGGAGTCTGAACTTGAAGCCAATGTGACAGCAGA
TGGAGCCTTGGCCATGGAAGAGGACTGGCCTCTCTGAAGAGTGAGATGAGGGAAGTGAAGGAGAGCTGGAAG
GAAGGAGCTGGAGTTTGACACGAATATGGATGAGTACAGATGGTGTATTACAGAAGCCAGAAGGTTGATACCAG
AGCCAAGAACGCTGGGGTTACAATCCAAGACACACTCAACACATTAGACGGCCTCCTGCATCTGATGGACCAGCC
TCTCAGTGTAGATGAAGAGGGGCTGGTCTTACTGGAGCAGAAGCTTTCCGAGCCAAGACCCAGATCAACAGCCA
ACTGCGGCCCATGATGTGAGAGCTGGAAGAGAGGGCACGTCAGCAGAGGGGCCACCTCCATTTGCTGGAGACAAG

WO 2004/030615

PCT/US2003/028547

560/6881
FIGURE 521B

CATAGATGGGATTCTGGCTGATGTGAAGAACTTGGAGAACATTAGGGACAACCTGCCCCAGGCTGCTACAATAC
CCAGGCTCTTGAGCAACAGTGAAGCTGCCATAAATATTTCTCAACTGAGGTTCTTGGGATACAGATCTCAGGGCT
CGGGAGCCATGTGATGTGAGTGGGTGGGATGGGGACATTTGAACATGTTTAATGGGTATGCTCAGGTCAACTGAC
CTGACCCCATTCCTGATCCCATGGCCAGGTGGTTGTCTTATTGCACCATACTCCTTGCTTCCTGATGCTGGGCAA
TGAGGCAGATAGCACTGGGTGTGAGAATGATCAAGGATCTGGACCCCAAAGAATAGACTGGATGGAAAGACAAAC
TGCACAGGCAGATGTTTGCCTCATAATAGTCGTAAGTGGAGTCCTGGAATTTGGACAAGTGCTGTTGGGATATAG
TCAACTTATTCTTTGAGTAATGTGACTAAAGGAAAAAACTTTGACTTTGCCAGGCATGAAATTCTTCCTAATGT
CAGAACAGAGTGCAACCCAGTCACACTGTGGCCAGTAAAATACTATTGCCTCATATTGTCTCTGCAAGCTTCTT
GCTGATCAGAGTTCCTCCTACTTACAACCCAGGGTGTGAACATGTTCTCCATTTTCAAGCTGGAAGAAGTGAGCA
GTGTTGGAGTGAGGACCTGTAAGGCAGGCCCATTCAGAGCTATGGTGCTTGCTGGTGCCCTGCCACCTTCAAGTTC
TGGACCTGGGCATGACATCCTTTCTTTTAATGATGCCATGGCAACTTAGAGATTGCATTTTTATTAAAGCATTTC
CTACCAGCAAAGCAAATGTTGGGAAAGTATTTACTTTTTTCGGTTTCAAAGTGATAGAAAAGTGTGGCTTGGGCAT
TGAAAGAGGTAAAATTCTCTAGATTTATTAGTCCTAATCAATCCTACTTTTCGAACACCAAAAATGATGCGCAT
CAATGTATTTTATCTTATTTTCTCAATCTCCTCTCTCTTTCCCTCCACCCATAATAAGAGAATGTTCCCTACTCACA
CTTCAGCTGGGTCACATCCATCCCTCCATTATCCTTCCATCCATCTTTCCATCCATTACCTCCATCCATCCTTC
CAACATATATTTATTGAGTACCTACTGTGTGCCAGGGGCTGGTGGGACAGTGGTGACATAGTCTCTGCCCTCATA
GAGTTGATTGTCTAGTGAGGAAGACAAGCATTTTTTAAAAATAAATTTAAACTTACAACTTTGTTTGTACAAG
TGGTGTATTATTGCAATAACCGCTTGGTTTGAACCTCTTTGCTCAACAGAACATATGTTGCAAGACCCTCCCATG
GGGGCACTTGAGTTTTGGCAAGGCTGACAGAGCTCTGGGTGTGCACATTTCTTTGCATTCCAGCTGTCACTCTG
TGCTTTTCTACAACCTGATTGCAACAGACTGTTGAGTTATGATAACACCAGTGGGAATTGCTGGAGGAACCAGAGG
CACTTCCACCTTGGCTGGGAAGACTATGGTGCTGCCTTGCTTCTGTATTTCTTGGATTTTCTGAAAGTGTTTT
TAAATAAAGAACAATTGTTAGA

PCT/US2003/028547

CCCAACCGCAGTTGACTAGCCTGCTACCGCGCCTTTGCTTCTCGGCACGCGGAGCCTCCTGGAGCCTGCCA
CCATCCTGCGCTACTACGTGCTGCGCCCGCAGCCATGTGCCGCAACCCTGGCCGCGCTTCCCCACCACCTGCG
TGGAGAGAGCCAAAGAGTTCAAGACACGTCTGGGGATCTTTCTTTCACAAATCAGAGCTGGGCTGCGATACTGGGA
GTACTGGCAAGTTTCGAGTGGGGCAGTAAACACAGCAAAAGAGAATAGAACTTCTCAGAAGATGTGCTGGGGTGG
GAGAGTCGTTTCGACCTGCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACGCTTTCTCTGAAGACAGAGTTCA
GTGAGGAGAACCCTGGAGTTCTGGCTGGCCTGTGAGGAGTTCAAGAAGATCCGATCAGCTACCAAGCTGGCCTCCA
GGGCACACCAGATCTTTGAGGAGTTCAATTTGCAGTGAGGCCCCCTAAAGAGGTCAACATTGACCATGAGACCCACG
AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGAAGACACGTACCCTGA
TGGAGAAGGACTCCTACCCACGCTTCTCTGAAGTCGCTTACCAGGACCTGGCTGCCCCAAGCCTCAGCCGCGCT
CTGCCACTGTCTGCTCCAGCTGCAGCCTGGACGAGCCCTCACACACCTGAGTCTCCACGGCAGTGAGGAAGCCAGCCG
GGAAGAGAGGTTGAGTCACCCATCCCCGAGGTGGCTGCCCCGTGTGTGGGAGGCAGGTTCTGCAAGCAAGTGCAA
GAGGACAAAAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
GATACTGTGGGACTCATGCTGGAGAGGAGCCGCCACTTCCAGGACCTGTGAATAAGGGCTAATGATGAGGGTTG
GTGGGGCTCTCTGTGGGGCAAAAAGGTGGTATGGGGGTTAGCACGGCTCTCGTTCTCACCAGGAGAAGGAAGTGT
TCTAGTGTGGTTTAGGAAACATGTGGATAAAGGGAAACCATGAAAATGAGAGGAGGAAAGACATCCAGATCAGCTG
TTTTGCGCTGTTGCTCAGTTGACTCTGATTGCATCCTGTTTTCTTAATTCCAGACTGTTCTGGGCACGGAAGGGA
CCCTGGATGTGGAGTCTTCCCCTTTGGCCCTCCTCACTGGCCTCTGGGCTAGCCAGAGTCCCTTAGCTTGTACC
TCGTAACACTCCTGTGTGCTGTCTCCAGCCTTGACAGTCAATGTCAAGGCCAGCAAGCTGATGTGACTCTTGCCCCAT
CGAGATATTTATACCTCAAACACTGGCCTGTGAGCCCTTTCCAAGTCAGTGGAGAGCCCTGAAAGGAGGCTCAC
TTGAAATCCAGCTCAGTGCTCTGGGTGGCCCCCTGCAGGTGGCCCCCTGACCTGCGTTGCAGCAGGGTCCACCTGT
GAGCAGGCCCGCCCTGGGGCCTCTTCTGGATGTGCCCTCTCTGAGTTCTGTGCTGTCTCTTGGAGGCAGGGCC
AGGAGAACAAAGTGTGGAGGCCCTCGGGGAGTGGCTTTTCCAGCTCTCATGCCCCGAGTGTGGAACAAGGCAGAA
AAGGATCCTAGGAAATAAGTCTCTTGGCGGTCCCTGAGAGTCTGCTGAAATCCAGCCAGTGTTTTTTGTGGTAT
GAGAACAGGCAAAAAGAGATGCCCGAGATAGAAGGGGAGCCTTGTTGTTTTCTTTCTGACAGCTGAGATGAACA
CTGGAGTGGGCAGAGGTGGCCAGGACCATGGCACCCTTAGAGTGCAGAAGCTGGGGGGAGAGGCTGCTTCGAAG
GGCAGGACTGGGGATAATCAGAACCTGCCTGTCACCTCAGGGCATCACTGAACAAACATTTCTGATGGCAACTC
CTGCGGCAGAGCCCAGGCTGGGGAAGTGAACCTACCCAGGGCAGCCCCCTTTGTGGCCAGGATAATCAACACTGTT
CTCTCTGTACCATGAGCTCCTCCAGGAGATTATTTAAGTGTATTGTATCATTGGTTTTCTGTGATTGTATAACA
TTGTTTTTGTATTATTGTTGGTGTCTGTTGTTATTTATTTATTGTAATTTTCAAGTTTGCTCTACTGGAGAATCTCAGCA
GGGGTTTCAGCCTGACTGTCTCCCTTTCTCTACCAGACTCTACCTCTGAATGTGCTGGGAACCTCTTGGAGCCTG
TCAGGAACCTCTCACTGTTTAAATATTTATTTATTTGTTGACAAATGGAGCTGGTTTCTTAGATATGAATGATGTT
GCAATCCCCATTTTCTGTTTCAGCATGTTATATTCTTATAAAATAAAAGCAAAAGTCAAATATG

WO 2004/030615

PCT/US2003/028547

562/6881
FIGURE 523

GGGTGCGGGGCTGCTGGCGGCTCTGCAGAGTCGAGAGTGGGAGAAGAGCGGAGCGTGTGAGCAGTACTGCGGCCCT
CCTCTCCTCTCCTAACCTCGCTCTCGCGGCCCTAGCTTTACCCGCCCGCTGCTCGGCGACCAGCGGGGATCCTCC
CCCAGCCGCAAGTCCACGAAGAAAGCAACGAATGAAAATTATGAAGACAACGAGAAGTCAGACTCCTCCGGGTGCG
CGCTCCAGCTGCTTCGGCTTCGTGCGCTACTCTGTGAACCTCCGGGGAGAGATCTCGAGTCAAGATTAAGACCTTA
ACCCACCAACCTGCCTGTTTCGGACACCCCCCGGGCCGGCCGCTGTCTGTCCCCCTTCTCCATCGCCCTCTCCCAGA
AAGCTCCGGTGCTTGGACCAGCTAGAGTCTGAGAAAGAGGAGAGGCGCAACGCCACTCCAAAAAGAGAAGGGTT
AAAGAGGGCAACCCCTAACGATACGCTTGACTTTCTGTGGCTGGGAACACCTTCCACCATGACCACCTCAGCAAGT
TCCCACTTAAATAAAGGCATCAAGCAGGTGTACATGTCCCTGCCTCAGGGTGAGAAAGTCCAGGCCATGTATATC
TGGATCGATGGTACTGGAGAAGGACTGCGCTGCAAGACCCGGACCTGGACAGTGAGCCCCAAGTGTGTGGAAGAG
TTGCCTGAGTGGAAATTTTCGATGGCTCTAGTACTTTACAGTCTGAGGGTTCCAACAGTGACATGTATCTCGTGCCCT
GCTGCCATGTTTCGGGACCCCTTCCGTAAGGACCCTAACAAAGCTGGTGTATGTGAAGTTTCAAGTACAATCGA
AGGCCTGCAGAGACCAATTTGAGGCACACCTGTAAACGGATAATGGACATGGTGAGCAACCAGCACCCCTGGTTT
GGCATGGAGCAGGAGTATACCCTCATGGGGACAGATGGGCACCCCTTTGGTTGGCCTTCCAACGGCTTCCCAGGG
CCCCAGGGTCCATATTACTGTGGTGTGGGAGCAGACAGAGCCTATGGCAGGGACATCGTGAGGGCCATTACCGG
GCCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTCATGCCTGCCAGTGGAATTTCAAGATT
GGACCTTGTGAAGGAATCAGCATGGGAGATCATCTCTGGGTGGCCCGTTTCATCTTGATCGTGTGTGTGAAGAC
TTTGGAGTGATAGCAACCTTTGATCCTAAGCCCATTCTGGGAAGTGAATGGTGCAGGCTGCCATACCAACTTC
AGCACCAAGGCCATGCGGGAGGAGAATGGTCTGAAGTACATCGAGGAGGCCATTGAGAACTAAGCAAGCGGCAC
CAGTACCACATCCGTGCCTATGATCCCAAGGGAGGCCCTGGACAATGCCCGACGTCTAAGTGGATTCCATGAAACC
TCCAACATCAACGACTTTTCTGCTGGTGTAGCCAATCGTAGCCAGCATACGCATTCCCCGGACTGTTGGCCAG
GAGAAGAAGGGTTACTTTGAAGATCGTCGCCCCCTTGCCAAGTCCGACCCCTTTTCGGTGACAGAAGCCCTCATC
CGCACGTGTCTTCTCAATGAAACCGCGATGAGCCCTTCCAGTACAAAAATTAAAGTGGACTAGACCTCCAGCTGT
TGAGCCCTCCTAGTTCTTTCATCCCACTCCAACCTTCTCCCTCTCCCAAGTTGTCCCGATTGTAAGTCAAAGGGT
GGAATATCAAGGTCGTTTTTTTTCATTCCATGCTGCCAGTTAATCTTGCTTTCTTTGTTTGGCTGGGATAGAGGGG
TCAAGTTATTAATTTCTTACACCTACCCTCCTTTTTTCCCTATCACTGAAGCTTTTGTAGTGCATTAGTGGGGA
GGAGGGTGGGGAGACATAACCACTGCTTCCATTTAATGGGGTGACCTGTCCAATAGGCGTAGCTATCCGGACAG
AGCACGTTTGCAGAAGGGGTCTCTTCTTCCAGGTAGCTGAAAGGGGAAGACCTGACGTACTCTGGTTAGGTTAG
GACTTGCCCTCGTGGTGGAACCTTTTCTTAAAAAGTTATAACCAACTTTTCTATTAAAAAGTGGGAATTAGGAGAG
AAGGTAGGGGTTGGGAATCAGAGAGAATGGCTTTGGTCTCTTGCTTGTGGGACTAGCCTGGCTTGGGACTAAATG
CCCTGCTCTGAACACGAAGCTTAGTATAAACTGATGGATATCCCTACCTTGAAAGAAGAAAAAGTTCTTACTGCT
TGGTCCTTGATTTATCACACAAAGCAGAATAGTATTTTTATATTTAAATGTAAAGACAAAAAACTATATGTATGG
TTTTGTGGATTATGTGTGTTTTGCTAAAGGAAAAAACCATCCAGGTCACGGGGCACCATAATTTGAGACAAATAGT
CGGATTAGAAATAAAGCATCTCATTTTGTAGTAGAGAGCAAGGGAAGTGGTTCTTAGATGGTGATCTGGGATTAGG
CCCTCAAGACCCCTTTTGGGTTTTCTGCCCTGCCACCCCTCTGGAGAAGGTGGGCACTGGATTAGTTAACAGACAAC
ACGTTACTAGCAGTCACTTGATCTCCGTGGCTTTGGTTTAAAGACACACTTGTCACATAGGTTTAGAGATAAG
AGTTGGCTGGTCAACTTGAGCATGTTACTGACAGAGGGGGTATTGGGGTTATTTTCTGGTAGGAATAGCATGTCA
CTAAAGCAGGCCTTTTGATATTAAATTTTTTAAAAAGCAAATTATAGAAGTTTAGATTTAATCAAATTTGTAG
GGTTTCTAGGTAATTTTTACAGAATTGCTTGTGTGCTTCAACTGTCTCCTACCTCTGCTCTTGAGGAGATGGGG
ACAGGGCTGGAGTCAAAACACTTGTAATTTTGTATCTTGATGTCTTTGTTAAGACTGCTGAAGAATTATTTTTTT
TCTTTTATAATAAGGAATAAACCCACCTTTATTCCTTCATTTCTATCTACCATTTTCTGGTTCTGTGTTGGCTG
TGGCAGGCCAGCTGTGGTTTTCTTTTGGCATGACAACCTTCTAATTGCCATGTACAGTATGTTCAAAGTCAAATAA
CTCCTCATTGTAAACAACTGTGTAAGTGCCTAAAGCAGCACTTATAAATCAGCCTAACAT

WO 2004/030615

PCT/US2003/028547

563/6881
FIGURE 524A

GCGGGGAGGGGCGGGGCTATGGAGAGGAGGAGGAAGATGGCGGGGCGGGCTGCTCTGAAGAGACCTCGGCGGGCGGCG
GGAGGAGGAGAGAAGCGCAGCGCCGCGCCGCGCCGGGGGCCCATGTGGGGAGGAGTCGGAGTCGCTGTTGCCGCCG
CCGCTGTAGCTGCTGGACCCGAGTGGGAGTGAGGGGGAAACGGCAGGATGAAGTTCGCCGAGCACCTCTCCGCG
CACATCACTCCCGAGTGGAGGAAGCAATACATCCAGTATGAGGCTTTCAAGGATATGCTGTATTACAGTCAGGAC
CAGGCACCTTCTGTGGAAGTTACAGATGAGGACACAGTAAAGAGGTATTTTGCCAAGTTTGAAGAGAAGTTTTC
CAAACCTGTGAAAAAGAACTTGCCAAAATCAACACATTTTATTAGAGAAGCTCGCAGAGGCTCAGCGCAGGTTT
GCTACACTTCAGAATGAGCTTCAGTCATCACTGGATGCACAGAAAGAAAGCACTGGTGTTACTACGCTGCGACAA
CGCAGAAAGCCAGTCTTCCACTTGTCCTCATGAGGAACGTGTCCAACATAGAAATATTAAAGACCTTAACTGGCC
TTCAGTGAGTTCTACCTCAGTCTAATCCTGCTGCAGAACTATCAGAATCTGAATTTTACAGGGTTTCGAAAAATC
CTGAAAAAGCATGACAAGATCCTGGAAACATCTCGTGGAGCAGATTGGCGAGTGGCTCACGTAGAGGTGGCCCCA
TTTTATACATGCAAGAAAATCAACCAGCTTATCTCTGAACTGAGGCTGTAGTGACCAATGAACCTGAAGATGGT
GACAGACAAAAGGCTATGAAGCGTTTACGTGTCCCCCTTTGGGAGCTGCTCAGCCTGCACCAGCATGGACTACT
TTTAGAGTTGGCCTATTTTGTGGAATATTCATTGTACTGAATATTACCCTTGTGCTTGCCGCTGTATTTAACTT
GAAACAGATAGAAGTATATGGCCCTTGATAAGAATCTATCGGGGTGGCTTTCTTCTGATTGAATTCCTTTTTCTA
CTGGGCATCAACACGTATGGTTGGAGACAGGCTGGAGTAAACCATGTACTCATCTTGAACCTTAATCCGAGAAGC
AATTTGTCTCATCAACATCTCTTTGAGATTGCTGGATTCTCGGGATATTGTGGTGCCTGAGCCTTCTGGCATGC
TTCTTTGCTCCAATTAGTGTCATCCCCACATATGTGTATCCACTTGCCCTTTATGGATTTATGGTTTTCTTCCTT
ATCAACCCCAACCAAACTTTCTACTATAAATCCCGGTTTTGGCTGCTTAACTGCTGTTTCGAGTATTTACAGCC
CCCTTCCATAAGGTAGGCTTTGCTGATTTCTGGCTGGCGGATCAGCTGAACAGCCTGTCAGTGATACTGATGGAC
CTGGAATATATGATCTGCTTCTACAGTTTGGAGCTCAAATGGGATGAAAGTAAGGGCCTGTTGCCAAATAATTCA
GAAGAATCAGGAATTTGCCACAAATATACATATGGTGTGCGGGCCATTGTTCACTGCATTCTGCTGGCTTCGC
TTCATCCAGTGCTGCGCCGATATCGAGACACAAAAGGGCCTTTCCTCATTAGTTAATGCTGGCAAATACTCC
ACAACCTTTCTTCATGGTGACGTTTGCAGCCCTTTACAGCACTCACAAAGAACGAGGTCAGTCCGACACTATGGTG
TTCTTTTACCTGTGGATTGCTTTTATATCATCAGTTCTGTCTATACCCTCATCTGGGATCTCAAGATGGACTGG
GGTCTCTTCGATAAGAATGCTGGAGAGAACACTTTCCTCCGGGAAGAGATTGTATACCCCAAAAAGCCTACTAC
TACTGTGCCATAATAGAGGATGTGATTCTGCGCTTTGCTTGGACTATCCAAATCTCGATTACCTCTACAACCTTG
TTGCTCATTCTGGGGACATCATTGCTACTGTCTTTGCCCACTTGAGGTTTTCCGGCGATTGIGTGGAACCTTC
TTCCGCTTGGAATGAACATCTGAATAACTGTGGTGAATTCGCTGTGTGCGGACATCTCTGTGGCCCCCTG
AACGCAGATGATCAGACTCTCCTAGAACAGATGATGGACAGGATGATGGGGTACGAAACCGCCAGAAGAATCGG
TCATGGAAGTACAACCAGAGCATATCCCTGCGCCGGCCTCGCCTCTCAATCCAAGGCTCGTGACACTAAG
GTATTGATAGAAGACACAGATGATGAAGCTAACACTTGAATTTCTGAAGTCTAGCTTAACATCTTTGGTTTTCC
TACTCTACAATCCTTTCTCGACCAACGCAACCTCTAGTACCTTTCCAGCCGAAAACAGGAGAAAACACATAACA
CATTTTCCGAGCTCTTCCGGATCGGATCCTATGGACTCCAAACAAGCTCACTGTGTTTTCTTTCTTTCTTCTGG
TTAATTTTAAATTTTCTATTTTCAAACAAATATTTACTTCAATTTGCCAATCAGAGGATGTTTTAAGAAACAAA
CATAGTATCTTATGGATTGTTTACAATCACAAGGACATAGATACCTATCAGGATGAAGAACAGGCATTGCAAGGA
CCCTCTGATGGGACGGTACTGAGATATCTCGGCTTCCGCTCAGCCCGGTTTTGACTGGTTGAAACCGGACATTGG
TTTTTAAATTTTTGTGAGTTTATGTGGAGAATTTTTTCTTTCTTTCTATACCCAGCGCAAAGGCACTGGCCGCA
CTTGACAGAAAAGTGCACCTTAAAGCAGTACCTTCATTTCATGAAGCTACTTTTTAATTTGATGTAACCTTTCTTA
TTTTGGGAAGGGTGTGCTGGGTGGGTGGGAAATATGATGATTTGTGTACACATAGTTTTCTCATTATTTATGAAAC
TTAACCATAACAGAAATGATATAACTCCTGTGCAATGAAGGTGATAACAGTAAAGAAGGCAGGGGAAACTTACGTT
GGATGACATTTATGAGGGTCAGTCCCACATACCTCTTTCAGGAGACAACCTTGACCCAGTTTGACCTTTTCTTTTC
TTGTTTTTATTTTAAAGCCAAAGTTTCATTGCTAACTTCTTAAGTTGCTGCTGCTTTAGAGTCTTGAGCATATCT
CTCATAACAAGGAATCCCACACTTCACACCACCGGCTGAATTTTCATGGAAGAGGTTCTGATAATTTTTTTAACTT
TTTAAGGAACAGATGTGGAATACACTGGCCCATATTTCAACCTTAACAGCTGAAGCTATGCCTTATTATGCATCC
ACATGTATGGTCCCTGTAGCGTGACCTTTACTAGCTCTGAATCAGAAGACAGAGCTATTTTCAGAGGCTCTGTGTG
CCCTCACTAGATAGTTTTTCTTCTGGGTTCAACCCTTTAGCCAGAATTTGATCAAATTTAAAGTCTGTCTATGGG
GAAACTATATTTTTGAGCACATGGAAACAAATTATACTTCTCATTATATTATGTTGATACAAAAGACCTTGCCA
GCCATTTCTCCCAGCAGTTTTTAAAGGATGAACATTGGATTTCATGCCATCCCATAGAAAACCTGTTTTTAAATTT

WO 2004/030615

PCT/US2003/028547

564/6881
FIGURE 524B

TAGGGATCTTTACTTGGTCATACATGAAAAGTACACTGCTTAGAAAATTATAGACTATTATGATCTGTCCACAGTG
CCCATTGTCACCTCTTTTGCTCATTCTTTCCCTTTGTTTCCTTAGTCATCCAAATAAGCCTGAAAACCATAAGAGA
TATTACTTTATTGAATATGGTTGGCATTAAATTTAGCATTTCATTATCTAACAAAATTAATATAAATTCCAGGAC
ATGGTAAAATGTGTTTTAATAACCCCCAGACCCAAATGAAAATTTCAAAGTCAATACCAGCAGATTCATGAAAGT
AAATTTAGTCCTATAATTTTCAGCTTAATTATAAACAAAGGAACAAATAAGTGGGAAGGGCAGCTATTACCATTCTG
CTTAGTCAAAACATTCGGTTACTGCCCTTTAATACACTCCTATCATCAGCACTTCCACCATGTATTACAAGTCTT
GACCCATCCCTGTCGTAACTCCAGTAAAAGTTACTGTTACTAGAAAATTTTTATCAATTAAGTACAAATAGTTT
CTTTTTAAAGTAGTTTCTTCCATCTTTATTCTGACTAGCTTCCAAAATGTGTTCCCTTTTTGAATCGAGGTTTTT
TTGTTTTGTTTTGTTTTCTGAAAAAATCATACAACTTTGTGCTTCTATTGCTTTTTTGTTGTTTGTAAAGCATGT
CCCTTGCCCCAAATGGAAGAGGAAATGTTTAATTAATGCTTTTTAGTTTAAATAAATTGAATCATTATAATAAT
CAGTGTTAACAATTTAGTGACCCTTGGTAGGTTAAAGGTTGCATTATTTATACTTGAGATTTTTTCCCCTAACT
ATTCTGTTTTTTGTACTTTAAACTATGGGGGAAATATCACTGGTCTGTCAAGAAACAGCAGTAATTATTACTGA
GTTAAATTGAAAAGTCCAGTGGACCAGGCATTTCTTATATAAATAAAATTGGTGGTACTAATGTG

WO 2004/030615

PCT/US2003/028547

565/6881
FIGURE 525

AATAAATTATTTTTGTTAAGGCAAGCATTGGTGTGTTCTTTAACTTGCTACTTGGAGACCTAGTGTCCAGTCTGG
ACAGAATGCACAGAGACCAGCCTCACCTGGAATGCAGCCAGACTCGATGTCCCTCAGCACACACAGCTCCTGGCC
ACAGACTGCCCATAGAAGTGTCTGCACCCAAACCCCATGGCCTTTTCATGCACGGAGACAGGCCTCTGGATGTGC
AGCCTTGCCACCCCTGCCCAATCCTCCCTGAGAGCTCCTGCCCTCAGTGCCCTGGGCTGGTGAGGGAGAAGCCT
GTCTGCACCTGCCTAATTCCAGCTCCTCCAGGAAGCAAGGGCTTGTGTCAGAGCTGCAGGGTTGGCCACTCGG
TGGGGAGGAGTCAGCCAGGATTAGAGAGCCTGCCCTAATCCGGCCTGCTGGGTTTTACAAGGATCAGAGCTGCT
GATAATGAACCTCATTAAAGGGGGAGCAGGAGCCTCAATCCGATTGGTTTTCTCTTTGACATCTTCACTCTGCTC
AGATGGCCTGGGTGCTATGTGGAGCAGGTGGGATGCCAAGGCCACTCCTGCTATGGGGCAGCTGGGGCTGGGGAG
GGATGGCAGTCTCCCTGCATGTTTCCCTCGACCTCTTTAGCTGCAGCGCCTTGCTGGGCTCCTGGGTTGGACTCC
CTCTCTGTGCCCTGCTCCAGGCACCCATTGGCTCCATCCTCCTGGTTGTGCTCTGCACCCCTGCTCCCTTGGG
CTGGCCCTGGCTGGGGGCTGAGAGACAGACAGGAACCCACAATCAGGAGGCAACCCTGGCCTGCAAGAGGAAGA
CAGAGGCTCCCAGGGCCGGTGCCCTGTGTGCCACTGCACCAAGGCCGCTGAATAAGCCTGCCCTTCAACCCCTA
AGGGCTCCTTGCCCAATGCCAAGTGTGGGGATTCTGTGCAGCAAGCCCTGTGGCTCCAGTGACGGTATTTCTAA
AGCCAAACTTAGTTACCTAGAATTAGCGCCATGTTGGAACACTGTGCGCAGCAGCCGGGCTGCACAGTGTGTAG
CCCAGCCTCCAGGTCCACGGAGTGGTGTGGACCTCCACCTCACAGCTGCCTCTGGCAGCCAAGCCTCTTTTCGC
CCGGCCCCAGCCCTCTGGTTGATAAACGGGTGGGCCTCCTCAGCAGCGTGGCTGCCTTTCACCTTGATTTCCCC
AGGGCTCTCGGCAACATCGATAAACAGCCTCGCCACCAGCTGGGCCCTCCCCACCCAGTCTGCCAGGCTGGG
AGCTGGAGCTTGCTGAGTCTTGAATGCCCTTCTAGATGGCTTCTCTAGAGGCTCTCCTGGCAAGAGAGGGTCCCA
AGGGGAGCCCTGCAAAGCAAAGGCTCCTTGTCTGGGGCGGGATAGAGAATCTCGCCTCTGTCTGGTGTGTTACCT
ACTGGGGGCACAGGAACAATTTCTCAAGGAGACAGTGGCATGGAGCTTTGAAAGACGAGTAGGTGTTAGCAAGG
AAATAAGGAGGAACGGGGGTACGGGCAGAGGAGAAAGCACATGCCAAGTCAGCAAAGAAAAGTAGAATTCGAAA
ACTTTTTAAAAATATTACTAAGGATTTTACAATGCTGCACTGGGCTAGAACTGAAGCTAAAACAGATACGTGG
TCCCTGCTGCTATGGGGCTTCCGTTCTAGAGGCAAGGACAGGTTGTGATGAGGGTTCTGAAGGATAGAGACCAAG
CAGGGAGGGTGTGAGGAGGCTTCTGCGAGACCTGAAGGATGGGAAGCCAGGAAGTGGGAGGGGTGGGGGTCCAG
GCTGGAGGGGCCAATGTAGGTGTAGAGGACTACAGCCCTGAGGGGCTGCTCCATGCGGCATTCTTGGAGGTCC
AAGAGGGGCAGCGCCACCTTGGGCCAGGCTCCTCTCCAGCAGCCTTGGTATGGGGTGGGGGTGGGAAGACCCCTG
ATGCAGCCTGTCTCTGGGTGTGGGGGTGGAGGAGAGGGCTCCAGGGGACCCAGCCAGCCTTGACCCTGGAGGAA
AGTCAGGTGGGCTCAGAGAGAGCCCTCAAATCTGGGCCCTGGGTGAGGGTGGGGTCAAGTCCAGCCTTGAAGAGA
ATGGACTCTGGAATCTGACGTCTGGGTTTGAATCCAGCTTCCAACACTCACTGGCTGTGTGACTTTGGGCAAGAT
AAGTTATCCCTTGTCCTCCATGTGTATTGGAGATAAACTACCCACCTACCAGATTGTGTACCATGCTGGGCAA
ACACTAAGTGCTTAATAATGGTAGCCCACTGCTC

WO 2004/030615

PCT/US2003/028547

566/6881
FIGURE 526

MHRDQPHLECSQTRCPSAHTAPGHRLPIELSAPKPHGLFMHGDRPLDVQPCHPLPQSSLRAPASVPWAGEGEACL
HLPNSSSSRKQGLVCQSCRVGHSVGRSQPGLESPLIRPAGFYKDQSC

WO 2004/030615

PCT/US2003/028547

567/6881
FIGURE 527

AGCCGGATGGTCCCGCAGCTCGGGGCCGGCCATGCTTCGCGGTCCGTGGCGCCAGCTTTGGCTCTTTCTCCTGCT
GCTGCTCCCGGGCGCGCCTGAGCCCCGCGGCGCCTCCAGGCCGTGGGAGGGAACCGACGAGCCGGGCTCGGCCTG
GGCCTGGCCGGGCTTCCAGCGCCTGCAGGAGCAGCTCAGGGCGGCGGGTGCCCTCTCCAAGCGGTACTGGACGCT
CTTCAGCTGCCAGGTGTGGCCCGACGACTGTGACGAGGACGAGGAGGCAGCCACGGGGCCCCCTGGGCTGGCGCCT
TCCTCTGTTGGGCCAGCGGTACCTGGACCTCCTGACCACGTGGTACTGCAGCTTCAAAGACTGCTGCCCTAGAGG
GGATTGCAGAATCTCCAACAACCTTTACAGGCTTAGAGTGGGACCTGAATGTGCGGCTGCATGGCCAGCATTGGT
CCAGCAGCTGGTCCTAAGAACAGTGAGGGGCTACTTAGAGACGCCCCAGCCAGAAAAGGCCCTTGCTCTGTCGTT
CCACGGCTGGTCTGGCACAGGCAAGAACTTCGTGGCACGGATGCTGGTGGAGAACCTGTATCGGGACGGGCTGAT
GAGTGACTGTGTGACGATGTTTCATCGCCACGTTCCACTTTCTCACCCCAAATATGTGGACCTGTACAAGGAGCA
GCTGATGAGCCAGATCCGGGAGACGCAGCAGCTCTGCCACCAGACCCTGTTTCATCTTCGATGAAGCGGAGAAGCT
GCACCCAGGGCTGCTGGAGGTCTTGGGCCACACTTAGAACGCCGGGCCCTGAGGGCCACAGGGCTGAGTCTCC
ATGGACTATCTTTCTGTTTCTCAGTAATCTCAGGGGCGATATAATCAATGAGGTGGTCTAAAGTTGCTCAAGGC
TGGATGGTCCCGGGAAGAAATTACGATGGAACACCTGGAGCCCCACCTCCAGGCGGAGATTGTGGAGACCATAGA
CAATGGCTTTGGCCACAGCCGTCTTGTGAAGGAAAACCTGATTGACTACTTCATCCCCTTCTGCCTTTGGAGTA
CCGTCACGTGAGGCTGTGTGCACGGGATGCCTTCCTGAGCCAGGAGCTCCTGTATAAAGAAGAGACACTGGATGA
AATAGCCCAGATGATGGTGTATGTCCCCAAGGAGGAACAACCTTTTTCTTCCCAGGGCTGCAAGTCTATTTCCTCA
GAGGATTAACACTTCTCTGTCATGAAGGCTAGAGGAAGACTTCCTGGAAGTGCCTTTCTTCCACTAACAGGACCC
TGGGACCTGTAGGAGCACCCCGTTTTGGGACTGTGAGGTGTTGAGGGTGTGGACTGGCATCCAGCAGCCACTAAC
AAACACACAACCTGGTGTGTAAAAGGCAGGCCTTACATTAGAAGCCAAGCCAATCCTTTTTCTTTTTTTTGGAGGT
CCCACCGAGATAGATAGGAACCTGGATTGCTGAATTCAAAAACAGAGCCCATTCTTAAGATCACTTGGTGCCTTA
AAGACACGCATTCCAAAGTGGAATGTGGTTGAAGAAAGTGGGCCAGGTGGTTGAAGAAAGCCATGTGGGAGCTCA
GCAAAATCCCAAGGGCTTATTATGACACTCCAGATGGTCTCCTTAGCATCTCAGCTCTTCTGCAAGGAAGAGCTTG
GGTGTAGGCCTCAGAGGCTGTAGGGTCCTTGGGTTACAGAGCCGGGAGAACGAAGTTCTGTGACCCAGGGGTG
GAGAATACACTCTAGGTTTGGCGGCTGGTGGGCTTTCAAATTGGTACTTCCAGAGGAAAGCCAAGCTGCTTCGT
TGTGAGCGAATCAGCCAAGAGCCTGAGGCTGAAGGGAAGTACACAGAGGAAGATATTTTACAAACCAGGTCAG
TGTAGGCCAAGACTTATGGTCTACAGATTTTGGCGGGGAGGGGGACCTTTTCAAAGACAATAGGGGGTCTTGA
CATGTTTGTGTATGTAAAGATGATAAGATTAATAATTTTTGATTTTTCTAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

568/6881
FIGURE 528

MLRGPWRQLWLFLLLLLPGAPEPRGASRPWEGTDEPGSAWAWPGFQRLQEQLRAGALSKRYWTLFSCQVWPDDC
DEDEEAATGPLGWRLPLLQRYLDLLTTWYCSFKDCCPRGDCRISNNFTGLEWDLNVRLHGQHLVQQVLVLRTVRG
YLETPQPEKALALSFHGWSGTGKNFVARMLVENLYRDGLMSDCVRMF IATFHFPHPKYVDLYKEQLMSQIRETQQ
LCHQTLFIFDEAEKLHPGLLEVLGPHLERRAPEGHRAESPWTIFLFLSNLRGDI INEVVLKLLKAGWSREEITME
HLEPHLQAEIVETIDNGFGHSRLVKENLIDYFIPFLPLEYRHVRLCARDALFSQELLYKEETLDEIAQMMVYVPK
EEQLFSSQGCKSISQRINYFLS

WO 2004/030615

PCT/US2003/028547

569/6881
FIGURE 529

ATTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTCTCTGCTGGATTAAAGACGGCCACAGACCAGAAC
TTCCACTATACTACTTAAAATTACATAGGTGGCTTGTCAAATTCATTGATTAGTATTGTAAAAGGAAAAAGAAG
TTCCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCACAGATGAACAAACTT
CTACACTGATTTTTTAAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAACAGACACAAAAGCTG
GCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAACCCAACGCATAGAAGACTTTTTTCTCTTCT
AAAAACAAC TAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAATGAAGACTTTTACCTG
GACCCTAGGTGTGCTATTCTTCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATTCAAAATTA AAAAAT
AAACCAGAGAAGATACCCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATACACATTCTTGGTACC
TGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCATTAAAGACATGATCAC
CAGGATGGACCTTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGTTCTGCAACTGGTGGT
GGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACATGAAGTCTCGTGTAC
TCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACTTGAAGTTTCCCAACTGGAAAA
CAAAATCCTCAATGTCAACACAGAAATGTTGAAGATGGCAACAAGATACAGGGAAGTAGAGGTGAAATACGCTTC
CTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTTGAGGATATTTCCCG
ACAAGACACCCATGTGTCTCCCCACTTGTCCAGGTGGTGGCACAACATATTCCTAACAGCCAACAGTATACTCC
TGGTCTGCTGGGAGGTAACGAGATTTCAGAGGGATCCAGGTTATCCAGAGATTTAATGCCACCACCTGATCTGGC
AACTTCTCCACCAAAAGCCCTTTCAAGATACCACCGTAACTTTCATCAATGAAGGACCATTCAAAGACTGTCA
GCAAGCAAAAGAAGCTGGGCATTTCGGTCAGTGGGATTATATGATTAAACCTGAAAACAGCAATGGACCAATGCA
GTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTCAGAAAAGAACAGACGGCTCTGTCAACTT
CTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGAAACATTGACGGAGAATACTGGCTTGGACTGGAAAATAT
CTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGATAAAAAAGTCTATGC
AGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAACTTACCAGGGAAATGC
AGGGGATTCTATGATGTGGCATAATGGTAAACAATTCAACCACTGGACAGAGATAAAGATATGTATGCAGGAAA
CTGCGCCCACTTTTATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAATGGAGTATGGTACAG
AGGAGGCCATTACAGAAGCAAGCACCAAGATGGAATTTTCTGGGCCGAATACAGAGGCGGGTCATACTCCTTAAG
AGCAGTTCAGATGATGATCAAGCCTATTGACTGAAGAGAGAGACTCGCCAATTTAAATGACACAGAAGTTTGTAC
TTTTAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTACACATAAAGTTTTTAA
AATGAATTTTACCGTAACCTATAAAAGGGAACCTATAAATGT

WO 2004/030615

PCT/US2003/028547

570/6881
FIGURE 530

MKTFTWTLGVLFFLLVDTGHCRRGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGPICVNTKGQDAST
IKDMITRMDLENLKDVLRSQKREIDVLQLVVDVDGNIVNEVKLLRKESRNMNSRVTLQLYMQLLHEIIRKRDNSLE
LSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQSVMITLLEEQLRIFSRQDTHVSPPLVQVVPQHIPP
SQQYTPGLLGGNEIQRDPGYPRDLMPPDLATSPTKSPFKIPPVTFINEGPFKDCQQAQAKEAGHSVSGIYMIKPEN
SNGPMQLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFNIDGEYWLGLENIYMLSNQDNYKLLIELEDWS
DKKVYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDKDKMYAGNCAHFHKGGWWYNACAHSNL
NGVWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

WO 2004/030615

PCT/US2003/028547

571/6881
FIGURE 531

ATGGGGCTGCTCACTGGCACTGGAGGCCGAAAGAAGGTGAGGGCAAGTGAGATGCAGGGACCTCTTCTCACAGCT
GTGCTGACAAGCACAAAAGGAGCCCCCACGTCCACACCAGGAAAGGGGGGATGGTGCACAAGATCCAGAGGCG
TCAACAGACACGTCCAGCGAACAAGCACAGGGTGGGCCGTCCGGGAGCCTTGTGCCGCCAGGAGGAAAGCCGCAC
CGAGGGCAGCAGGGAGGCTCTGATGGCTGCCAAGAGGGTCTGATCCAGAAATATGGCCTCAATATGTGCCCCCAG
TGTTTCCGTCAGTACGCGAAGGATATCGGTTTCATTAAATTGGACTAA

WO 2004/030615

PCT/US2003/028547

572/6881
FIGURE 532

TAGGTTTCATTGGGAAGCTTGAGTTTTATCATTGGCAACAAATGCCATCAGTTTTTTCCAAGCTGACTTGTCTT
TTTTGAGCAAATCTCTGCCAAAATTACCCCTAAAAATATGAATAATCAATTTGTCAGGTTTTTTCAAACATAAAAT
GTTCTGTGAAAACAAGCAGCTAGTTCAGCTTGATCTCAAACAATTGTAACACTTTTTCTAGGGAAAAAAAAT
CTAGACATCCATACTTTATGGCAGATGTGCTTCATGCATACTTCCCATTGTCACACAGAATATCAAAATAACG
TGTACTCAAGGTCAAGATTTACTAACAACATAAAATTCAAAACTGCTAAACAACAGAATGCTGAATAAGGTGATC
CAATTTTTAATATTTTATTTGAGACAACATCTCACCTGTCAACCCAGGCTGGAATCCAGTGGTGTGACACAGCTC
ACTGCATCCTCAACCTCCTGGGCTCAAGCGATCGTCCCACCTCAGTCTCATGAGTGGTTGGGACTACAGGCATGC
ACCATCATGCCCGGCTCACTTTTTTTTTCTTTTTTTTTTAAATTGTAGACACAGGGTCTCACTATGTTGCCAGG
CCGGTCTTGAATCCTGGACTCAAGCAATCCCCCACCTTGGTTTCCCAAAGTGTTGGGATTACAGGCATGAGCT
ACTACATACAACTGAAATCTTTAATATGCTTGTCAAAAAGTTTTCTGATTACAGCAAATGGCACTTATATATAAA
AGAGAGAACAAGAAGCTGGATGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTAGGTGGGCAGATCA
CGAGGTGAGGAGTTCGAGACCAGCCTGGCCAACGTGGTGAAACCCCTCTCTACTAAAAATACAAAAATAGCCAG
GCATGGTGGCCACGCCTGTAATCCCAGCTACTTGGAAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGTGG
AGGTTGCAGTGAGCCAAGATTGCGCCGCTACATTCCAGCCTGGGCAACACGAGCGAAACTCCGTCTCAAAAAAAA
AAAAAAAAGAATAGAACTTGGCTGGATGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGGCAGGGCAG
TTGGATCACTTGAGGCCAGGAGTTCAAGACTAGCCTGGCTGACATGGTGAAACTCCATCTCTACTAAAAATACAG
AAAAAAAATTAGCTGGGAGTGGTGGCACACACCTGTATCCCAGCTACTCAGGTAGTTGAGGCACAACAATCAC
TTGAGCCTAGGAGGCCAGGCTGGAGTGAGGTGGCACGATCTTGGTTCACTGCAACCTCCACCTCCAGGGTTCAG
AGTAGCTGGGACTACAGGCCCCACACTACCACACCCGGCTAATTTTCGCTTTTTTTTCAGTAGAGACCGGGTTTTGC
CATGTTGGCCAGGCTGGTCTCGAAGCCTGAGCCATAACCTGGCGAAAAGATACTTTGAAATGTAACATCGTTTTT
CACTTCAAAATCAAGGTATTTTACCAACTTGTCTTTGGTACCTCCCCAAAACCTGATCTACTACATTTGCAGTTT
CATTCAATTTTCCAACATTAAGGAATAAACTTGAAGCGCTTACATTCTTGTGGGGGAAGTAAGAACAAAACACAT
AATAGGTCATGGTGGTCACATGAAAAGTAAAGGGTAACCGATTGGGGTAGGTGGTGGTAGTTTTGTGTGTGTGTT
TTTTTTTGAGACCAAGTCTCGCCGTTGCCAGGCTGGAGTGCGGTGGCATGATCTCAGTTCAGTCAACCTCCAC
TTCCTAGGTTCAAGCAATTCCTGCCTCAGCTACTCAAGAGGCTGAGGCAGGAGAATTCCTTGAACCTGGGAGG
CAGAGGTTGCAGTGAACGTGATAGTGCCGCTGCACTCCATTCTGGGCAAGAGCTAGACTCTTGTCTAAAAAAA
AAAAAATACCTTGAACGTGCTATACCTTTGCTTCTTTAAACCTTGCTCCACACAGTGTAGTCAAGCCGACTCTCCA
TACCTGTAGAAATTTAATCTCCTTTACCAATAGGTAGTAATAGGTGGATTTCTAAAAGATTTCCCACTACTGTT
TCAGTTTAAGATTAATCTCCATTTTCTTTCTCAGAGAGATTCCCATCTGCTTTAATTTTAAATCATCACTAACA
GTAGCTCAATCAATTAACGTTAACATCAATAAACATGTACCTTTAAAAGGTATGACAGGAACTGTCTTCATGTC
CTTACCCAAGCAAGTCATCCATGGATAAAAACGTTACCAGGAGCTGGAATACAAATGAGGACTTCCATTAAAAATG
CTAAACATCATTAACCTCTTTTCAAAGTTGTCTGTC

WO 2004/030615

PCT/US2003/028547

573/6881
FIGURE 533

MCFMHTSHFVTQNIKITCTQGQDLLTTKIPKLLNNRMLNKVIQFLIFYLRQHLLTSPRLESSGVTQLTASSTSWA
QAIVPPQSHEWLGLQACTIMPGSLFFSFFF

WO 2004/030615

PCT/US2003/028547

574/6881
FIGURE 534

ATCTGTAGATGGGAGTGATTAGCTGTTTTAAAAGTTAAATGTGACTGAGAAGGAAATTGAGTAGGGCAAATTTTA
AATGGGTATTATTTTTTCATCTTCAAACAGGCAGACCTGTTATCCTAAACTAGGTGAGTCAGCTTTTGGTACATGT
GATGATTTTCAGTGTAACCAATGATGTAATGATTCTGCCAAATGAAATATAATGATATCACTGTAAAACCGTTCC
ATTTTGATTCTGAGGTTACTCTACTAACAAGCATCACACATTTGTATTTTGCCCTGATTAATATGTTGGCTTCGC
TTTCAGGGTTTTTAATGACCACAACAAGCAAGCATGCAGCTTACTGCTTGAAAGGGTCTTGCCTCACCCAAGCTA
GAGTGCAGTGGCCTTTGAAGCTTACTACAGCCTCAAACCTTCTGGGCTCAAGTGATCCTCAGCCTCCCAGTGGTCT
TTGTAGACTGCCTGATGGAGTCTCATGGCACAAGAAGATTAAAACAGTGTCTCCAATTTTAATAAATTTTGCAA
TCC

WO 2004/030615

PCT/US2003/028547

575/6881
FIGURE 535

AGTTAAACAGCTGAGCTTCTGAATGCCTGCAAGAAGCTGCCCTTTGAAATTAAGAACTTCGTGAAGAAAACAGA
GGCTCTTCGGTTGCAGTATCGCTACTTAGACTTGCCTAGTTTCCAAATGCAGTATAACCTGCGACTGAGGTCCCA
GATGGTCATGAAAATGCGGGAATATCTCTGTAATCTGCATGGGTTTGTGGATATAGAAACCCCCACATTGTTTAA
GAGGACCCACAGGGGTGCCAAAGAGTTTTTAGTACCATCCAGGGAACCTGGAAAGTTTTGTTCTCTCCCTCAGAG
TCCTCAACAGTTTAAGCAACTTCTGATGGTTGGCGGTTTAGACAGATATTTTCAGGTTGCCCGATGTTATCGAGA
TGAAGGTTCAAGACCAGACAGACAGCCTGAGTTTACTCAGATTGACATAGAGATGTCATTTGTAGACCAGACTGG
GATCCAGAGTTTAATTGAGGGTTTGCTCCAGTATTCCTGGCCCAATGACAAAGATCCTGTGGTTGTTCCCTTTCC
TACTATGACTTTTGCTGAGGTGCTGGCCACCTATGGAACCTGATAAACCTGACACTCGCTTTGGAATGAAGATTAT
AGATATCAGTGATGTGTTTAGAAACACAGAGATTGGATTTCTTCAAGATGCACTTAGTAAGCCCCATGGAACCTGT
GAAAGCCATATGTATCCCTGAAGGAGCAAAATACTTAAAAAGGAAAGACATTGAATCCATTAGAACTTTGCAGC
TGACCATTTTAATCAGGAAATCTTACCTGTATTCCTTAACGCCAATAGAACTGGAATTCTCCAGTTGCTAATTT
CATAATGGAGTCACAAAGACTGGAATTAATCAGACTAATGGAGACCCAAGAGGAAGATGTGGTCTACTAAGTGC
TGGAGAGCACAATAAAGCATGCTCTTTGTTAGGAAATTACGACTGGAATGTGCTGACCTTCTAGAAACAAGAGG
AGTGGTGCTCCGTGACCCCACTCTGTTCTCTTTCCTTTGGGTGGTAGATTTCCCACTCTCTCTGCCAAGGAGGA
AAGTCCCAGAGAGCTGGAATCGGCCCACCACCCATTTACTGCTCCCCACCCAGTGACATACATCTCCTGTACAC
TGAGCCCAAAAAGGCCCGTAGCCAACACTATGACTTGGTTTTAAATGGCAATGAAATAGGAGGTGGTTCAATTCCG
AATTCACAATGCAGAGCTGCAGCGTTATATCCTGGCAACCTTACTAAAGGAGGATGTGAAAATGCTCTCCCATCT
GCTCCAGGCTTTAGATTATGGGGCACCCCTCATGGAGGAATTGCCTTAGGGTTAGACAGACTGATATGCCTTGT
CACTGGATCTCCAAGCATCAGAGATGTCATAGCCTTCCCAAAGTCCTTCCGGGGACATGACCTCATGAGCAATAC
CCCAGATTCTGTCCCTCCTGAGGAACTGAAGCCCTATCATATCCGAGTCTCCAAGCCAACAGACTCCAAAGCAGA
AAGAGCTCATTGAATCATGCATACCATGCAGAAAGTTGAGCTTTTAGGTTTGTCTCTTTGCTTCCCCAAGGCT
AAAGTCAGATCTAGAGTTCTGCCACAGGTCTAACAATCAAGTCTTTAGATGGAAGGAATCCAGGCAACATTCTTC
ACCACAACGAAGAAACAGATAAAAGATAACCAATTTTGACTTGATTTCATGCATCATTTGGATTTTTTTTTGGTTA
GGACTTTTTTTGAAGTTCCTTTTTTACTTAGGTGTGAAAGATGGTTCTTTGTTGAAATAATATAGTGGTTTTAGTGT
TTTCAAATCATGTTTCTCATACCCAGATAGTAGATTATTCACCTTAGGACAGAGGTAATCAAATTATGTGTGAAAT
GTAGGAAAATGCTTGCCCTGTAACTAGTGAGTTGATGGAGCATTGCTTCATCATCCTCATCAAGAGAATCAT
ATAAATTAAGCTTTATAATGACATTTCAACCATCAACATAATATAGTGAGGAGTAGCATAATTTTTTTAATAAT
GCAGAAAACATCACTGAAATGAGAGTCACAAATTTTCTTCAGTGTTTCAGCCTGAGTAAGTTACATAAACCTCG
CTTAGCCTCCCTTCTGCTAATGTGTAAAATACATACTTGCCCTGGCTACCTCACCGGGCTGTTATTGCTGGAAT
CAGAGGAGATAACATATATGGAAGATAAAGTGAATAAAAGTACTTTGAAAAACT

WO 2004/030615

PCT/US2003/028547

576/6881
FIGURE 536

MQYNLRLRSQMVMKMREYLCNLHGFVDIETPTLFKRTPGGAKEFLVPSREPGKFCSLPQSPQQFKQLLMVGGLDR
YFQVARCYRDEGSRPDRQPEFTQIDIEMSFVDQTGIQSLIEGLLQYSWPNDKDPVVVFPPTMTFAEVLATYGTDK
PDTRFGMKIIDISDVFRNTEIGFLQDALSKPHGTVKAICIEGAKYLKRKDIESIRNFAADHFNQEILPVFLNAN
RNWNSPVANFIMESQRLELIRLMETQEEDVLLTAGEHNKACSLGKLRLECADLLETGRGVVLRDPTLFSFLWVV
DFPLFLPKESPRELESAAHPFTAPHPSDIHLTYTEPKKARSQHYDLVLNGNEIGGGSIRIHNAELQRYILATLL
KEDVKMLSHLLQALDYGAPPHGGIALGLDRLICLVGTGSPSIRDVIAFPKSFRGHDLMSTPDSPVPPEELKPYHIR
VSKPTDSKAERAH

WO 2004/030615

PCT/US2003/028547

577/6881
FIGURE 537

GCCTGTCTGCATTCTACTATATAAAGCAGCAGAGACGTTGACTAGCGCATATTTGCTAAGAGCACCATGCGCGCA
GCAGCCATCTCCACTCCAAAGTTAGACAAAATGCCAGGAATGTTCTTCTCTGCTAACCCAAAGGAATTGAAAGGA
ACCACTCATTCACTTCTAGACGACAAAATGCAAAAAGGAGGCCAAAGACTTTTGGAATGGATATGAAAGCATAC
CTGAGATCTATGATCCCACATCTGGAATCTGGAATGAAATCTTCCAAGTCCAAGGATGTACTTTCTGCTGCTGAA
GTAATGCAATGGTCTCAATCTCTGGA AAAACTTCTTGCCAACCAAACCTGGTCAAAATGTCTTTGGAAGTTTCCTA
AAGTCTGAATT CAGTGAGGAGAATATTGAGTTCTGGCTGGCTTGTGAAGACTATAAGAAAACAGAGTCTGATCTT
TTGCCCTGTAAAGCAGAAGAGATATATAAAGCATTGTGTCATT CAGATGCTGCTAAACAAATCAATATTGACTTC
CGCACTCGAGAATCTACAGCCAAGAAGATTAAAGCACCAACCCCCACGTGTTTTGATGAAGCACAAAAAGTCATA
TATACTCTTATGGA AAAAGGACTCTTATCCCAGGTTCC TCAAATCAGATATTTACTTAAATCTTCTAAATGACCTG
CAGGCTAATAGCCTAAAGTGACTGGTCCCTGGCTGAAGGGAATTAACAGATAGTATCAAGCGCAGAAGGAATGTG
CCAGTATGGCTCCCTGGGTGAACAGCTTGGCCTTTTTTGGGTGTCTTGACAGGCCAAGAAGAACAAATGACTCAG
AATGGATTAACATGAAAGTTATCCAGGCGCAGAGTTGAAGAAGCATAAGCAAGACAAAAACAGAGAGACCGCAGA
AGGAGGAAGATACTGTGGTACTGTCATAAAAAACAGTGGAGCTCTGTATTAGAAAGCCCTCAGAACTGGGAAGG
CCAGGTAAC TCTAGTTACACAGAACTGTGACTAAAGTCTATGAACTGATTACAACAGACTGTAAGAATCAAAG
TCAACTGACATCTATGCTACATATTATTATATAGTTTGTACTGAGCTATTGAAGTCCCATTA ACTTAAAGTATAT
GTTTTCAAATTGCCATTGCTACTATTGCTTGTCTGGTGTATTTTATTTTATTGTTTTTGACTTTGGAAGAGATGA
ACTGTGTATTTAACTTAAGCTATTGCTCTTAAAACAGGGAGTCAGAATATATTTGTAAGTTAAATCATTGGTGC
TAATAATAAATGTGGATTTTGTATTAAAATATATAGAAGCAATTTCTGTTTACATGTCTTGCTACTTTTAAAAA
CTTGCATTTATTCCTCAGATTTTAAAAATAAATAAATAATTCATTT

WO 2004/030615

PCT/US2003/028547

578/6881
FIGURE 538

CTTTTCGATCCGCCATCTGCAGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTATGGGGAAGACCA
TCACCCTCGAGGTTGAACTCTCGGATACAATAGATAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAATTCCTC
CTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGTTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAA
AGGAGTCTACTCTTCATCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTC
CCAGGAAGAATAAGCACAAGAGAAAAGAAGGTTAAGCTGGCTCTCCTGAAATATTATAAGGTGGATGAGAATGGCT
TTATGGCAAGCCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGACA
AGTAACTGTATGACTTAATAA

WO 2004/030615

PCT/US2003/028547

579/6881
FIGURE 539

MQIFVKTLMGKTIITLEVELSDTIDNVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYNIQKESTLHLVLRRLRG
GAKKRKKKSYTTPRKNKHKRKKVKLALLKYYKVDENGFMASHFDRHYCGKCCLTYCFNKPEDK

WO 2004/030615

PCT/US2003/028547

580/6881
FIGURE 540

AAAACAGCCGGGGCTCCAGCGGGAGAACGATAATGCAAAGTGCTATGTTCTTGGCTGTTCAACACGACTGCAGAC
CCATGGACAAGAGCGCAGGCAGTGGCCACAAGAGCGAGGAGAAGCGAGAAAAGATGAAACGGACCCCTTTTAAAG
ATTGGAAGACCCGTTTGAGCTACTTCTTACAAAATTCTCTACTCCTGGGAAGCCCCAAAACCGGCCAAAAAAGCA
AACAGCAAGCTTTTCATCAAGCCTTCTCCTGAGGAAGCACAGCTGTGGTCAGAAGCATTGACGAGCTGCTAGCCA
GCAAATATGGTCTTGCTGCATTACAGGGCTTTTTTAAAGTCGGAATTCTGTGAAGAAAATATTGAATTCTGGCTGG
CCTGTGAAGACTTCAAAAAACCAAATCACCCCAAAAGCTGTCCTCAAAAAGCAAGGAAAATATATACTGACTTCA
TAGAAAAGGAAGCTCCAAAAGAGATAAACATAGATTTTCAAACCAAAACTCTGATTGCCCAAGATATACAAGAAG
CTACAAGTGGCTGCTTTACAACCTGCCAGAAAAGGGTATACAGCTTGATGGAGAACAACCTCTTATCCTCGTTTCT
TGGAGTCAGAATTCTACCAGGACTTGTGTAAAAAGCCACAAATCACACAGAGCCTCATGCTACATGAAATGTAA
AAGGGAGCCCAGAAATGGAGGACATTTCAATCTTTTTCTGAGGGGAAGGACTGTGACCTGCCATAAAGACTGAC
CTTGAATTCAGCCTGGGTGTTTCAGGAAACATCACTCAGAACTATTGATTCAAAGTTGGGTAGTGAATCAGGAAGC
CAGTAACTGACTAGGAGAAGCTGGTATCAGAACAGCTTCCCTCACTGTGTACAGAACGCAAGAAGGGAATAGGTG
GTCTGAACGTGGTGTCTCACTCTGAAAAGCAGGAATGTAAGATGATGAAAGAGACAATGTAATACTGTTGGTCCA
AAAGCATTAAAAATCAATAGATCTGGGATTATGTGGCCTTAGGTAGCTGGTTGTACATCTTCCCTAAATCGATC
CATGTTACCACATAGTAGTTTTAGTTTAGGATTCAGTAACAGTGAAGTGTTTACTATGTGCAAGGGTATTGAAGT
TCTTATGACCACAGATCATCAGTACTGTTGTCTCATGTAATGCTAAAACCTGAAATGGTCCGTGTTTGCATTGTTA
AAAATGATGTGTGAAATAGAATGAGTGCTATGGTGTGAAAACCTGCAGTGTCCGTTATGAGTGCCAAAAATCTGT
CTTGAAGGCAGCTACACTTTGAAGTGGTCTTTGAATACTTTTAATAAATTTATTTTGATAAATAATATTG

WO 2004/030615

PCT/US2003/028547

581/6881
FIGURE 541

MQSAMFLAVQHDCRPMDKSAGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGKPKTGKKSQQAFIKPSPE
EAQLWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACEDFKKTKSPQKLSSKARKIYTDFIEKEAPKEINI
DFQTKTLIAQNIQEATSGCFTTAQKRVYSLMENNSYPRFLESEFYQDLCKKPQITTEPHAT

WO 2004/030615

PCT/US2003/028547

582/6881
FIGURE 542

TGAAGATGAAAAAGAAGATCATAAAATGTGCGCCAACAACGGCAGGCGGCATCTAAAGCAGCTTCTAAACAGAG
AGAGATGCTCATGGAAGATGTGGGCAGTGAGGAAGAACAAGAAGAGGAGGATGAGGCACCATTCCAGGAGAAAGA
TTCCGGCAGCGATGAAGATTTCTAATGGAAGATGATGACGATAGTGACTATGGCAGTTCGAAAAAGAAAAACAA
AAAGATGGTTAAGAAGTCCAAACCTGAAAGAAAAGAAAAGAAAATGCCCAAACCCAGACTAAAGGCTACAGTGAC
GCCAAGTCCAGTGAAAGGCAAAGGGAAAGTGGGTGCCCCACAGCTTCAAAGGCATCAAAGGAAAAGACTCCTTC
TCCCAAAGAAGAAGATGAGGAACCGGAAAGCCCGCCAGAAAAGAAAACATCTACAAGCCCCCACCAGAGAAATC
TGGGGATGAAGGGTCTGAAGATGAAGCCCCTTCTGGGGAGGATTAAAAGTGATGATGGTCTGGGGAGAGATTTTA
TTAAAAAAGAAAAGAGGGAGGAAAAAAGAACCTACTTAAGATAGAACATGGTTTTGGCTATGGCTT
GACTCATGGGCTTTCAGTGCTTTTTTCCATTTGTTGAAAGTAACATTTCTCTCTCTCTCTTT

WO 2004/030615

PCT/US2003/028547

583/6881
FIGURE 543

AGCCTGAGGAGCTATTTTGAGCAATGGGGAATGCTCACGGACTGTGTGGTAATGAGAGACCCAAACACCAAGTGC
TCCAGGGGCTTTGGGTTTGTACATATGCCATTGTGGAGGAGGTGGATGCAGCCATGAATGCAAGGCCACACAAG
GTGGATGGAAGAGTTGGAGAACCAAAGAGAGCTGTTTCAAGGGAAGATTCTCAAAGACCAGGTGCTCACTTAACT
GTGAAAAAGATATTTGTTGGCAGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATAATTTGAACAGTTTG
GAAAAACGGAAGTGATTGAAATCATGACTGACTGAGGCAGTGGCAAGAAAAGGGGCTTTGCCTTTGTAACTTTG
ATGACCATGACTCTGTGAATAAGACTGCCATTACAGAAATACCATCCTACGAATGGCCATAACTGTGAAGTTAGGA
AAGCCCTGTCAAAGTAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAAGTCGAAGTGGTTCTGGAACTTTGGTT
TGGTCGTGGAGGTGGTTTCGGTTGGCATGACAGCCGTGGTGGTGGTGGTGGATATGGTGGCAGTGAGGATGGCGA
TAATGGATTTGGTAATGATGGAAGCAATTTTGGAGGTGGTGGAAAGCTACAGTGATTTTGGCACTACAATAATCA
GTCTTCAAATTTTGGACCCATGAAGGGAGGAACTTTGGAGGCAGAAGCTCTGGGCCCTATGGCGGTGGAGGCC
AATACTCTGCCAAACCACGAAACCAAGGTGGCTATGGTGGTTTCAGTAGCAGCAGTAGCTATGGCAGTGGCAGAA
GATTTTAATTAGGAAACAAAGCTTAGCTGGAGAGGAGAGCCGGAGAAGTGACAGGGAAGCTACAGGTTACAACAG
ATTTGTGAACCTAGCCAAGCACAGTGGTGGCAGGGCCTAACTGCTACAAAGGAGACATGTTTGTAGACAAATACTC
ATGTGTATGGGCAAAAACTCGAGGACTGTATTTGTGACTAATTGTGTAAACAGGTTATTTTAGTTTCTGTTCTGT
GGAAAGCGTAAAGCATTCCAACAAAGGGTTTTAATGCAGATTTTTTTTTTTTTTGGCACCCATGCTGTTGATTGCT
AAATGTAATAGTCTGATGGTGTGCTGAATAAATGTCTT

WO 2004/030615

PCT/US2003/028547

584/6881
FIGURE 544

AGGCAGAGCCCGCGAGGAGGTGACGCGGCTGCGGAGGTGACGCGGGAGGTGCGCGCCCCCTCCGGCGCGGGGAG
GGCGCTGAAGATCGGGGCCGCTCGGGCCGACGGCCGCTCCAGCGCCGCGGGATGTAGCGCGGGGACCGCGGGCCC
CCAGCAGAGCCCGCCTGCCCGGCTTTTAGAAGACCAAACCTGGACAATGGACTTTGCTCACTATGATGACATGATC
TCCATTGACCTCCATTTGTCTACCATCAGAGGGAGATCTCTGCCCCCTGGGGCTGAGAGACCCCAACCTTTCCCC
AAGCTGAAGCTGCAGGGTATTGAGGTACCAGCCAGATGTCTTCCACAAAGGATCTGTGGTGGCACAGGGGAATG
GGGCTCCTGCCAGTAACAGGGAAGCTGACACGGTGGAACCTGGCTGAACTGGGACCCCTGCTAGAAGAGAAGGGCA
AACGGGTAATCGCCAACCCACCCAAAGCTGAAGAAGAGCAAACATGCCCAGTGCCCCAGGAAGAAGAGGAGGAGG
TGCGGGTACTGACACTTCCCTTGCAAGCCCACCACGCCATGGAGAAGATGGAAGAGTTTGTGTACAAGGTCTGGG
AGGGACGTTGGAGGGTCATCCCATATGATGTGCTCCCTGACTGGCTAAAGGACAACGACTATCTGCTACATGGTC
ATAGACCTCCCATGCCCTCCTTTTCGGGCTTGCTTCAAGAGCATCTTCCGCATTACATACAGAACTGGCAACATCT
GGACCCATCTGCTTGGTTTCGTGCTGTTTCTCTTTTGGGAATCTTGACCATGCTCAGACCAAAATGTACTTCA
TGGCCCCCTCTACAGGAGAAGGTGGTTTTTGGGATGTTCTTTTGGGTGCAGTGTCTGCTCAGCTTCTCCTGGC
TCTTTACACCGTCTATTGTCAATTCAGAGAAAGTCTCTCGGACTTTTTCCAACTGGACTATTCAGGGATTGCTC
TTCTAATTATGGGGAGCTTTGTCCCCTGGCTCTATTATTCCTTCTACTGCTCCCCACAGCCACGGCTCATCTACC
TCTCCATCGTCTGTGTCTGGGCATTTCTGCCATCATTGTGGCGCAGTGGGACCGGTTTGCCACTCCTAAGCACC
GGCAGACAAGAGCAGGCGTGTTCCTGGGACTTGGCTTGAGTGGCGTCGTGCCACCATGCATTTACTATCGCTG
AGGGCTTTGTCAAGGCCACCACAGTGGGCCAGATGGGCTGGTTCTTCTCATGGCTGTGATGTACATCACTGGAG
CTGGCCTTTATGCTGCTCGAATTCCTGAGCGCTTCTTTCTGGAAAATTTGACATATGGTTCCAGTCTCATCAGA
TTTTCCATGTCCTGGTGGTGGCAGCAGCCTTTGTCCACTTCTATGGAGTCTCCAACCTTCAGGAATTCGGTTACG
GCCTAGAAGGCGGCTGTACTGATGACACCCTTCTCTGAGCCTTCCACCTGCGGGGTGGAGGAGGAACCTTCCCAA
GTGCTTTTAAAAATAACTTCTTTGCTGAAGTGAGAGGAAGAGTCTGAGTTGTCTGTTTCTAGAAGAAACCTCTTA
GAGAATTCAGTACCAACCAAGCTTCAGCCCACTTTACACCCACTGGGCAATAAACTTTCCATTTCATTCTCCT
AGCTGGGGATGGGGCATGGTCAAACCTTAGCCATCCCCTCCTCAGCAAGGCATCTACCGGCCCTCACAGAGACAG
TACTTTGAACTCATGTTGAGATTTTACCCTCTCCTCCAACCATTTTGGGAAAATTATGGACTGGGACTCTTCAG
AAATTCTGTCTTTTCTTCTGGAAGAAAATGTCCCTCCCTTACCCCATCCTTAACCTTTGTATCCTGGCTTATAAC
AGGCCATCCATTTTGTAGCACACTTTTCAAAAACAATTATATACCTGGTCCCATCTTTCTAGGGCCTGGATCT
GCTTATAGAGCAGGAAGAATAAAGCCACCAACTTTTACCTAGCCCGGCTAATCATGGAAGTGTGTCCAGGCTTCA
AGTAACCTTGAGTTTTAATTTTTTTTTTTTCTTGGCAGAGTAATGTAAATTTAAATGGGGAAAGATATTTAATAT
TTAATACTAAGCTTTAAAAGAAACCTGCTATCATTGCTATGTATCTTGATGCAAAGACTATGATGTTAATAAAA
GAAAGTACAGAAGACACTTGGCATTCAAAGATTTT

WO 2004/030615

PCT/US2003/028547

585/6881
FIGURE 545

GGCCGCGGAGCCGGGCGGAGCTGGCTTGCGGCTCCCGGGGCCGGCTCTCCGGCCGGAGACATGSCCCGGGGGGCCC
GGCCCGCTAGGCAGGCCTCGCCCCGATACGGTCGCCATGCCCAAGAGAGGAAAGCGACTCAAGTTCCGGGGCCAC
GACGCCTGCTCCGGCCGAGTGACCGTGCGGATTACGCCAACTCGGATCCGGCGGTCTGTGAGGTCTGGACGAGTC
AAGAAAGCCGTAGCCAACGCTGTTTACGAGGAAGTAAATCTCTTTGTGGCTTGGAAGCCTCTCAGGTTTCTGCA
GAGGAAGCTCTTTCTGGGGCTGGTGAGCCCTGTGACATCATCGACAGCAGTGATGAGATGGATGCCAGGAGGAA
AGCATCCATGAGAGAACTGTCTCCAGAAAAAGAAAAGCAAGAGACACAAAGAAGAACTGGACGGGGCTGGAGGA
GAAGAGTATCCCATGGATATTTGGCTATTGCTGGCCTCCTATATCCGTCCTGAGGACATTGTGAATTTTCCCTG
ATTTGTAAGAATGCCTGGACTGTCACTTGCACTGCTGCCCTTTGGACCAGGTTGTACCGAAGGCACTACACGCTG
GATGCTTCCCTGCCTTTGCGTCTGCGACCAGAGTCAATGGAGAAGCTGCGCTGTCTCCGGGCTTGTGTGATCCGA
TCTCTGTACCATATGTATGAGCCATTTGCTGCTCGAATCTCCAAGAATCCAGCCATTCCAGAAAGCACCCCCAGC
ACATTAAAGAATTCCAAATGCTTACTTTTCTGGTGCGAAAGATTGTTGGGAACAGACAGGAACCAATGTGGGAA
TTCAACTTCAAGTTCAAAAAACAGTCCCCTAGGTTAAAGAGCAAGTGTACAGGAGGATTGCAGCCTCCCGTTTCA
TACGAAGATGTTTATACCAATCCAGACCAGGACTGCTGCCTACTGCAGGTCACCACCCTCAATTTTATCTTTATT
CCGATTGTATGGGAATGATATTTACTCTGTTTACTATCAATGTGAGCACGGACATGCGGCATCATCGAGTGAGA
CTGGTGTTCGAAGATTCCCCTGTCCATGGTGGTCGGAACTGCGCAGTGAACAGGGTGTGCAAGTCATCCTGGAC
CCAGTGACACAGCGTTCCGGCTCTTTGACTGGTGGCATCCTCAGTACCCATTCTCCCTGAGAGCGTAGTTACTGCTT
CCCATCCCTTGGGGGCAGCCTCGAGTGTAGTCCATTAGTAATCAGATTCCAGTTTGGACAGGGTGGCTGGATTGT
ATATCTCGTTAGTAATGTACATGCTCTTACAGTTCTAGGGCTCCTGTTAGGGGAGGGAGAAATGTTGAATCAAGA
GGGAAACAACACTACTATGATTTATAAACATATTTAATGTAAAAATTTGCATTTAAAGGAGTGGCCCTGTTTTC
TGTGTTAAACCCCATTTGGTGCTATTGAGTTTGTCTTTATCTTTATCCCAGTGAAAATTGTTGATCTTGCT
GTAGGGAAAAATTAACCTCTTTGAATCTCCAAACAAGGAAGTTTACGATTCCCTTATGGATCAGAGGAACCTTA
GAGGCCTGAAATTGTTGCTTCCAGTTTAGCTGCCCTCAAATTCAAGTGAATATTTCCCTTCTCCCTTTACCCCT
TCTCCAGAAATAAAGCAGGTGACAGGGTTTTCAGAACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

586/6881
FIGURE 546

MARGPGPLGRPRPDTVAMPKRGKRLKFRAHDACSGRVTVADYANS DPAVVRSGRVKKAVANAVQQEVKSLCGLEA
SQVPAEEALSGAGEPCDIIDSSDEMDAQEESIHERTVSRKKKSKRHKEELDGAGGEEYPMDIWLLLASYIRPEDI
VNFS LICKNAWTVTCTAAFWTRL YRRHYTL DASLP LRLRPESMEKLRCLRACVIRSLYHMYEPFAARISK NPAIP
ESTPSTLKN SKCLLFWCRKIVGNRQEP MWEFNFKFKKQSPRLKSKCTGGLQPPVQYEDVHTNPDQDCCLLQVTTL
NFI FIP IVMGMIFTLFTINVSTDMRHHRVRLVFQDSPVHGGRKLRSEQGVQVILDPVHSVRLEFDWWHPQYPFSLR
A

WO 2004/030615

PCT/US2003/028547

587/6881
FIGURE 547

AGTGGAGTGGGACAGGTATATAAAGGAAGTACAGGGCCTGGGGAAGAGGCCCTGTCTAGGTAGCTGGCACCAGGA
GCCGTGGGCAAGGGAAGAGGCCACACCCCTGCCCTGCTCTGCTGCAGCCAGAATGGGTGTGAAGGCGTCTCAAACA
GGCTTTGTGGTCTCTGGTGTCTCCAGTGTCTGCTCTGCATACAACTGGTCTGCTACTACACCAGCTGGTCCCA
TACCGGGAAGGCGATGGGAGCTGCTTCCAGATGCCCTTGACCGCTTCTCTGTACCCACATCATCTACAGCTTT
GCCAATATAAGCAACGATCACATCGACACCTGGGAGTGAATGATGTGACGCTCTACGGCATGTCTAACACACTC
AAGAACAGGAACCCCAACCTGAAGACTCTCTTGTCTGTCTGGAGGATGGAACCTTTGGGTCTCAAAGATTTTCCAAG
ATAGCCTCCAACACCCAGAGTCGCCGGACTTTCATCAAGTCAGTACCGCCATTTCTGCGCACCCATGGCTTTGAT
GGGCTGGACCTTGCTGGCTCTACCCCTGGACGGAGAGACAAACAGCATTTTACCACCCTAATCAAGGAAATGAAG
GCCGAATTTATAAAGGAAGCCAGCCAGGGAAAAAGCAGCTCCTGCTCAGCGCAGCACTGTCTGCGGGGAAGGTC
ACCATTGACAGCAGCTATGACATTGCCAAGATATCCCAACACCTGGATTTTATTAGCATCATGACCTACGATTTT
CATGGAGCCTGGCGTGGGACCACAGGCCATCACAGTCCCCTGTTCCGAGGTGAGGAGGATGCAAGTCTTGACAGA
TTCAGCAACACTGACTATGCTGTGGGGTACATGTTGAGGCTGGGGGCTCCTGCCAGTAAGCTGGTGATGGGCATC
CCCACCTTCCGGGAGGAGCTTCACTCTGGCTTCTTCTGAGACTGGTGTGGAGCCCCAATCTCAGGACCGGGAATT
CCAGGCCGGTTTACCAAGGAGGACAGGGACCCTTGCCCTACTATGAGATCTGTGACTTCCTCCGCGGAGCCACAGTC
CATAGAATCCTCGGCCAGCAGGTCCCCTATGCCACCAAGGGCAACCAGTGGGTAGGATACGACGACCAGGAAAGC
GTCAAAGCAAGGTGCAGTACCTGAAGGACAGGCAGCTGGCGGGCGCCATGGTATGGGCCCTGGACCTGGATGAC
TTCCAGGGCTCCTTCTGTGGCCAGGATCTGCGCTTCCCTCTCACCATGCCATCAAGGATGCACTCGCTGCAACG
TAGCCCTCTGTTCTGCACACAGCACGGGGGCCAAGGATGCCCCGTCCCCCTCTGGCTCCAGCTGGCCGGGAGCCT
GATCACCTGCCCTGCTGAGTCCCAGGCTGAGCCTCAGTCTCCCTCCCTTGGGGCCTATGCAGAGGTCCACAACAC
ACAGATTTGAGCTCAGCCCTGGTGGGCAGAGAGGTAGGGATGGGGCTGTGGGGATAGTGAGGCATCGCAATGTAA
GACTCGGGATTAGTACACACTTGTGATTAAATGGAAATGTTTACAGATCCCCAAGCCTGGCAAGGGAATTTCTTC
AACTCCCTGCCCCCAGCCCTCCTTATCAAAGGACACCATTTTGGCAAGCTCTATCACCAGGAGCCAAACATCC
TACAAGACACAGTGACCATACTAATTATACCCCTGCAAAGCCAGCTTGAAACCTTCACTTAGGAACGTAATCG
TGTCCCTATCCTACTTCCCCTTCTAATTCCACAGCTGCTCAATAAAGTACAAGAGCTTAACAGTGTGTTGGCG
CTTTGCTTTGGTCTATCTTTGAGCGCCCACTAGACCCACTGGACTCACCTCCCCCATCTCTTCTGGGTTCCCTCC
TCTGAGCCTTGGGACCCCTGAGCTTGCAGAGATGAGGCCGCCATGT

WO 2004/030615

PCT/US2003/028547

588/6881
FIGURE 548

CAGGGTAACGCTGTCTTGTGGACCCGCACTTCCCACCCGAGACCTCTCACTGAGCCCCGAGCCGCGCGGACATGA
GCCACGGGAAGGGAACCGACATGCTCCCGGAGATCGCCGCCGCCGTGGGCTTCCTCTCCAGCCTCCTGAGGACCC
GGGGCTGCGTGAGCGAGCAGAGGCTTAAGGTCTTCAGCGGGGCGCTCCAGGAGGCACTCACAGAGCACTACAAAC
ACCACTGGTTTTCCGAAAAGCCGTCCAAGGGCTCCGGCTACCGCTGCATTTCGCATCAACCACAAGATGGACCCCA
TCATCAGCAGGGTGGCCAGCCAGATCGGACTCAGCCAGCCCCAGCTGCACCAGCTGCTGCCAGCGAGCTGACCC
TGTGGGTGGACCCCTATGAGGTGTCTACCGCATTTGGGAGGACGGCTCCATCTGCGTCTTGTACGAGGAGGCC
CACTGGCCGCTCCTGTGGGCTCCTCACCTGCAAGAACCAAGTGCTGCTGGGCCGAGCAGCCCCCTCCAAGAACT
ACGTGATGGCAGTCTCCAGCTAGGCCCTTCCGCCGCCGCCGTGGGCGCCGCCGTGCTCATGCTGCCGTGACAACA
GGCCACCACATACTCAACCTGGGGAAGTGTATTTTAAATGAAGAGCTATTTATATATATTATTTTTTTTAAAG
AAAGGAGGAAAAGAAACCAAAAGTTTTTTTTTAAGAAAAAAATCCTTCAAGGAGCTGCTTGGAAGTGGCCTCCC
CAGGTGCCTTTGGAGAGAACTGTTGCGTGTCTGAGTCTGTGAGCCAGTGTCTGCCTATAGGAGGGGGAGCTGTTA
GGGGGTAGACCTAGCCAAGGAGAAGTGGGAGACGTTTGGCTAGCACCCAGGAAGATGTGAGAGGGGAGCAAG
GGTTAGCAACTGTGAACAGAGAGGTGCGGATTTGCCCTGGGGGAGGAAGAGAGGCCAAGTTTCAGAGCTCTCTGTC
TCCCCAGCCAGACACCTGCATCCCTGGCTCCTCTATTACTCAGGGGCATTTCATGCCTGGACTTAAACAATACTA
TGTTATCTTTTCTTTTATTTTTCTAATGAGGTCTGGGCAGAGAGTGAAGGCCCTCTCCTGATTCCTACTGTCC
TAAGCTGCTTTTCTTGAAATCATGACTTGTCTTAATTCTACCTCAGGGGCCTGTAGATGTTGCTTTCCAGCCA
GGAATCTAAAGCTTTGGGTTTTCTGAGGGGGGAGGAGGGAAGTATTGGGGTTAGGATGGAAGGGAAC
TCTGCACAAAACCTTTGCTTTGCTAGTGTCTTTGTGTGTATGTGTGGCAAATAATTGGGGGTGATTTGCAAT
GAAATTTGGGACCCAAAGAGTATCCACTGGGGATGTTTTTGGCCAAAACCTCTTCCTTTTGAACCACATGAAA
GTCTTGATGTCTGTGCCATGATCCCTTTGAGAGGTGGCTCAAAAGCTACAGGGAAGTCCAGGTCTTTTATTACTG
CCTTCTTTTCAAAAGCACAACTCTCCTCTAACCTCCCTCCCCCTTCCCTTCTGGTCCGGTTCATAGAGCTACCG
TATTTTCTAGGACAAGAGTTCTCAGTCACTGTGCAATATGCCCCCTGGGTCCCAGGAGGGTCTGGAGGAAAAGT
GCTATCAGAACCTCCTGATGCCCTGGTGGGCTTAGGGAACCATCTCTCCTGCTCTCCTTGGGATGATGGCTGGCT
AGTCAGCCTTGCATGTATTCTTGGCTGAATGGGAGAGTGCCCCATGTTCTGCAAGACTACTTGGTATTCTTGTA
GGCCCGACACTAAATAAAAGCCAAACCTTGGGCACTGTTTTTCTCCCTGGTGTCTCAGAGCACCTGTGGGAAAGG
TTGCTGTCTGTCTCAGTACAATCCAAATTTGTCTGACTTGTGCAATATATACTGTTGTGGGTGGAGAAAAGT
GGAAAGCTACACTGGGAAGAACTCCCTTCCCTTCAATTTCTCAGTGACATTGATGAGGGGTCTCAAAGACCTC
GAGTTTCCCAAACCGAATCACCTTAAGAAGGACAGGGCTAGGGCATTGGCCAGGATGGCCACCCCTCCTGCTGTT
GCCCCTTAGTGAGGAATCTTACCCCACTTCCCTTACCCCAAGGTTCTCCTCCCCACAGCCAGTCCCCCTTCCCTG
GATTTCTAAACTGCTCAATTTTGAATCAAAGGTGCTATTTACCAAACACTCTCCCTACCCATTCTGCCAGCTCT
GCCTCCTTTTCAACTCTCCACATTTTGTATTGCCTTCCCAGACCTGCTTCCAGTCTTTATTGCTTTAAAGTTTAC
TTTGGGCCCACAGACCCAAGAGCTAATTTTCTGGTTTGTGGGTGAAACAAAGCTGTGAATCACTGCAGGCTGTG
TTCTTGCATCTTGTCTGCAACAGGTCCCTGCCTTTTTAGAAGCAGCCTCATGGTCTCATGCTTAATCTTGTCTC
TCTTCTCTTTTATGATGTTCACTTTAAAAACAACAAAACCCCTGAGCTGGACTGTTGAGCAGGCCTGTCTCTC
CTATTAAGTAAAAATAAATAGTAGTAGTATGTTTGAAGCTATTCTGACAGAAAAGACAAAGGTTACTAATTGTA
TGATAGTGTTTTTATATGGAAGAATGTACAGCTTATGGACAAATGTACACCTTTTTGTACTTTAATAAAAATGT
AGTAGGATAAAAAAAA

WO 2004/030615

PCT/US2003/028547

589/6881
FIGURE 549

MSHGKGT DMLPEIAAAVGFLSSLLRTRGCVSEQRLKVFSGALQEALTEHYKHHWFPEKPSKSGSYRCIRINHKMD
PIISRVASQIGLSQPQLHQLLPSELTLWVDPYEVSYRIGEDGSICVLYEEAPLAASCGLLTCKNQVLLGRSSPSK
NYVMAVSS

WO 2004/030615

PCT/US2003/028547

590/6881
FIGURE 550

ATGTCCATGAGGAGCCCCATCTCTGCCAGCTGGCCCTGGATGGCGTTGGCACCATGGTGAAGTGCACCATCAAG
TCAGAGGAGAAGAAAGAGCCTTGCCACGAGGCCCCCAGGGCTCAGCCACTGCCGCTGAACCTCAGCCTGGAGAC
CCAGCCCCGGGCCTCCCAGGATAGTGCTGACCCCCAAGCTCCAGCCCAGGGGAATTTAGGGGCTCCTGGGACTGT
AGCTCTCCAGAGGGTAATGGGTCCCCAGAACCCAAGAGACCAGGAGCGTCGGAGGCTGCCTCTGGAAGCCAGGAG
AAGCTGGACTTCAACCGAAATTTGAAAGAAGTGGTGCCAGCCATAGAGAAGCTGTTGTCCAGTGACTGGAAGGAG
AGGTTTCTAGGAAGGAACTCTATGGAAGCCAAAGATGTCAAAGGGACCCAAGAGAGCCTAGCAGAGAAGGAGCTC
CAGCTTCTGGTCATGATTACACAGCTGTCCACCCTGCGGGACCAGCTCCTGACAGCCCCACTCGGAGCAGAAGAAC
ATGGCTGCCATGCTGTTTGAGAAGCAGCAGCAGCAGATGGAGCTTGCCCGGCAGCAGCAGGAGCAGATTGCAAAG
CAGCAGCAGCAGCTGATTACGACAGCAGCATAAGATCAACCTCCTTCAGCAGCAGATCCAGCAGGTTAATATGCCT
TATGTCTATGATCCCAGCCTTCCCCCAAGCCACCAACCTCTGCCTGTACCCCTGACTCCCAGCTGGCCTTACCC
ATTCAGCCCATTCCCTGCAAACAGTGGAGTATCCGCTGCAGCTGTGTCACAGCCCCCTGCCCAAGTGGTGAAG
AGGCCTGGGGCCATGGCCACCCACCACCCCTGCAGGAGCCCTCCCAGCCCCTGAACCTCACAGCCAAGCCCCAAG
GCCCCGAGCTGCCAACACCTCCAGCTCCCCAAGCCTGAAGATGAGCAGCTGTGTGCCCCGCCCCCAGCCAT
GGAGGCCCCACGCGGGACCTGCAGTCCAGCCCCCGAGCCTGCCTCTGGGCTTCCTTGGTGAAGGGGACGCTGTC
ACCAAAGCCATCCAGGATGCTCGGCAGCTGTGTCACAGCCACAGTGGGGCCTTGATGGCTCCCCAACACCCCC
TTCCGTAAGGACCTCATCAGCCTGGACTCATCCCCAGCCAAGGAGCGGCTGGAGGACGGCTGTGTGACCCACTG
GAGGAAGCCATGCTGAGCTGCGACATGGATGGCTCCCGCCACTTCCCCGAGTCCCGAAACAGCAGCCACATCAAG
AGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGATCCTGCAAGCCTTCCCAGACATGCAC
AACTCCAGCATCAGCAAGATCCTTGGATCTCGTGGAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAG
GAACAGGCGCGGCTGAGCCGGCAGCACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGGCCCAAGCGACC
TGCATCGTGGAGGGCAAGCGGCTGCGCGTGGGAGAGTACAAGGCCCTGATGAGGACCCGCGCTCAGGATGCCCGC
CAGAGCTACGTGATCCCCCGCAGGCTGGCCAGGTGCAGATGAGCTCCTCAGATGTCTGTACCTCGGGCAGCA
GGCATGCCGCTGGCACAGCCACTGGTGGAGCACTATGTCCCTCGTAGCCTGGACCCCAACCTGCTGTGATCGTC
AACACCTGCAGCCTCAGAGAGGAGGGTGAAGGAGAGCAGATGACAGCACTCGGTGGCTGATGGCGAGATGTACCGG
TACAGCGAGGACGAGGACTCGGAGGGTGAAGAGAAGAGCGATGGGGAGTTGGTGGTGTCTACAGACTGATCCCCG
CTGGGTGGGCTGGCCCCCTTCTCCTCTGGGGAAGACCTTGTCCCAACTCGATGGGCACAGCCAGCCAACCTAAGA
CTATGTTGGTACTTGGACTTGTTCGTGCCCCAGAGATGGGCAAGCTGTGCACTTGCAGATACATTCATGAGGGG
AGAGGCGCCCTCCCTTCCCTGAGGAGCTGTTGGCCTGGGTGGGCAGGAACTGCAGTATGGCCATGGGCTGAGCAGG
CTGAGCACCTCAGCCTTTAGGGCTTATGGCCAGGGGACACTGTATGACTCTCCTCTCCTGCAGGTGTCTATCCAC
CTGGGGTATGGCATCTACCGACCTGTCTCCCTGGGGTCACATGCTTTGTTTCCATTCTTGTCTGGCTGGACCAG
CCACTGTGGGACCAACACCCCTCCCACACTCCCCCAGACTGCTCGTCTATCACCAGGATCGCTTTGTACTTTGTG
CAAAAGGGTCTGGCTGTCCCTTGTGTTTTTCTCTCTGCCAAGCCTATTGTGCCCTCTGGCTGCTGTATGTGTGCG
CGTGCACGTGTGTGTGTTTCTCTGTTTCTATTCTGACACAAGATATTTATTGAGTGCCCACTACGTGCCAGGCAC
TGTGCTGAGTTCTGTGGGTGTGTCTCTCGATGCCACTCCTGCTTCTCTGGGGGCTCTTTCTGTGCTTCTCTT
TGTCCCCAAATTGCTACCTCTTTGTGAGTCTGGGTGTCTCAGGTTCTGTGTGCTTGTGTGCAATTTCTGTCTCT
CTCTGTCTCTCTCTCTGCAAGGCCCTCTATTTCTCTCTTTCTTGGTGTCTGTCTTTGCCCCCTGTGCCCTCT
GGATTCTCTGGGTCTATGTAGGCCCTGGTCTGCCCTGGGCTCATCAGCCTTCTGACCTCCTCCTGCCCTCCCC
TTCACTCCCTCCCTGGCTCTGCCAGTCGGTTCACGAGGCCATTTTGTAGCTCTGATCAGCATGGGAATGTGCCT
CGGCCTCCAAGGGGCTTTGTCTGGTGCCCCCGCCCCCTGGTCCCAACCTGATCCCACGAGGGAGTTGGGACAGGA
GGATTGATGGTGTCTCCCTTCTGTCAGCGTCAGAGGCCCTGGAGAGGGGCTGTCCATGGCAGCTGGTCTTTATT
CCTCCCTCATGAGCACAGGGTCGGGGGGGTCCCCATTCTTGAAGAGGTTGAGAAGACTCCTGGGCTTCAGCCTC
TCCCACCCAGCCCTGCCCTCACCTGCCCTGCCCTCCCCCTCCCCACTCTATACTAGGGACTGGATCTCAGCCTCT
GATCAGTTTCAAAAGTTTGTTCCTAAGGAAATCAAAATCCCATTTGTACCTAACTCTGAAGATCTAAATAGCCC
TTGGATCAGTATGGGAACCCCAAATCCCACAGGGCCAGATGTGGAGTCTGTGTCTGCCCCGCTTCTCTCCATC
CTCAAAGCCCCCACTTCTCTCCAGGCTGTTTCTTTTTTATGACTGTAAACATAGATAGTCTTTATTTTGTAA
TAATAAGATAATGATGAGTAACTTAACCAGCACATTTCTCCTGTTTACACTCGGGGGATTTTTTTGTTTTCTGAT
GACATAATAAAGACAGATCATTTTCAGAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

591/6881
FIGURE 551

MSMRSPISAQLALDGVGTMVNCTIKSEEKKEPCHEAPQGSATAAEPQPGDPARASQDSADPQAPAQGNFRGSWDC
SSPEGNGSPEPKRPGASEAASGSQEKLDNFNRNLKEVVPAIEKLLSSDWKERFLGRNSMEAKDVKGTQESLAEKEL
QLLVMIHQLSTLRDQLLTAHSEQKNMAAMLFQKQQQMEELARQQEQIAKQQQQLIQQQHKINLLQQQIQQVNMP
YVMIPAFPPSHQPLPVTQDSQLALPIQPICKPVEYPLQLLHSPAPVVKRPGAMATHHPLQEPSQPLNLTAKPK
APELPNTSSPSLKMSSCVPRPPSHGGPTRDLQSSPPSLPLGFLGEGDAVTKAIQDARQLLHSHSGALDGSPTNP
FRKDLISLDSSPAKERLEDGCVHPLEEAMLSCDMDGSRHFPESRNSSHIKRPMAFMVWAKDERRKILQAFPMH
NSSISKILGSRWKSMTNQEKQPYEEQARLSRQHLEKYPDYKYKPRPKRTCIVEGKRLRVGEYKALMTRRRQDAR
QSYVIPPQAGQVQMSSSDVLYPRAAGMPLAQPLVEHYVPRSLDPNMPVIVNTCSLREEGEGTDDRHSVADGEMYR
YSEDEDSEGEKSDGELVVLTD

WO 2004/030615

PCT/US2003/028547

592/6881
FIGURE 552

AACTGCCATCTTCCAGTAATTCGCCAAAATGACGAATACAAAGGGAAAGAGGAGAGGCACCCGATGTATGTTCTC
TAGGCCTTTTAGAAAACATGGAGTTGTTCCCTTTGGCCACGTATAIGCGAGTCTATAAGAAAGGTGATATTGTAGA
CATCAAGGGAATGGGTACTGTTCAAAAAGGAATGCCCCACACGCGTTACCACGGCAAACTGGAAGAGTCTACAA
TGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAAGGCAAGATTCTTGCCAAGAGAATTAATGT
GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATGATCAGAAAAA
GAAAGAAGCCAAAGAGAAAAGTTACCTGGATTCAACTAAAGCGCCAGCCTGCTCCACCCAGAGAAGCACACTTTGT
GAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCTATGAATTCATGGCATAATAGGTGTTAAAAA
AAAAA

WO 2004/030615

PCT/US2003/028547

593/6881
FIGURE 553A

GCTTTTCAGGCGATCTGGAGAAAGAACGGCAGAACACACAGCAAGGAAAGGTCCCTTTCTGGGGATCACCCCCATTGG
CTGAAGATCAGACCATTCTTCCTCTTGTGTTTTGCCCTGCCCTGGCCTCCTGCATGCCCCAACAGCCTGCTCCCGT
GGGGCCTGCTATCCACCTGTTGGGGACCTGCTTGTGGGAGGACCCGGTTTCTCCGAGCTTCATCTACCTGTGGA
CTGACCAAGCCTGAGACCTACTGCACCCAGTATGGCGAGTGGCAGATGAAATGCTGCAAGTGTGACTCCAGGCAG
CCTCACAACCTACTACAGTCACCGAGTAGAGAATGTGGCTTCATCCTCCGGCCCCATGCGCTGGTGGCAGTCCAG
AATGATGTGAACCCTGTCTCTCTGCAGCTGGACCTGGACAGGAGATTCCAGCTTCAAGAAGTCATGATGGAGTTC
CAGGGGCCCCATGCCCGCCGGCATGCTGATTGAGCGCTCCTCAGACTTCGGTAAGACCTGGCGAGTGTACCACTAC
CTGGCTGCCGACTGCACCTCCACCTTCCCTCGGGTCCGCCAGGGTCCGGCTCAGAGCTGGCAGGATGTTCCGGTGC
CAGTCCCTGCCTCAGAGGCCTAATGCACGCCTAAATGGGGGGAAGGTCCAACCTTAACCTTATGGATTTAGTGTCT
GGGATTCCAGCAACTCAAAGTCAAAAAATTCAAGAGGTGGGGGAGATCACAACTTGAGAGTCAATTTACCAGG
CTGGCCCCCTGTGCCCCAAAGGGGGCTACCACCTCCAGCGCCTACTATGCTGTGTCCAGCTCCGTCTGCAGGGG
AGCTGCTTCTGTACGGCCATGCTGATCGCTGCGCACCCAAGCCTGGGGCCTCTGCAGGGCCCCCTCCACCGCTGTG
CAGGTCCACGATGTCTGTGTCTGCCAGCACAACTGCCGGCCCCAAATTGTGAGCGCTGTGCACCTTCTACAAC
AACCGGCCCTGGAGACCGGCGGAGGGCCAGGACGCCCATGAATGCCAAAGGTGCGACTGCAATGGGCACTCAGAG
ACATGTCACTTTGACCCCGCTGTGTTTGGCGCCAGCCAGGGGGCATATGGAGGTGTGTGTGACAATTGCCGGGAC
CACACCGAAGGCAAGAACTGTGAGCGGTGTGAGTGCATATTTCCGGAACCGGCGCCCGGGAGCTTCCATTGAG
GAGACCTGCATCTCCTGCGAGTGTGATCCGGATGGGGCAGTGCCAGGGGCTCCCTGTGACCCAGTGACCGGGCAG
TGTTGTGTGCAAGGAGCATGTGCAGGGAGAGCGCTGTGACCTATGCAAGCCGGGCTTCACTGGACTCACCTACGCC
AACCCGCGAGGGCTGCCACCGCTGTGACTGCAACATCCTGGGGTCCCGGAGGGACATGCCGTGTGACGAGGAGAGT
GGGCGCTGCCTTTGTCTGCCAACGTGGTGGGTCCCAATGTGACCAGTGTCTCCCTACCACTGGAAGCTGGCC
AGTGGCCAGGGCTGTGAACCGTGTGCCTGCGACCCGCACAACCTCCCTCAGCCACAGTGCAACCAAGTTCACAGG
GCAGTGCCCTGTGCGGAAGGCTTTGGTGGCCTGATGTGCAGCGCTGCAGCCATCCGCCAGTGTCCAGACCCGAGC
TATGGAGACGTGGCCACAGGATGCCGAGCCTGTGACTGTGATTTCCGGGGAACAGAGGGCCCCGGGTGCGACAAG
GCATCAGGCCGCTGCCTCTGCCGCCCTGGCTTGACCGGGCCCCGCTGTGACCAGTGCCAGCGAGGCTACTGCAAT
CGCTACCCGGTGTGCGTGGCCTGCCACCTTGCTTCCAGACCTATGATGCGGACCTCCGGGAGCAGGCCCTGCCG
TTTGGTAGACTCCGCAATGCCACCGCCAGCCTGTGGTCAGGGCCTGGGCTGGAGGACCGTGGCCTGCCCTCCCGG
ATCCTAGATGCAAAGAGTAAGATTGAGCAGATCCGAGCAGTTCTCAGCAGCCCCGAGTCACAGAGCAGGAGGTG
GCTCAGGTGGCCAGTGCCATCCTCTCCCTCAGGCGAACTCTCAGGGCCTGCAGCTGGATCTGCCCTGGAGGAG
GAGACGTTGTCCCTTCCGAGAGACCTGGAGAGTCTTGACAGAAGCTTCAATGGTCTCCTTACTATGTATCAGAGG
AAGAGGGAGCAGTTTGAAAAAATAAGCAGTGTGATCCTTCAGGAGCCTTCCGGATGCTGAGCACAGCCTACGAG
CAGTCAGCCCAGGCTGCTCAGCAGGTCTCCGACAGCTCGCCCTTTTGGACCAGCTCAGGGACAGCCGGAGAGAG
GCAGAGAGGCTGGTGGCGCAGGCGGGAGGAGGAGGACCGGCAGCCCCAAGCTTGTGGCCCTGAGGCTGGAG
ATGTCTTCGTTGCCTGACCTGACACCCACCTTCAACAAGCTCTGTGGCAACTCCAGGCAGATGGCTTGACCCCCA
ATATCATGCCCTGGTGAAGTATGTCCCCAAGACAATGGCACAGCCTGTGGCTCCCGCTGCAGGGGTGTCTTCCC
AGGGCCGGTGGGGCCTTCTTGATGGCGGGCAGGTGGCTGAGCAGCTGCGGGGCTTCAATGCCAGCTCCAGCGG
ACCAGGCAGATGATTAGGCGAGCCGAGGAATCTGCCTCAGAGATTCAATCCAGTGCCAGCGCTTGGAGACCCAG
GTGAGCGCCAGCGCTCCAGATGGAGGAAGATGTGACAGCGCACACGGCTCCTAATCCAGCAGGTCCGGGACTTC
CTAACAGACCCCGACACTGATGCAGCCACTATCCAGGAGGTGAGCAGGCGCTGCTGGCCCTGTGGCTGCCACA
GACTCAGCTACTGTTCTGCAGAAGATGAATGAGATCCAGGCCATTGCAGCCAGGCTCCCCAACGTGGACTTGGTG
CTGTCCCAGACCAAGCAGGACATTGCGCGTGGCCGCGGTTGACAGGCTGAGGCTGAGGAAGCCAGGAGCCGAGCC
CATGCAGTGGAGGGCCAGGTGGAAGATGTGGTTGGGAACCTGCGGCAGGGGACAGTGGCACTGCAGGAAGCTCAG
GACACCATGCAAGGCACCGAGCCGCTCCCTTCGGCTTATCCAGGACAGGGTTGCTGAGGTTACGACAGTACTGCGG
CCAGCAGAAAAGCTGGTGACAAGCATGACCAAGCAGCTGGGTGACTTCTGGACACGGATGGAGGAGCTCCGCCAC
CAAGCCCGGCAGCAGGGGGCAGAGGCAGTCCAGGCCAGCAGCTTGGCGAAGGTGCCAGCGAGCAGGCATTGAGT
GCCCAAGAGGGATTGTGAGAGAATAAAACAAAAGTATGCTGAGTTGAAGGACCGGTTGGGTGAGTTCATGCTG
GGTGAGCAGGGTGCCCGGATCCAGAGTGTGAAGACAGAGGCAGAGGAGCTGTTGGGGAGACCATGGAGATGATG
GACAGGATGAAAGACATGGAGTTGGAGCTGCTGCGGGGACGCCAGGCCATCATGCTGCGCTCGGCGGACCTGACA
GGACTGGAGAAGCGTGTGGAGCAGATCCGTGACCACATCAATGGGCGCGTGTCTACTATGCCACCTGCAAGTGA

WO 2004/030615

PCT/US2003/028547

594/6881
FIGURE 553B

TGCTACAGCTTCCAGCCCGTTGCCCCACTCATCTGCCGCCTTTGCTTTTGGTTGGGGGCAGATTGGGTTGGAATG
CTTTCCATCTCCAGGAGACTTTTCATGCAGCCTAAAGTACAGCCTGGACCACCCCTGGTGTGTAGCTAGTAAGATT
ACCCTGAGCTGCAGCTGAGCCTGAGCCAATGGGACAGTTACACTTGACAGACAAAGATGGTGGAGATTGGCATGC
CATTGAAACTAAGAGCTCTCAAGTCAAGGAAGCTGGGCTGGGCAGTATCCCCGCCTTTAGTTCTCCACTGGGGA
GGAATCCTGGACCAAGCACAAAACTTAACAAAAGTGATGTAAAAATGAAAAGCCAAATAAAAAATCTTTGG

WO 2004/030615

PCT/US2003/028547

595/6881
FIGURE 554

MRPFFLLCFALPGLLHAQQACSRGACYPPVGDLLVGRTRFLRASSTCGLTKPETYCTQYGEWQMKCKCDSRQPH
NYYSHRVENVASSSGPMRWWQSQNDVNPVSLQLDLDRRFQLQEVMMEFQGPMPAGMLIERSSDFGKTWRVYQYLA
ADCTSTFPRVRQGRPQSWQDVRCQSLPQRPNARLNGGKVQLNMDLVSGIPATQSQKIQEVGEITNLRVNFTRLA
PVPQRGYHPPSAYYAVSQLRLQGSCFCHGHADRCAPKPGASAGPSTAVQVHDVCVCQHNTAGPNCERCAPFYNNR
PWRPAEGQDAHECQRCDNCNGHSETCHFDPAVFAASQGAYGGVCDNCRDHTEGKNCERCQLHYFRNRRPGASIQET
CISCECDPDGAVPGAPCDPVTGQCVCKEHVQGERCDLCKPGFTGLTYANPQGCHRCDCNILGSRDMPDCDEESGR
CLCLPNVVGPCKDQCAPYHWKLASGQGCEPCACDPHNSPQPTVQPVHRAVPCREGFGGLMCSAAAIQCPDRTYG
DVATGCRACDCDFRGTEGPGCDKASGRCLCRPGLTGPRCDQCQRGYCNRYPCVACHPCFQTYDADLREQALRFG
RLRNATASLWSGPGLEDRLASRILDAKSKIEQIRAVLSSPAVTEQEVASAILSRLRTLQGLQLDLPLEEET
LSLPRDLESIDRSFNGLLTMYQRKREQFEKISSADPSGAFRMLSTAYEQSAQAAQVSDSSRLLDQLRDSRREAE
RLVRQAGGGGGTGSPKLVALRLEMSSLPDLTPTFNKLCGNSRQMACTPISCPGELCPQDNGTACGSRRCRGLPRA
GGAFLMAGQVAEQLRGFNAQLQRTQMIRAAEESASQIQSSAQRLETQVSASRSQMEEDVRRTRLIIQQVRDFLT
DPDTDAATIQEVSEAVLALWLPTDSATVLQKMNEIQAIARLPNVDLVLSQTKQDIARARLQAEAEARSRAHA
VEGQVEDVGNLRQGTVALQEAQDTMQGTSRSLRIQDRVAEVQQVLRPAEKLVTSMKQLGDFWTRMEELRHQA
RQQGAEAVQAQQLAEGASEQALSAQEGFERIKQKYAELKDRLGQSSMLGEQGARIQSVKTEAEELFGETMEMMDR
MKDMELELLRGSQAIMLRADLTGLEKRVEQIRDHINGRVLYYATCK

WO 2004/030615

PCT/US2003/028547

596/6881
FIGURE 555

GCGGAGTCTCCAACCTGGGAGAGCTGCAGCTGCCGAGAGGAGGAGAACGCTGAGGTCTGGTCTGGACCAACGGACGCG
CTGACCGCTGCCAACTGCAGCTCGCGCTGCCTCCTGCTCGCGCCGTGCCACTAAGGTCACTCCCGCCTCCGAGAG
CCCAGAGCCGAGATGGAAACGGTCCAGGAGCTGATCCCCCTGGCCAAGGAGATGATGGCCCAGAAGCGCAAGGGG
AAGATGGTGAAGCTGTACGTGCTGGGCAGCGTGCTGGCCCTCTTCGGCGTGCTGCTCGGCCTGATGGAGACTGTG
TGCAGCCCCTTACGGCCGCCAGACGTCTGCGGGACCAGGAGGCAGCCGTGGCGGAGCTGCAGGCCGCCCTGGAG
CGACAGGCTCTCCAGAAGCAAGCCCTGCAGGAGAAAGGCAAGCAGCAGGACACGGTCTTCGGCGGCCGGGCCCTG
TCCAACCGGCAGCACGCCTCTTAGGAACTGTGGGAGACCAGCGGAGTGGGAGGGAGACGCAGTAGACAGAGACAG
ACCGAGAAGGAAGGGAGAGACAGAGGGGGCGCGCGCACAGGAGCCTGACTCCGCTGGGAGAGTGCAGGAGCACGT
GCTGTTTTTTTATTTGGACTTAACTTCAGAGAAACCGCTGACATCTAGAACTGACCTACCACAAGCATCCACCAA
GGAGTTTGGGATTGAGTTTTGCTGCTGTGCAGCACTGCATTGTCATGACATTCCAACACTGTGTGAATTATCTA
AATGCGTCTACCATTTTGCAGTAGGGAGGAAGGATAAATGCTTTTTATGTTATTATTATTAAATTATTACAATGAC
CACCATTTTGCATTTTGAAATAAAAACTTTTTATACCAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

597/6881
FIGURE 556

METVQELIPLAKEMMAQKRKGKMKVLYVLGSLALFGVVLGLMETVCSPFTAARLRDQEAAVAELQAALERQAL
QKQALQEKGKQQDTVLGGRALSNRQHAS

WO 2004/030615

PCT/US2003/028547

598/6881
FIGURE 557

CCCGCCTCCGAGAGCCCAGAGCCGAGATGGAAACGGTCCAGGAGCTGATCCCCCTGGCCAAGGAGATGATGGCCC
AGAAGCGCAAGGGGAAGATGGTGAAGCTGTACGTGCTGGGCAGCGTGCTGGCCCTCTTCGGCGTGGTGCTCGGCC
TGATGGAGACTGTGTGCAGCGGAGTGGGAGGGAGACGCAGTAGACAGAGACAGACCGAGAGAGGAATGGAGAGAC
AGAGGGGGCGCGCGCACAGGAGCCTGACTCCGCTGGGAGAGTGCAGGAGCACGTGCTGTTTTTTATTTGGACTTA
ACTTCAGAGA

WO 2004/030615

PCT/US2003/028547

599/6881
FIGURE 558

CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCC GGCGGCGCGCTCCTTGTTCTAACCCGGCGCGCCATGACCGTCCG
CGCGGCCGAGCGTGCCCCGCGGCGCTGCCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCC
TGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAA
GTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG
TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGC
TAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGT
GCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAACTA ACTTGCCTTCAGAATTTAAATGGTCCACAG
CAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG
GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTT
GTCTTATTTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGACAGAGAAATTTATTGTCCAGCACCAC
CACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA
ATAAAGGATTACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC
CACCACCTGAATGCAGAGGAAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATG
TTCCAACACAGAAAGTCTCACCAACTTCTCAGAAAAACCACCAAAAAACCACCAACCAATGCTCAAGCAACAC
GGAGTACACCTGTTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGAACCACTTCAG
GTAATACCCGCTCTTCTATCTGGGCACACGTGTTTACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT
TGCTGACTTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCTAGTTTCTTAGACTTA
TCTGCATATTGGATAAAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGG
AATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAG
AACAACTTGCAGAATTGAGAGTGATTCTTTCTAAAAGTGTAAGAAAGCATAGAGATTTGTTGATTTTAGAAT
GGGATCACGAGGAAAAAGAGAAGGAAAGTGATTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGGAA
ATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAAACCAATTCAGTCTCTTCTAAGCAAAATTGC
TAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAA
TATTTTAAAGGTAAACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG
AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGCTTCTTTGACTTAATGTCTTTAAA
AGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAA
ATTTGTAAATCTTATCTTTTGTAAATATTTATTTATATTATTTATGACAGTGAACATTCTGATTTTACATGTAA
AACAAAGAAAAGTTGAAGAAGATATGTGAAGAAAATGTATTTTTCTAAATAGAAATAAATGATCCCATTTTTTG
GT

WO 2004/030615

PCT/US2003/028547

600/6881
FIGURE 559

MTVARPSVPAALPLLGLPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGE
KDSVICLKGSQWSDIEEFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLK
WSTAVEFCCKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYC
PAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRTTKHFHETTPNKGSGTTS GTTRLLSGHTCFTLTGLLGLTV
TMGLLT

WO 2004/030615

PCT/US2003/028547

601/6881
FIGURE 560A

GTGGATTTGGTCTCTCCCTGATTCCGAGCTGCGGGCAGGGAGAGGGGCCTCGCGCCGCCCTCAGCAGCCGGCGG
CGGCCGAGGTAGACCGAGCGGGGACGGAAGGACAGACCGACGTCGCCGAGCTGGAATCATGTGAGGGCCAACCGG
GGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCGGC
CCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGTCGGCCCCC
CAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGTCC
ACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCAACCTGACCATCCAGG
TGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTTGTTACCCGCCCTCATCGTGACGCCCTGCAGCGAAG
TGCTCACCTCACCAACAATGTCAACAAGCTGCTCATATTGACTACTCTGAGAACCCTGCTGGCCTGTGGGA
GCCTCTACCAGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTATCCTGGTGGAGCCATCCCAAGAAGG
AGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCA
AGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCAGCCGGAAGCTGCCCGAG
ACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCTCTCTCATCAAGATCCCTTCAG
ACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTC
TCACTGTCCAGCCCGAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCG
TGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGCCGGGTGG
AATACCGCTCCTGCAGGCTGCTTACCTGGCCAAGCTGGGGACTCACTGGCCAGGCCTTCAATATCACCAGCC
AGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACCACCGCCCGATGACTCTGCCCTGT
GTGCCTTCCCTATCCGGGCCATCAACTTGAGATCAAGGAGCGCTGCAGTCTGTACCAGGGCGAGGGCAACC
TGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGACCAAGGCGCTGTCCCATCGATGATAACTTCTGTG
GACTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCACCAGCAGGGACC
GCATGACCTCTGTGGCTCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGGACTAAGAGTGGCAAGCTGA
AAAAGATTGGGGCCGACGGTCCCCCCCCATGGTGGGGTCCAGTACGAGATGGTCTCTGTGCTCAAGGACGGAAGC
CCATCCTCCGGGACATGGCCTTCTCCATTGATCAGCGCTACCTGTACGTCTGTCTGAGAGACAGGTCAACAGG
TCCCGTGGAGTCACTGTGAGCAGTATACGACTTGTGGGAGTGCCTGAGCTCTGGGGACCTCACTGTGGCTGGT
GTGCCCTGCACAACATGTGCTCCCGCAGGGACAAATGCCAACAGGCCTGGGAACCTAATCGATTTGTGCCAGCA
TCAGCCAGTGTGTGAGCCTTGCAAGTGCATCCAGCAGCATCTCAGTATCTGAGCACAGCCGGTTGCTTAGCCTGG
TAGTGAGTGATGCTCCTGATCTATCTGCGGGTATCGCCTGTGCCTTTGGGAACCTGACAGAGGTGGAGGGGCAGG
TGTCCGGGAGCCAGGTCACTGTCATCTACCTGGGCCAAGGATGTCCCTGTCTATCCCGCTGGATCAAGACTGGT
TTGGGCTGGAGCTACAGGTGCAAGGAGACAGGGAAGATATTTGTAGCACCGAGTTCAAGTTTACAACCT
GCAGTGCCCAACCACTGTGCTGTCTGTGTCACAGCGCTTCCGCTGCCATTGGTGCAAGTACCGCAACCTCT
GCACATGAGACCCACCACTGCTCCTTCCAGGAGGGCCGGATCAATATTTAGAGGACTGTCCCCAGCTGGTGC
CCACAGAGGAGATCTTGATTCCAGTCCGGGAGGTAAAGCCAATCACCTTAAGGCGCGAAATCTGCCCCAGCCGC
AGTCCGGCCAGCGAGGCTATGAGTGTGCTCAACATACAAGGAGCCATCCACCGGTCCCGCTCTGCGCTTCA
ACAGCTCCAGCGTTCAAGTGTGAGAACAGCTCGTACCAGTATGATGGCATGGACATCAGCAATCTGGCCGTGGATT
TCGCTGTGGTGTGGAACGGCAATTTTCATCATTGACAACCTCAGGACCTGAAAGTCCATCTCTACAAGTGTGCAG
CCCAGCGGGAGAGCTGCGGCCTCTGCCTCAAGGCCGACCGGAAGTTTGAGTGTGGCTGGTGCAGCGGCGAGCGCA
GGTGCACCTCCACCAGCACTGTACCAGCCCTTCCAGCCCTGGCTCGACTGGTCCAGCCACAATGTCAAGTGCT
CCAACCTCAAATCACCGAGATTTTGACGGTGTCTGGACCGCCGGAAGGAGGGACGCGAGTGACCATCCATGGCG
TGAACCTGGGTCTGGACTTCTCCGAGATCGCCCACCATGTGCAGGTGGCTGGGGTGCCCTGCACGCCCCCTCCAG
GGGAATACATCATCGCTGAGCAGATTGTCTGTGAGATGGCCATGCCCTCGTGGGAACCACTCCGGGCCAGTAC
GCCTGTGTATTGGCGAGTGTAAGCCAGAGTTCATGACGAAGTCCCATCAGCAGTACACCTTCGTGAACCTTCTG
TGCTGTCACTCAACCAATCCGAGGTCCCGAGTCAGGAGGCACTATGGTGACCATTACCGGCCATTACCTTGGGG
CTGGGAGCAGCGTGGCAGTCTACCTGGGCAACCAGACCTGCGAGTTCTACGGGAGGTCAATGAGTGAGATCGTGT
GTGTCTACCCCCATCATCCAATGGCCTTGGCCCGGTCCCTGTTTCTGTGAGTGTGACCGAGCCCATGTGGATA
GCAACCTGCAGTTTGAGTACATAGATGACCCTCGGGTCCAGCGCATCGAGCCAGAGTGGAGCATTGCCAGTGGCC
ACACACCCCTGACCATCACAGGCTTCAACCTGGATGTCAATTAGGAGCCAAGGATCCGAGTCAAATTCATGGCA
AAGAATCTGTCAATGTGTGTAAGTTGTGAACACAACCACCTCACCTGCCTGGCACCTCTCTGACCACGGACT
ACCGCCCTGGCCTGGACACTGTGGAACGCCCAGATGAGTTGGATTGTCTTTAACAATGTCCAATCCTTGCTAA

WO 2004/030615

PCT/US2003/028547

602/6881
FIGURE 560B

TTTACAACGACACCAAGTTTATCTACTACCCCAACCCGACCTTTGAACTGCTTAGCCCTACTGGAGTCTTGGATC
AAAAGCCAGGATCGCCCATCATTCTGAAGGGCAAAAACCTCTGCCCTCCTGCCTCTGGAGGGGCCAAACTCAACT
ACACTGTGCTCATCGGAGAGACCCCTTGTGCTGTACCGTATCTGAGACCCAGCTTCTCTGCGAGCCTCCCAACC
TCACCGGGCAGCACAAGGTCATGGTTTACGTGGGCGGGATGGTGTCTCGCCTGGCTCGGTGAGTGTCATCTCAG
ACAGCTTGCTGACCCTGCCAGCCATCGTCAGCATCGCGGCCGGCGGCAGCCTCCTCCTCATCATCGTCATCATCG
TCCTCATTGCCTACAAGCGCAAGTCTCGAGAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGATGGACAATC
TGGAGTCCCGTGTGGCCTTGGAGTGCAAGGAAGCTTTTGTGCTGAGCTCCAGACGGATATCAATGAGTTGACCAGTG
ACCTGGACCGCTCAGGAATCCCTTACCTGGACTATCGTACCTACGCTATGCGAGTCCTGTTCCCGGGCATCGAGG
ACCACCCCGTCTCGGGGAGCTGGAGGTACAAGGAAACGGGCAGCAGCACGTGGAGAAGGCCCTGAAGCTCTTTG
CCCAGCTCATCAACAACAAGGTGTTCTGTGCTGACCTTCATCCGCACCCTGGAGCTGCAGCGCAGTTTCTCCATGC
GCGACCGGGGCAACGTGGCTTCGCTCATCATGACCGGCCTGCAGGGCCGCTGGAATATGCCACTGATGTCTCA
AGCAGCTGCTCTCTGACCTCATCGATAAGAACCTGGAGAACAAGAACCACCCCAAGCTGCTACTCCGGAGGACAG
AGTCTGTGGCTGAAAAGATGTGACCAATTGGTTTCGCCTTCTCCTGCAACAAGTTCCTAAAGGAGTGCGCAGGGG
AGCCACTCTTCATGCTATACTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATTGATGCCATCACGGGCGAGG
CCCCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCAGATCGAGTACAAGACCCTGATCCTGAACTGCGTCA
ACCCTGACAACGAGAACAGTCCAGAGATCCCAGTGAAGGTGTTAAACTGTGACACCATCACACAGGTCAAGGAGA
AGATTCTTGATGCCGTGTATAAGAATGTGCCCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGGAGTGGC
GCCAAGGCCGGATCGCCCGGGTCTGTGCTGCAAGATGAGGACATCACCACCAAGATTGAGGGTGACTGGAAGCGGC
TCAACACACTGATGCATTATCAGGTGTGACAGGTGGTGGTGGCTCTGGTCCCCAAACAGACCTCCTCTACA
ACATCCCTGCCCTCTGCCAGCATCTCCCGGACGTCCATCAGCAGATACGGTGACTCCTCCTTCAGGTATACGGGCA
GCCCCGACAGCCTGCGGTCCCCGGGCCCCGATGATCACCCAGACCTGGAAAGTGGGGTCAAGGTGTGGCATCTGG
TGAAGAACCATGACCACGGTGACCAGAAGGAGGGTGACCGGGGCAGCAAGATGGTGTCCGAGATCTACCTGACCC
GGCTACTGGCCACCAAGGGCACCCCTGCAGAAAGTTTGTGGACGACTTGTGTTGAGACCTTGTTCAGCACTGTGCACC
GGGGCAGCGCTCTCCCCCTGGCCATCAAGTACATGTTTGATTTCTTAGATGAGCAGGCAGACAGGCACAGCATCC
ATGACACAGATGTGCGGCACACCTGGAAAAGCAACTGCCTCCCTCTGCGCTTCTGGGTGAACGTGATTAAGAACC
CCCAGTTCGTGTTTGACATCCACAAGGGCAGCATCACGGACGCCTGCCTCTCTGTGGTGGCCAGACCTTCATGG
ACTCTTGTTCACGTCAGAGCACCGGCTGGGCAAGGACTCCCCCTCCAACAAGCTGCTCTATGCCAAGGACATCC
CCAGCTACAAGAGCTGGGTGGAGAGATACTACGCAGACATCGCCAAGCTCCCAGCCATCAGTGACCAGGACATGA
ATGCCTACCTCGCCGAGCAGTCCCGCCTGCACGCCGTGGAGTTCAACATGCTGAGTGCCCTCAATGAGATCTACT
CCTATGTCAGCAAGTATAGTGAGGAGCTCATCGGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCAGCGGCTGG
CTTATAAGGTGGAGCAGCTCATTAAATGCCATGTCCATTGAGAGCTGAGAGGAGGAGCCTCGCATTCTCTGGGAAGA
GGGACCTGTCCAAGCTGTCACACTGGGAGTCTCAGATGGAAGGACAAGTGATGGGGATCAGGCCCCAGAGCTTGC
TGTCCTCTGAGACCCCATCCTGGGGAGAGGGGAGGACTCCTCTCCCTACGCCAGCCAAGTTTCGTATAGCCAGT
TCCAGCTGGGAGAGACAGTGGGCGTCTGTCATCCTCAGTGAGAACACCAGAGAACCCGGGGCCGGGAGAAGGTGG
TTCTTCAAGCCGAGAGGCACGAGCTGGGGACAGTTCTGCCTCTGTGACTGCTTTGCATGAAAACCTATTTGA
TGATATTGGGGAAATAATGAGAACTTTATTTAATTTTTTAAGAAAAAGGGAAAAAACAGAAATAAAACAAA
AGCCGCCCTGTTAATCCAAATTAAAAA

WO 2004/030615

PCT/US2003/028547

603/6881
FIGURE 561

ACTGAATTCAACAATTATTTATTGAGTGTCTATTATGTGCTAGATACTGAGACACATCAGAGAACAAAACCAAAA
GCCCTGCCCTCGTCGGGCTTACAGTCTAGCACTTACTGCCAGTTAACCTGGAGGCTACCTGGAACCCCGGGCAAG
TCACCGCACCTCTGTGCCTCGGTCCTCAGCTGCCTAATGGGAGAATAAGCAGACCTGGCTCAGACATGAATCATG
TGCTTGGTGTACTGCAGATGCCAACTGCATCCCCATAACCCACCACCCAGACAGTAGATAGGGCTGGAAGTTGA
TTTTTAATGATCAAGTACAATGGAGGGAGGGCAGAGGGGCTAAGCCTAGCTGTCTGGGGTGCTGTGGTGGTGGTG
GGCTGGCTACACAACTGTTGCTGCTGCTGCTGCTTCTTGGTGGCTGCCTTGCTGGCGAGGTCCTTGGCCTTCTC
TGCTAGCTGCCAGTGCTGTCTCCTTTGCCTTCTCCTTGGCTTCCTTGGCTGTCTCAACAAGTGTGTTTGAAGGGGC
CTCGCCTTGCAGCTTTGCCAAGATATATTCAAACCCCTTCATAGTCTTGGTCACATTGCTTTTGAACCAGGCAAG
ACCAAATTCCTGGACAGCTCTGGAGACACCAAATAAGCTAGAGGAGACCCAGGCTTCCCGGCGGATTTCGGTCCG
GCCACTGTTGTCAGAGTTCACACAGTAAACACATCGTTCCTCCACCACC

WO 2004/030615

PCT/US2003/028547

604/6881
FIGURE 562

TTTCGGCCGGAACCGCCATCTTCCAGTAATTCGCCAAAATGACAAACACAAAGGGAAAGAGGAGAGGCACCCGAT
ATATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTTCCTTTGGCCACATATATGCGAATCTATAAGAAAGGTG
ATATTGTAGACATCAAGGGAACGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAACTGGAA
GAGTCTACAATGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGA
GAATTAATGTGCGTATTGAGCACATTAAGCATTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATG
ATCCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCTATG
AATTCATGGCATAATAGGTGTT

WO 2004/030615

PCT/US2003/028547

605/6881
FIGURE 563

MTNTKGKRRGTQYMF SRPFRKHGVVALATYMQIYKKGDIVDIKGMGTVQKGMPhKCYHGKTGRVYNVPQHAVGIV
VNTQVKGKILAKRINVRIEHIKHSKS

WO 2004/030615

PCT/US2003/028547

606/6881
FIGURE 564

ATGAAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAAGAGTTCTGAA
GATATCCGGTGCAAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCCAG
AAGGACTGCAACTGCCTGCACGTGGTGGAGCCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTG
TGCGAGTGCAGGTACGAGGAGCGCAGCACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGT
GCCCTGTTGCTCTACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATATACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCA
AACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTC
TTCGATCGGCACAAGATGCTCAGCTAG

WO 2004/030615

PCT/US2003/028547

607/6881
FIGURE 565

MKLLSLVAVVGCLLVPPAEANKSSDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

WO 2004/030615

PCT/US2003/028547

608/6881
FIGURE 566

ACCTGCACTGACTTTTTTCTCCTTTTGGAGGGAGAGCAGAGACCATGTCTGACATAGAAGAGGTGGTGGAAGAGT
ACGAGGAGGAGGAGCAGGAAGAAGCAGCTGTTGAAGAGCAGGAGGAGGCAGCGGAAGAGGATGCTGAAGCAGAGG
CTGAGACCGAGGAGACCAGGGCAGAAGAAGATGAAGAAGAAGAGGAAGCAAAGGAGGCTGAAGATGGCCCAATGG
AGGAGTCCAAACCAAAGCCCAGGTCGTTTCATGCCCAACTTGGTGCCTCCCAAGATCCCCGATGGAGAGAGAGTGG
ACTTTGATGACATCCACCGGAAGCGCATGGAGAAGGACCTGAATGAGTTGCAGGCGCTGATCGAGGCTCACTTTG
AGAACAGGAAGAAAGAGGAGGAGGAGCTCGTTTCTCTCAAAGACAGGATCGAGAGACGTCGGGCAGAGCGGGCCG
AGCAGCAGCGCATCCGGAATGAGCGGGAGAAGGAGCGGCAGAACCGCCTGGCTGAAGAGAGGGGCTCGACGAGAGG
AGGAGGAGAACAGGAGGAAGGCTGAGGATGAGGCCCGGAAGAAGAAGGCTTTGTCCAACATGATGCATTTTGGGG
GTTACATCCAGAAGXXXXXXXXXACAGAGCGGAAAAGTGGAAGAGGCAGACTGAGCGGGAAAAGAAGAAGA
TTCTGGCTGAGAGGAGGAAGGTGCTGGCCATTGACCACCTGAATGAAGATCAGCTGAGGGAGAAGGCCAAGGAGC
TGTGGCAGAGCATCTATAACTTGGAGGCAGAGAAGTTCGACCTGCAGGAGAAGTTCAAGCAGCAGAAATATGAGA
TCAATGTTCTCCGAAACAGGATCAACGATAACCAGAAAGTCTCCAAGACCCGCGGGAAGGCTAAAGTCACCGGGC
GCTGGAAATAGAGCCTGGCCTCCTTCACCAAAGATCTGCTCCTCGCTCGCACCTGCCTCCGGCCTGCACTCCCC
AGTTCGCGGGCCCTCCTGGGCACCCAGGCAGCTCCTGTTTGGAAATGGGGAGCTGGCCTAGGTGGGAGCCACCA
CTCCTGCCTGCCCCACACCCACTCCACACCAGTAATAAAAAGCCACCACACTG

WO 2004/030615

PCT/US2003/028547

609/6881
FIGURE 567

CCAGCCTTGCCCGGCAGAGGACTCTGGAGGATGAGGAGGAACAGGAGCGCGCGAXGGCGGCGGCACCGCAACCTG
AGCTCCACCACGGACGATGAGGCTCCCAGGCTCAGCAGAATGGAGACCGGCAGCCTCTGCTTCTGAGAGACTACC
GAGCGTGGAAGAAGCAGAGGTGCCCAAGCCACTGCCCCAGCCTCCAAAGATGAGGACGAGGACATCCAGAGCAT
CCTCAGAACACGGCAGGAGCGGAGGCAGAGGCGGCAGGTGGTGGAGGCTGCACAGGCCCCCATCCAGGAGAGGCT
GGAGGCAGAGGAGGGGAGGAACAGCTTGAGCCCTGTGCAGGCCACACAGAAACCCCTAGTCTCCAAGAAGGAACCT
GGAAATCCACCTCGCCGGAGACTGAGTCGGGAACAGCGGGGCCCCCTGCGCTGGAGGAGGAGAGCTTGGTGGGCA
GGGAGCCAGAAGAGAGGAAGAAAGGGGTTCAGAAAAGTCCCCAGTCTTGGAGAAATCCTCCATGCCAAAGAAGA
CGGCACCTGAAAAGAGCCTGGTCTCCGATAAAACCTCCATCTCTGAGAAGGTGCTGGCCTCAGAGAAGACATCTC
TATCAGAGAAGATAGCAGTGTGAGAGAAAAGAAACAGCTCAGAGAAGAAGTCTGTTCTAGAAAAAACAGTGTCT
CTGAGAAGTCGCTGGCCCCAGGGATGGCACTGGGCTCAGGAAGGAGGCTGGTGTCTGAGAAAGCTTCCATCTTTG
AGAAGGCACTGGCCTCAGAGAAGAGCCCAACTGCAGATGCTAAGCCGGCCCCAAAGAGGCCACAGCCTCAGAGCA
GCCCCCTGGCGCAGGAGCCGCCAGCCTCTGGGGGAAGCCAGCCACCACCAAGGAGCAGAGAGGAAGGGCCCCCTCC
TGGAAGAACCTGCCCTCTTTGGCAGAGCAGGGGGCTTCAGACCTCCGACTGTGGCCTCCCGCTCCCACCCGT
CACACTCCAGGTGAAAATCCCCAGCAAGGAGGAAGAGGCAGATATGTCTCACCACACAGCGAACCTACAGCAG
CTCCCTCAAACGCTCCAGCCCCAGGACCATCTCCTTTCCGATGAAACCAAGAAAGAAAACCTCGGAAACAACCCCT
AACTCGCAGTGCCAGCATGAAGCTCCAGACAACACAGTGAAGTTGGGAGAGAAGCTGGAGAGATACCACACGGC
CATACGGAGATCAGAATCTGTCAAGTCTCGGGGTCTGCCTTGCACTGAGTTATTCTGTGGCTCCTGTGGGTGTAGC
CAGCAAGCGCCACCTCTTTGAGAAGGAACCTGGCGGGCCAGAGCCGAGCAGAACCAGCCTCCAGCCGGAAGGAGAA
CTTGAGGCTCTCAGGGGTTGTGACATCAAGGCTCAACCTGTGGATCAGCAGGACCCAGGAATCTGGAGATCAGGA
CCCCCAGGAGGCACAGAAAGCATCATCTGCAACCGAGAGGACTCAGTGGGGACAGAAATCTGACTCCTCGCTGGA
CGCTGAGGTGTGACAAGCCCCGCCAAGACAGACCTGCAAGTCTTCGTCTCAAGGGACCTCCCTCATGCCAGGCCC
CTGCCTCTCACAGCAGCACCCCTTTCTCTCATTGTCCCTGTTCCCTTTTTTGCTGTGGATCTGTTTGGCCAGGGT
CCCTGGGGTTCAGGAATATTTGCAAGACTCAGCCAGCTCCTTCCCAGCCAGCCTCTTGGGGTGGGACTTTCTCA
CCCTGCGGCAGGCACAACAGATGCTGGGACCCAGTCTCTGCCAGGTACAGCACAAAGTGACATCAGCACTATG
GGGCCTATGTCCTGCCAGAGACCTCTGCTCCTTCTGCTCACATCCACAGTCAGGGCACGGCGCCCCCTCAAGAA
CTCCAGAGTCACCTGTCTCATCGGCTCCAGCAAGTGCCCTCTTTGTCTATGATGTCCCCCTTCTCTGAGGCCTGG
ACCCACCCATCTTTGTCCCTGGGGCTGCTCCAGCCACTGAGGCCCGCTCTGGCCAGGGGAGAAGGAGCTGCCG
TGCGTCTTCCCTGTGCCCGCTCTCCCTGCTTGGTTCTCCCTCCCTTCCCTGGCCGGCTGCCATGGCCAGGAGCT
AAGTGCCCTTTTTGTGTGCAACCACTTACCCTTTCTCTGAAAACCTGTTCTCAGGAAGGATCTGATAAACTCATT
TACTCTCAGGTGTAAGAGACTGATGAGACCTTAGAAGCGAATTCCTCTCTGGAGGCCTTGCTTTCTAGCAGAGTC
ACCTGAAGTGTGTGAGGAGGATCATATTTTCTCATCCCCCTCTTCTCACATTAAGGTGGTGGCTTGCCACTC
AGCAGTCTAGCTTGGTGACTGGGAACCTGCCACATACAGGGCCAGGCCTACCCTCCTTCCCCACAAGCCCCCTCC
AACCCCAACCCCATGCTCTGGACCTCATGGCTCCTATGAGCTTGGAGCATGGTGAACCATCAGAGAATCTAGAA
CCAACCAAGCTAGGAACATCAGCCTGGTGCCTGTTAACCCTTAAAGCTGTGGTTTACAACTTTTCAAAAATTTA
AATCATTAG

WO 2004/030615

PCT/US2003/028547

610/6881
FIGURE 568

ATTCAAGGCCTGGGGGAGCTGCGGTTCCGAGAAGCGGCAGACGGCAGCCAGAAGGCTTGGGCTGTTGAGTAAGCA
GCCCCCTCTCAGTCCCGGCCCTCCCCGCCCCGCGCCCTGCGCCTCCAGTGAGTGACTGAGCCCCGCTGCGGCCC
CGCCCCCGGGGCCCTGCCGGAGCTGGTGCGCGGCGCGGAGGGGAGGGCCGGCCAGGGTAGGAATGCGCTGCGGGC
GGGCGGCGCAGGAGGCGAGCGGCGGAACATGTAAGGGCACATCCCGCAGCTGCCGCCAGCGCGCAGACAGAGC
CCAGGGGAGCAAGAGAACGGGCGGGCGGTGGGGCTCACGGCCTAGGGAGGCGCGGAGGCATCTGGCAGAGGCGGG
TCGGGCTGGGCCAGCTGGGGTAGAGCGGAGGAGCGGGTGCCGGCTGAAGCGGGGCGGTGGGCGCGGAGCGCGCTG
GGGGCACCGACACCACTCACCGGCAGCCGGGTGCTGAGGGCCGCGGTGTGGGTGCGCGGAGCAGTCAGGGCGCA
GGTGGGCAGCGCGCACGGCCTGCCAGCCGGGGCGCCAGAATCCTGCGCTGCGGGGCCAGAGGGGGCGCCGCGCC
CGCCGCAGCCTGGAGCTTTCCGCGAACCTCGGGGCGCCCATGACGGCGGCGGCGACGGCTACCGTGCTCAAGGAG
GGCGTGCTGGAGAAGCGCAGCGGCGGGCTGCTGCAGCTGTGGAAGCGGAAGCGCTGCGTCCTACCGAACGCGGG
CTGCAGCTCTTCGAGGCCAAGGGCACGGGCGGCCGCGCCCAAGGAGCTCAGCTTCGCCCGCATCAAGGCCGTGGAG
TGCGTGGAGAGCACCGGGCGCCACATCTACTTCACGCTGGTGACCGAAGGGGGCGGCGAGATCGACTTCCGCTGC
CCCCTGGAAGATCCCGGCTGGAACGCCCAGATCACCTAGGCCTGGTCAAGTTCAAGAACCAGCAGGCCATCCAG
ACAGTGCGGGCCCGGCAGAGCCTCGGGACCGGGACCCCTCGTGTCTTAACACCGGGCGCACCATCTTTCCTTCA
TGCTACCCACCACCTCAGTGCTGAGGTCAAGGCAGCTTCGTTGTTCCCTCTGGCTTGTGGGGGCACGGCTGTGCT
CCATGTGGCAAGGTGGAAGGAATGGACGAGCCCTGGGAGGAGGGCAGAAGGCTACGCAGGGCTGAGGATGAAGAT
GCAGCCCCCTGGATGGTCCCAGACTCTCAGGACATGCCCAGCTCAGGGGCTTCGAGCCACAGGCCTGGCCTCATAT
GGCATGAGGGGGAGCTGGCATAGGAGCCCCCTCCCTGCTGTGGTCTCTGCCCTCTGTCTCTGCAGACTGCTCTTAGC
CCCCTGGCTTTGTGCCAGGCCTGGAGGAGGGCAGTCCCCCATGGGGTGCCGAGCCAACGCCTCAGGAATCAGGAG
GCCAGCCTGGTACCAAAGGAGTACCCAGGGCCTGGTACCCAGGCCCACTCCAGAATGGCCTCTGGACTCACCTT
GAGAAGGGGGAGCTGCTGGGCCTAAAGCCCACTCCTGGGGGTCTCCTGCTGCTTAGGTCTTTTGGGACCCCCAC
CCATCCAGGCCCTTTCTTTGCACACTTCTTCCCCCACCTCTACGCATCTTCCCCCACTGCGGTGTTTCGGCCTGA
AGGTGGTGGGGGTGAGGGGGGGTTTGGCCATTAGCATTTTCATGTCTTTCCCCAA

PCT/US2003/028547

ATGGCGCGCGCGCGCGCGGACGCTGGTGCGGCCCTCCGGGCTGCCGGGTCCAGTGGGCACAAGGATTAAAGGAAGACGTTA
TGGGATACGCTCACCGGGATCCTATCCCCAGTACAGGAGGTGCGGGCGGCTGCTGAAGAACAGATTAAGGTGCTG
GAGGTGACGGAGGAATTTGGTGTTCACCTTGGCAGAACTGACTGTAGATCCCCAGGGGGCACTGGCAATCCGTGAG
CTGGCATCAGTCATCTTGAAACAATATGTGGAGACTCACTGGTGTGCCCAATCAGAGAAATTTAGGCCTCCTGAA
ACTACAGAAAGGGCAAAAATTGTTATCCGGGAGCTATTGCCTAATGGGTTGAGAGAATCGATAAGCAAAGTGCGC
TCCAGTGTGGCCTATGCAGTGTGAGCCATTGCCCACTGGGACTGGCCTGAAGCTTGGCCCCAACTCTTCAACCTG
CTCATGGAGATGTTGGTGAGCGGAGACTTAAATGCCGTCCATGGAGCCATGCGTGTGCTGACAGAATTCACCTGT
GAAGTTACAGACACACAGATGCCACTTGTTGCTCCTGTGCTATTCTCCCAGAGATGTATAAGATCTTCACCATGGC
GAGGTGTATGGTATTTCGAACCCGTTCCCGAGCCGTGGAGATTTTTTACCACCTTGTGCCCATATGATCTGTAACAIG
GAGGAGCTGGAAAAGGGTGAGCCAAAGTCTGTATCTTTCCCGTGGTACAGCAGTTTACAGAGGCCTTTGTTTACG
GCCCTCCAGATACCAGATGGCCCCACATCTGACAGTGGGTTTAAGATGGAGGTCTAAAGGCAGTGACAGCCCTA
GTGAAAAACTTCCCAAAGCACATGGTGTCTCTCATGCAGCAGATTCTGCCTATTGTTTGGAAACACCCTAACCGAG
AGTGCAGCTTTTTATGTGAGGACAGAAGTAAATTACACAGAAGAAGTAGAAGATCCTGTGGATTCTGATGGTGAA
GTCCTGGGCTTTGAAAACTCTCGTCTTTAGCATTTTTTGAATTTGTCCATGCTCTACTAGAAAATAGCAAATTCAAA
AGCACTGTTAAGAAAGCCTTGCTGAATTGATTTATTATATTATCCTGTACATGCAAATCACTGAGGAGCAGATT
AAAGTATGGACAGCCAACCCCCAACAAATTTGTAGAAGATGAAGATGATGATACATTCTCCTATACTGTTAGAATA
GCAGCTCAAGACTTGTGTGCTGGCTGTGGCCACAGATTTCCAGAATGAAAGTGCAGCAGCCCTGGCTGCTGCAGCC
ACTCGACATTTACAAGAAGCTGAGCAAACCAAAACAGTGGCACTGAGCACTGGTGGAAAGATCCATGAGGCATGC
ATGCTTGCCCTAGGCTCAGTGAAGGCCATCATCACTGACAGTGTGAAAAATGGCAGGATTTCATTTTGACATGCAT
GGGTTCTTGACCAATGTCATCCTTGAGACCTCAACCTCTCAGTGTCTCCTTTCTCTTGGGCGGGGCACTTTGG
GCTGCCAGTCGGTTTACTGTTGCTATGTCCCCTGAAGTATCCAGCAGTTTCTACAGGCAACAGTTAGTGGTCTT
CACGAGACACAGCCCCCATCAGTTTGAATTTCTGCAGTGAGAGCCATCTGGGGTTATTGTGACCAACTGAAAGTC
TCAGAGAGTACCCACGTGCTCCAGCCCTTCTCCTCCCGAGCATCCTTGATGGCTTAATTCACCTAGCAGCCAGTTT
AGCTCAGAGGTCTTCAACCTGGTGATGGAGACCCCTGTGCATCGTTTGTACAGTAGACCCCGAATTCACAGCAAGC
ATGGAAAGCAAAATCTGCCCTTTCACCATCGCCATTTTCTTAAAGTACAGTAATGATCCCGTCTGTCGCCCTCACTG
GCTCAGGACATCTTCAAGGAGCTGTCCAGATTGAAGCCTGTCAGGGCCCAATGCAAATGAGGCTGATTCCCACT
CTGGTCAGCATAATGCAGGCCCCAGCAGACAAGATTCTGTCAGGGCTTTGTGCGCAGAGCCATTGATATCCTGACA
ACAGTAGTACGAAATACAAAGCCTCCCCTTTCCAGCTTCTCATCTGCCAAGCTTTCCCTGCTGTGGCACAGTGT
ACCCTTCACACAGATGACAATGCCACCATGCAGAATGGCGGAGAGTGTCTGCGGGCCTATGTGTGATGACCCCTG
GAACAAGTAGCCAGTGGCATGATGAGCAGGGCCACAATGGACTGTGGTATGTGATGCAAGTGGTGAGCCAGCTC
CTGGACCCCCGCACCTCAGAGTTCACCTGCGGCCTTTGTGGGCCGCCCTTGTTTCCACCTCATCTCCAAGGCAGGG
CGGGAACTCGGGGGAGAATCTAGACCAGATTCTTCGTGCCATCCTCAGTAAGATGCAGCAGGCAGAGACGCTCAGT
GTATGCAGTCCCTGATCATGGTGTTCGCTCATCTGGTGCACTCAGCTAGAACCTCTCTTGAGTTCCTGTGT
AGCTCCCAGGACCTACTGGCAAACCTGCTCTAGAGTTTGATGAGTGGTGTGAGTGGACAAGCCGACAGCACCTGTTC
TATGGACAGTATGAAGGCAAAGTCAGCTCTGTGGCACTCTGTAAGCTGCTCCAGCATGGCATCAATGAGATGAC
AAACGGCTACAGGATATCCGTGTGAAGGGAGAGGAGATCTACAGCATGGATGAGGGCATCCGACCCGCTCTAAG
TCAGCCAAAACCCGAGAAGCTGGACAACACATTCTTGTCTGGTCAAGATCTTAAGCTGATCATCAACAGGACTC
TCCAACGTCTATGGAGGCTAATGCCGCTCGCCAGGCCATCCTGCAGAGTGGAGTCAAGATGACTCCAATGATATG
TGGGAGGACCAGGAGGAGGAAGAGGAGGAGGAGGAGGATGGTTTAGCTGGCCAACTTTTATCTGACATTCTTGCT
ACAAGTAAATATGAGGAGGATTACTACGAGGATGATGAGGAAGATGACCTGATGCCCTGAAGGATCCTCTCTAT
CAGATTGATCTGCAGGCATATCTCACAGATTTCTCTGCCAGTTTGTCTAGCAGCCCTGCTACATAATGTTTTTCA
GGCCACCTTAATGACAATGAGAGGCGAGTTCTACAGACCATCGGCATCTAA

WO 2004/030615

PCT/US2003/028547

612/6881
FIGURE 570

MAAAAAAGAASGLPGFVAQGLKEALVDTLTGILSPVQEVRAAAEEQIKVLEVTEEFVHLELTVDPQGALAIRQ
 LASVILKQYVETHWCAQSEKFRPPETTERAKIVIRELLPNGLRESISKVRSSVAYAVSAIAHWDWPEAWPQLFNL
 LMEMLVSGDLNAVHGAMRVLTFTREVTDQTQMPVLVAPVILPEMYKIFTMAEVYGIRTRRAVEIFTTCAHMICNM
 EELEKGAAKVLIFPVVQQFTEAFVQALQIPDGPTSDSGFKMEVLKAVTALVKNFPHMVSSMQQILPIVWNTLTE
 SAAFYVRTEVNYTEEVDPVDSGGEVLGFENLVFSIFEVHALLENSFKKSTVKKALPELIYYIILYMQITEEQI
 KVWTANPQQFVEDEDDDTFSYTVRIAAQDLLLLAVATDFQNESAAALAAAATRLQEAQTKNSGTEHWWKIHEAC
 MLALGSVKAIITDSVKNRIHFDMHGFLTNVILADNLNSVSPFLLGRALWAASRFTVAMSPELIQQFLQATVSGL
 HETQPPSVRISAVRAIWGYCDQLKVSESTHVLQFFLPSILDGLIHLAAQFSSEVLNLVMTLCIVCTVDPEFTAS
 MESKICPFTIAIFLKYSNDPVVASLAQDIFKELSQIEACQGPMQMRILPTLVSIMQAPADKIPAGLCATAIDILT
 TVVRNTKPPLSQLLICQAFPAVAQCTLHTDDNATMQNGGECLRAYVSVTLEQVAQWHDEQGHNGLWYVMQVVSQ
 LDPRTSEFTAFAVGRVSTLISKAGRELGENLDQILRAILSKMQQAETLSVMQSLIMVFAHLVHTQLEPLLEFLC
 SLPGPTGKPALEFVMAEWTSRQHLYGQYEGKVSSVALCKLLQHGINADDKRLQDIRVKGEEIYSMDEGIRTRSK
 SAKNPERWTNIPLLVKILKLIINELSNVMEANAARQATPAEWSQDDSDNMWEDQEEEEEEEDGLAGQLLSDILA
 TSKYEEDYYEDEDDPDALKDPLYQIDLQAYLTDFLCQFAQQPCYIMFSGHLNDNERRVLQTIGI

WO 2004/030615

PCT/US2003/028547

613/6881
FIGURE 571

AGTCAAGATGGAGGAGTACGCGGAGAGCCTTGCCCATGGCGAATTGTGGATGACTGTGGTGGGGCCTTTACGAT
GGGTACCAATTGGTGGTGGTATCTTTCAAGCAATCAAAGGTTTTTCGCAATTCTCCAGTGGGAGTAAACCACAGACT
ACGAGGGAGTTTGACAGCTATTAAAACCAGGGCTCCACAGTTAGGAGGTAGCTTTGCAGTTTGGGGAGGGCTGTT
TTCCATGATTGACTGTAGTATGGTTCAAGTCAGAGGAAAGGAAGATCCCTGGAATCCATCACAAGTGGTGCCTT
AACGGGAGCCATACTGGCAGCAAGAAATGGACCAGTGGCCATGGTTGGGTCAGCCGCAATGGGTGGCATTCTCCT
AGCTTTAATTGAAGGAGCTGGTATCTTGTGACAAGATTTGCCTCTGCACAGTTTCCCAATGGTCCTCAGTTTGC
AGAAGACCCCTCCAGTTGCCTTCAACTCAGTTACCTTCCTCACCTTTTGGAGACTATCGACAATATCAGTAGGA
CTTCTTTCCTAGGATTTCTTTAACAGAACGAGTTGTGGTTCGAGAAGGATTTCAGAAGATCAAGTTACAGTCTGT
TTTTAAAACCATAGGTGGGACAGCTATGGCCAATAGGCTATAAAGAGACATTTAGCACTTTTTTCTATTTAAAGG
AACAAGCGGGGAAGGGTGCTAAAAGATAATACGTTTTATTTATTCACACTTGAATTGCATTTGTGATCAAAATAAA
TGTTTAAATCGCTAAAGGAAAATACAGTAAGTGCTTGAAAGATGAAGGACCAAAAGGCCAAAAAACAGTGAAATA
TGATCATCATCTCTTGCGGACTTCTCTGCCTGGTTTTGTGTGTTCTGTATTCAAACAATAAAAAGCTGGTGGAA
CTTACTCTTTCTTTTAAGATAAGTTGTAGACTTCGATGTTTCATGCTCATGTACTTCAAATAATGCATGTTTTAT
AGTTAGTCCCTCATCACTTGAAGTGACTTCTGAGAATTATGCAGAGTCAACATGGATCATTTCACAGTGAGATGC
TTTATGGATTGAAGGATAAGGTAAAATGTTTATAGTTTACTTTGAAAGTAAAATATACTATGTCTTGGTTTTGAG
GATATTGGATACAAAACCTCTCTTCCTTTAGGGCTACTGAGTCTTGATTCTGATCATCAGAAATTTACCAGAAA
CAACTTGCTTCCAATATACCAATTCTATATGAAGAATTCATGGAGAGTGTACTGGCACTGGAAGAGTTTAGTGT
TTCTTGATGCTTGAAAATAAAGTATGTACTGTTTTGAATGTGTTCCAAGTCTCTGCATAAACGATGTATTTTG
GGGTCTGGTTGGGCCTGGAAAATGGATGAGCACTTCAGAACAGGTCAATTTTCTGATATTGGAAGTGACATGTGG
CCCTATAGGAGGCATGATGTTAGTTAATTACACATTTGCCTACATCTGTGGGAAATGGAGAACAAAGCCATGTGG
GTACTGTAAACACACGTTTTATCTTTTGCCCAATGCCATACATATGGTAGGCATTTAATTACTGATTGTGTTTGG
ATAATTTGGGAATTTTCGACTGTGGTAAAATATACATAAAATAATACTTATTAAAAA

WO 2004/030615

PCT/US2003/028547

614/6881
FIGURE 572

MEEYAREPCPWRIVDDCGGAFTMGTIGGGIFQAIKGFRNSPVGVNHLRGSLTAIKTRAPQLGGSFAVWGGLFSM
IDCSMVQVRGKEDPWNSITSGALTGAILAARNGPVAMVGSAMGGILLALIEGAGILLTRFASAQFPNGPQFAED
PSQLPSTQLPSSPFGDYRQYQ

WO 2004/030615

PCT/US2003/028547

615/6881
FIGURE 573

GGCCATGGCGAGCGGCGAGCATTCCCCCGGCAGCGGCGCGGCCCGGCGGCGCTGCACTCCGCGCAGGCTGTGGA
CGTGGCCTCGGCCTCCAACCTCCGGGCGCTTIGAGCTGCTGCACTTGACCTGGACCTGCGGGCTGAGTTCGGGCC
TCCAGGGCCCGGCGCAGGGAGCCGGGGGCTGAGCGGCACCGCGGTCTGGACCTGCGCTGCTGGAGCCCGAGGG
CGCCGCCGAGCTGCGGCTGGACTCGCACCCGTGCCTGGAGGTGACGGCGGCGGCGCTGCGGCGGGAGCGGCCCGG
CTCGGAGGAGCCGCTGCGGAGCCCGTGAGCTTCTACACGCAGCCCTTCTCGCACTATGGCCAGGCCCTGTGCGT
GTCTTTCGCGCAGCCCTGCCGCGCGCCGAGCGCCTCCAGGTGCTGCTCACCTACCGCGTCGGGGAGGGACCCGG
GGTTTGCTGGTTGGCTCCCGAGCAGACAGCAGGAAAGAAGAAGCCCTTCGTGTACACCCAGGGCCAGGCTGTCTT
AAACCGGGCCTTCTTCCCTTGCTTCGACACGCCTGCTGTTAAATACAAGTATTAGCTCTTATTGAGGTCCAGA
TGGCTTCACAGCTGTGATGAGTGCTAGCACCTGGGAGAAGAGAGGTCCAAATAAGTTCTTCTCCAGATGTGTCA
GCCCATCCCCTCCTATCTGATAGCTTGGCCATCGGAGATCTGGTTTCGGCTGAAGTTGGACCCAGGAGCCGGT
GTGGGCTGAGCCCTGCCTGATTGATGCTGCCAAGGAGGAGTACAACGGGGTGATAGAAGAATTTTGGCAACAGG
AGAGAAGCTTTTGGACCTTATGTTTGGGGAAGGTATGACTTGCTCTTCATGCCACCGTCCTTCCATTGGAGG
AATGGAGAACCCTTGCTGACCTTTGTCACCCCTGCCTGCTAGCTGGGGACCGTCCTTGGCAGATGTCATCAT
CCATGAGATCTCCACAGTTGGTTTGGGAACCTGGTCACCAACGCCAACTGGGGTGAATCTGGCTCAATGAAGG
TTTACCATGTACGCCAGAGGAGGATCTCCACCATCCTCTTGGCGCTGCGTACACCTGCTTGGAGGCTGCAAC
GGGGCGGGCTCTGCTGCGTCAGCACATGGACATCACTGGAGAGGAAAACCACTCAACAAGCTCCGCGTGAAGAT
TGAACCAGGCGTTGACCCGGACGACACCTATAATGAGACCCCTACGAGAAAGGTTCTGCTTTGTTTCATACCT
GGCCCACTTGGTGGGTGATCAGGATCAGTTTGACAGTTTTCTCAAGGCCTATGTGCATGAATTCAAATTCCGAAG
CATCTTAGCCGATGACTTTCTGGACTTCTACTTGGAATATTTCCCTGAGCTTAAGAAAAAGAGAGTGGATATCAT
TCCAGGTTTTGAGTTTGATCGATGGCTGAATACCCCGGCTGGCCCCGTACCTCCCTGATCTCTCCCTGGGGA
CTCACTCATGAAGCCTGCTGAAGAGCTAGCCCACTGTGGGCAGCCGAGGAGCTGGACATGAAGGCCATTGAAGC
CGTGGCCATCTCTCCCTGGAAGACCTACCAGCTGGTCTACTTCTGGATAAGATCCTCCAGAAATCCCCTCTCCC
TCCTGGGAATGTGAAAAAATTTGGAGACACATACCCAAGTATCTCAAATGCCCGGAATGCAGAGCTCCGGCTGCG
ATGGGGCCAAATCGTCCTTAAGAACGACCACCAGGAAGATTTCTGGAAAGTGAAGGAGTTCCTGCATAACCAGGG
GAAGCAGAAGTATACACTTCCGCTGTACCACGCAATGATGGGTGGCAGTGAGGTGGCCAGACCCTCGCCAAGGA
GACTTTTGATCCACCGCCTCCAGCTCCACAGCAATGTTGTCAACTATGTCCAGCAGATCGTGGCACCCAGGG
CAGTTAGAGGCTCGTGTGCATGGCCCCCTGCCTCTTCAGGCTCTCAGGATATCTATTCTCTAGCTTAGGTATCTGTGA
TTCTTGTTCCCTGATCAACTTCTGGAGTTTATATCCCCTCAGGATAATCTATTCTCTAGCTTAGGTATCTGTGA
CTCTTGGGCTCTGCTCTGGTGGGAACCTTACTTCTCTATAGCCCACTGAGCCCCGAGACAGAGAACCTGCCACA
GCTCTCCCCGCTACAGGCTGCAGGCACTGCAGGGCAGCGGTATTCTCTCCCCACCTAAGTCTCTGGGAAGAAG
TGGAGAGGACTGATGCTCTTCTTTTTCTCTTTCTGCTTTTTCTTGCTGATTTTATGCAAGGGCTGGCATT
TGATTGTTCTTTTTTCAGGTTTAATCCTTATTTTAATAAAGTTTTCAAGCAAAAT

WO 2004/030615

PCT/US2003/028547

616/6881
FIGURE 574

MASGEHSPGSGAARRPLHSAQAVDVASASNFRAFELLHLHLDLRAEFGPPGPGAGSRGLSGTAVLDLRCLEPEGA
AELRLDSHPCLEVTAALRRERPGSEEPFAEPVSFYTQPF SHYGQALCVSFPQPCRAAERLQVLLTYRVGEGPGV
CWLAP EQTAGKKKPFVYTQQA VLNRAFFPCFDTPAVKYKYSALIEVPDGF TAVMSASTWEKRGPNKFFFQMCQP
IPSYLIALAIGDLVSAEVGPRSRVWAEFCLIDAAKEEYNGVIEEFLATGEKLF GPYVWGRYDLLFMPPSFPGGM
ENPCLTFVTPCLLAGDRSLADVIIHEISHSWFGNLVTNANWGEFWLNEGFTMYAQRRISTILFGAAYTCLEAATG
RALLRQHMDITGEENPLNKL RVKIEPGVDEDDTYNETPYEKGFCFVSYLAHLVGDQDQFDSFLKAYVHEFKFRSI
LADDFLD FYLEYFPELKKKRVDIIPGFEEFDRWLNTPGWPPYLPDLSPGDSL MKPAEELAQ LWAAEELDMKAIEAV
AISPWKTYQLVYFLDKILQKSPLPPGNVKKLGDTPSISNARNAELRLRWGQIVLKNHQEDFWKVKEFLHNQ GK
QKYTLPLYHAMMGSEVAQTLAKETFASTASQLHSNVVNYVQQIVAPKGS

WO 2004/030615

PCT/US2003/028547

617/6881
FIGURE 575

AGGCTCTATTTAGAGCCGGGTAGGGGAGCGCAGCGGCCAGATACCTCAGCGCTACCTGGCGGAACTGGATTTCTC
TCCCGCCTGCCGGCCTGCCTGCCACAGCCGGACTCCGCCACTCCGGTAGGATTCCCCGCCTGTCATTCCCTAGCC
CAGCTCTTGGGAACTGCAGAGGGGTCCAGAGGATTTCAGATTCTGAACCTGCACACTCCAGTCTAGGATCTCCG
AGCAAGAGCGTAGCCTCATGGCTGCAACCTGTGAGATTAGCAACATTTTATAGCAACTACTTCAGTGCATGTACA
GCTCGGAGGACTCCACCCTGGCCTCTGTCCCCCTGCTGCCACCTTTGGGGCCGATGACTTGGTACTGACCCTGA
GCAACCCCCAGATGTCATTGGAGGGTACAGAGAAGGCCAGCTGGTTGGGGGAACAGCCCCAGTTCTGGTCGAAGA
CGCAGGTTCTGGACTGGATCAGCTACCAAGTGGAGAAGAACAAGTACGACGCAAGCGCCATTGACTTCTCACGAT
GTGACATGGATGGCGCCACCCTCTGCAATTGTGCCCTTGAGGAGCTGCGTCTGGTCTTTGGGCCTCTGGGGGACC
AACTCCATGCCCAGCTGCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGGATCATTGAGCTGCTGGAGA
AGGATGGCATGGCCTTCCAGGAGGCCCTAGACCCAGGGCCCTTTGACCAGGGCAGCCCCCTTTGCCCAGGAGCTGC
TGGACGACGGTCAGCAAGCCAGCCCCCTACCACCCCGCAGCTGTGGCGCAGGAGCCCCCTCCCCGGCAGCTCTG
ACGTCTCCACCGCAGGGACTGGTGCTTCTCGGAGCTCCCACTCCTCAGACTCCGGTGGAAGTGACGTGGACCTGG
ATCCCACTGATGGCAAGCTCTTCCCCAGCGATGGTTTCGTGACTGCAAGAAGGGGGATCCCAAGCACGGGAAGC
GGAAACGAGGCCCGGCCCGAAAGCTGAGCAAAGAGTACTGGGACTGTCTCGAGGGCAAGAAGAGCAAGCACGCGC
CCAGAGGCACCCACCTGTGGGAGTTCATCCGGGACATCCTCATCCACCCGGAGCTCAACGAGGGCCCTCATGAAT
GGGAGAATCGGCATGAAGGCGTCTTCAAGTTCCTGCGCTCCGAGGCTGTGGCCCACTATGGGGCCAAAAGAAAA
AGAACAGCAACATGACCTACGAGAAGCTGAGCCGGGCCATGAGGTACTACTACAAACGGGAGATCCTGGAACGGG
TGGATGGCCGGCGACTCGTCTACAAGTTTGGCAAAACTCAAGCGGCTGGAAGGAGGAAGAGGTTCTCCAGAGTC
GGAAGTGAAGGTTGGAAGTATACCCGGGACCAAACTCACGGACCACTCGAGGCTGCAAACTTCTCTGGGAGGAC
AGGCAGGCCAGATGGCCCCCTCCACTGGGGAATGCTCCAGCTGTGCTGTGGAGAGAAGCTGATGTTTTGGTGAT
TGTCAGCCATCGTCTCTGGGACTCGGAGACTATGGCCTCGCCTCCCCACCCTCCTCTTGAATATACAAGCCCTGGG
GTTTGAAGCTGACTTTATAGCTGCAAGTGTATCTCCTTTTATCTGGTGCTCCTCAAACCCAGTCTCAGACACTA
AATGCAGACAACACCTTCTCCTGCAGACACCTGGACTGAGCCAAGGAGGCTGGGGAGGCCCTAGGGGAGCACC
GTGATGGAGAGGACAGAGCAGGGGCTCCAGCACCTTCTTCTGGACTGGCGTTCACCTCCCTGCTCAGTGCTTGG
GCTCCACGGGCAGGGGTGAGAGCACTCCCTAATTTATGTGCTATATAAATATGTCAGATGTACATAGAGATCTAT
TTTTTCTAAACATTTCCCTCCCCACTCCTCTCCCACAGAGTGTGACTGTTCCAGGCCCTCCAGTGGGCTGAT
GCTGGGACCCTTAGGATGGGGCTCCCAGCTCCTTTCTCCTGTGAATGGAGGCAGAGACCTCCAATAAAGTGCCTT
CTGGGCTTTTTCTAACCTTTGTCTTAGCTACCTGTGTACTGAAATTTGGGCCTTTGGATCGAATATGGTCAAGAG
GTTGGAGGGGAGGAAAATGAAGGTCTACCAGGCTGAGGGTGAGGGCAAAGGCTGACGAAGAGGGGAGTTACAGAT
TTCCTGTAGCAGGTGTGGGCTTACAGACACATGGACTGGGCTGGGAGGCGAGCAAAGGAAGCAGCTGAGACTGTT
GGAGAACGCTTACAAGACTTCATGCAAGCAAGGACATGAACTCAGAACACTGAGGTGAGAAGCATCCTGCTGTCA
TGACACCGCTCGAGTGACCTTGACCTTGACCAAGTCTGTCTGTTTAGGACTGATTTTTCTATTAGGCTAGGGT
TTGGACCTGATGTTCTCAAGATGTCTAGAATTGCATGGCTGGCCTTGTGGAATAGATGGTTTTGCATTCCAGCCA
AGTGTGCTGTAACTGTATATCTGTAATATGAATCCCAGCTTTTGAGTCTGACAAAATCAGAGTTAGGATCTTGT
AAAGGA

WO 2004/030615

PCT/US2003/028547

618/6881
FIGURE 576

CGGGTACAGGGGGCCCAAGAGCTGGGCTGGCTGTCTCCTGCTCATCCAGCCATGCGGTGGCTGTGGCCCCTGGCT
GTCTCTCTTGCTGTGATTTTGGCTGTGGGGCTAAGCAGGGTCTCTGGGGGTGCCCCCTGCACCTGGGCAGGCAC
AGAGCCGAGACCCAGGAGCAGCAGAGCCGATCCAAGAGGGGCACCGAGGATGAGGAGGCCAAGGGCGTGCAGCAG
TATGTGCCTGAGGAGTGGGCGGAGTACCCCGGCCATTACCCCTGCTGGCCTGCAGCCAACCAAGCCCTTGGTG
GCCACCAGCCCTAACCCCGACAAGGATGGGGGCACCCAGACAGTGGGCAGGAAGTGGGGGCAATCTGACAGGG
GCACCAGGGCAGAGGCTACAGATCCAGAACCCCTGTATCCGGTGACCGAGAGCTCCTACAGTGCCTATGCCATC
ATGCTTCTGGCGCTGGTGGTGTTTGGCTGGGCATTGTGGGCAACCTGTGGTTCATGTGCATCGTGTGGCACAGC
TACTACCTGAAGAGCGCCTGGAAGTCCATCCTTGCCAGCCTGGCCCTCTGGGATTTTCTGGTCCTCTTTTCTGC
CTCCCTATTGTCTCTTCAACGAGATCACCAAGCAGAGGCTACTGGGTGACGTTTCTTGTCTGCGTGGCCTTTC
ATGGAGGTCTCCTCTCTGGGAGTCACGACTTTTCCAGCCTCTGTGCCCTGGGCATTGACCGCTTCCACGTGGCCACC
AGCACCTTGCCCAAGGTGAGGCCCATCGAGCGGTGCCAATCCATCCTGGCCAAGTTGGCTGTCTGCGTGGGCTGGC
TCCATGACGCTGGCTGTGCTGAGCTCCTGCTGTGGCAGCTGGCACAGGAGCCTGCCCCACCATGGGCACCCCTG
GACTCATGCATCATGAAACCCCTCAGCCAGCCTGCCCCGAGTCCCTGTATTCACTGGTGATGACCTACCAGAACGCC
CGCATGTGGTGGTACTTTGGCTGCTACTTCTGCCTGCCCATCCTCTTACAGTCACCTGCCAGCTGGTGACATGG
CGGGTGCGAGGCCCTCCAGGGAGGAAGTCAGAGTGCAGGGCCAGCAAGCACGAGCAGTGTGAGAGCCAGCTCAAC
AGCACCGTGGTGGGCTGACCGTGGTCTACGCCTTCTGCACCCCTCCCAGAGAACGTCTGCAACATCGTGGTGGCC
TACCTCTCCACCGAGCTGACCCGCCAGACCCCTGGACCTCCTGGGCCTCATCAACCAGTTCTCCACCTTCTTCAAG
GGCGCCATCACCCAGTGCTGCTCCTTTGCATCTGCAGGCCGCTGGGCCAGGCCTTCTGGACTGCTGCTGCTGCTG
TGCTGCTGTGAGGAGTGCGGCGGGGCTTCGGAGGCCTCTGCTGCCAATGGGTGCGGACAACAAGCTCAAGACCGAG
GTGTCTCTTCCATCTACTTCCACAAGCCCAGGGAGTCACCCCACTCCTGCCCCTGGGCACACCTTGCTGAGGC
CCCAGTAGGGGTGGGGAGGGAGGGAGAGGCCGCCACCCCGCCGGTGTCTGCTGTTCTTTCCCATAGGTCTTGC
TTTGTTCCTGTCTTGCTGTCTAGGGATGGACTTGGTTCTTGTCAAGGTTTGGGAATCCG

WO 2004/030615

PCT/US2003/028547

619/6881
FIGURE 577

MRWLWPLAVSLAVILAVGLSRVSGGAPLHLGRHRAETQEQQSRSKRGTEDEEAKGVQQYVPEEWAHEYPRPIHPAG
LQPTKPLVATSPNPDKDGGTPDSGQELRGNLTGAPGQRLQIQNPLYPVTESSYSAYAIMLLALVVFVAVGIVGNLS
VMCIVWHSYYLKSANWSILASLALWDFLVLFCLPIVIFNEITKQRLLDVSCRAVPFMEVSSLGVTTFSLCALG
IDRFHVATSTLPKVRPIERCQSILAKLAVIWVGSMTLAVPELLWQLAQEPAPTMGTLDSCIMKPSASLPESLYS
LVMTYQNARMWWYFGCYFCLPILFTVTCQLVTWRVRGPPGRKSECRASKHEQCESQLNSTVVGLTVVYAFCTLPE
NVCNIVVAYLSTELTRQTLDLLGLINQFSTFFKGAITPVLLLCICRPLGQAFLDCCCCCCECGGASEASAANG
SDNKLKTEVSSSIYFHKPRESPPLLPLGTPC

WO 2004/030615

PCT/US2003/028547

620/6881

FIGURE 578

GC GCGCAGCGCTGGTACCCCGTTGGTCCGCGCGTTGCTGCGTTGTGAGGGGTGTCAGCTCAGTGCATCCCAGGCA
GCTCTTAGTGTGGAGCAGTGAAGTGTGTGTGGTTTCCTTCTACTTGGGGATCATGCAGAGAGCTTCACGTCTGAAG
AGAGAGCTGCACATGTTAGCCACAGAGCCACCCCCAGGCATCACATGTTGGCAAGATAAAGACCAAATGGATGAC
CTGCGAGCTCAAAATATTAGGTGGAGCCAACACACCTTATGAGAAAGGTGTTTTTAAGCTAGAAGTTATCATTCCCT
GAGAGGTACCCATTTGAACCTCCTCAGATCCGATTTCTCACTCCAATTTATCATCCAAACATTGATTCTGCTGGA
AGGATTGTCTGGATGTTCTCAAATTGCCACCAAAAGGTGCTTGGAGACCATCCCTCAACATCGCAACTGTGTTG
ACCTCTATT CAGCTGCTCATGTCAGAACCAACCCTGATGACCCGCTCATGGCTGACATATCCTCAGAATTTAAA
TATAATAAGCCAGCCTTCCTCAAGAATGCCAGACAGTGGACAGAGAAGCATGCAAGACAGAAACAAAAGGCTGAT
GAGGAAGAGATGCTTGATAATCTACCAGAGGCTGGTGACTCCAGAGTACACAACTCAACACAGAAAAGGAAGGCC
AGTCAGCTAGTAGGCATAGAAAAGAAATTCATCCTGATGTTTACGGGACTTGTCCTGGTTTCATCTTAGTTAATG
TGTTCTTTGCCAAGGTGATCTAAGTTCCTACCTTGAATTTTTTTTTAAATATATTTGATGACATAATTTTGTG
TAGTTTATTTATCTTGTACATATGTATTTTGAAATCTTTTAAACCTGAAAAATAAATAGTCATTTAATGTTGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

621/6881
FIGURE 579

MQRASRLKRELHMLATEPPPGITCWQDKDQMDDLRAQILGGANTPYEKGVFKLEVIIPERYPFEPPIRFLTPIY
HPNIDSAGRICLDVLKLPPKGAWRPSLNIATVLTISIQLLMSEPNPDDPLMADISSEFKYNKPAFLKNARQWTEKH
ARQKQKADEEEMLDNLPEAGDSRVHNSTQKRKASQLVGIEKKFHPDV

WO 2004/030615

PCT/US2003/028547

622/6881
FIGURE 580A

ATGCTGCAAAATGCCGAAGTTAAATGAAATACCTCCGGGGAGGGCAGGCCGAGGGAGGCTCGGGGGGAGGGAAGA
TGGCCTGGACAAACAGGTCTCTGAAGCTGCGAGGCTGGAGTGGAGGGCGCAGGGGCGAGGGCGGCCAGAGCT
CCATGGGACAGCTGGGGAAGCTCCAGGCTACCTACACAACCTGGCCCAGGCTGGTCACGGTGTCCCCCTCCCTG
CTCTGTGCCCTCTCCTTCCAGAAATCCACCATGGAGAGTAAGGATGAGGTCAGCGACACCGACAGTGGCATCATC
CTGCAGTCTGGCCCCGACAGCCCGGTCTCCCAATGAAGGAGCTGACCCATGCAGTGCACAAGCAGCAGAGGGCC
CTGGAAGCGAGGCTGGAGGCCTGCCTGGAGGAGCTGAGGAGACTCTGCCTTCGGGAAGCGGAGCTGACGGGCACC
TTGCCAGCGGAGTATCCCCTCAAACAGGGGAAAAGGCCCCCAAGGTTGCGCGCAGGATCGGAGCGGCTTACAAA
CTGGATGACTGGGCCTTGACAGAGAGGACCCCTAAGCAGCCTGGAGCGCCAGCTGGCCCTGCAGCTGCAGATC
ACAGAGGCAGCCCGTGGCTGTGCCTGGAGGAGAACCTCAGCAGGCAGGCTCGGCGGCAGCGGAAGCACTCCATG
CTGCAGGAGGAGAAGAAGCTGCAGGAGCTCCAGCGCTGCCTGGTTCGAGCGGCGGCGCAATAGCGAGCCACCTCCG
GCTGCTGCTCTCCCCCTGGGCGGAGAGCTCAGTGCCTCTGATGACAGCTCCCTGTGAGATGGGCTCCTCTGGAG
GAAGAGGAAATCCCAAGTGCCAAAACCTCCTCCAGAGTCTCCAGCCCCACCTTCTCGGCCTCTCCACCCCCAAACC
CTTGAGGGTCTGCAGCCAACAGGACCTGAGGCTGGGAGCCGAGGCTCCAGTCCAGAACAGCCCCCTGGAAG
GAAACCAGCCTGGACCACCCCTATGAGAAGCCAGGAAGTCTTCTGAGCCCTGGAGCGAGTCCAGCAGCCAGCC
ACCACACCACAGGATGGGCCCAGTGCCTCCAGCCTGTGGCTTCTGGAGCCTGCCTCCTACCACGTGGTTCCCATC
CGTGGTGTTCCTGGCCAGTGGCAGGGCCGACCAAGTGCACCCACCCCTGAGATACAGGGGAGGAGGGGCCAG
TCGCAGTCTCTGAGGGTGGATTCTTCCGGGCGGGTCTGAGGGCCGAGGTTCGACGCGCTTTCGCCGCGCCGC
CCCACTCACTACACGGTGACAGTGCCAGATTCTGTCTTCCCGCGACCAAGCCCCCGCTGCCCCACGCCGCTGC
CACTCCTGCTCAGAAGACAGTGGCTCTGACGTCTCCAGCATCTCCACCCCACTTTCGCCGGGCGAGCAGCCCC
GACATCTCCTTTCTGCAGCCTCTCTCCCTCCCAAGACCCATCGTCACCGCGGGCCTGGGTCCAGCCGGCAGC
AGAGAGCTGGTCGCCCCACCACCCCAAGCTACTGCTGCCGCTGGCTATTTCCCGGCGGGGCGGTACGTGGTGGTG
GCTGAGAGCCCCCTGCCGCTGGCGAGTGGGAGCTGCGCCGCGCAGCCCCGGGCCCTGCTTACGAGGAGGAGGGC
ACTCCCTTGCGCTACCAGCGTCTGGTGCCTCCCGCAGCCGCATCGTGCAGGACGCCCTCCCTGAAGGACAGCCCG
GCAGGCCGGGGGCTCAGCAAGGCCGCGCTGTCCGAGGAGCTCAAGTGGTGGCACGAGCGTGCACGCCTCCGGAGC
ACCCGCCCCCACTCACTGGACCGCCAAGGAGCTTTCCGGGTGAGGAGCCTGCCCCCTGGGAGAGAGGGCTTCGGA
CGAGCCCTGGGACCCCGGGCACAGGTGCCACAGTTTGTGTGCTGCGGAGATCGCCTGATGGGGCCCCCTGTGCAA
GTCTTTGTACCTGAAAAAGGAGAGATCATCAGCCAGGTGTAAGTCTGCGCCCCACGCTGGAAAAAACTGTTTCAT
AGAGGGGCTGGGCTGAGACCCCCCACCCTGAGTGCCTCTTTCAGCTCCCCATCCCCATCGCAGGCCGATGAC
CTGGAGCTGAGACCTTTTATTATTTTATTTTACACGACTTTTTCAGAAGCCCTGACCTAAGGATTTATATATG
TGGATTGTCTCAATACCCCTGTGATATGATTATGTTTATCCCCCAGAGTTGGCCTACTGGACTTAAGGCCTT
GCCTGTCTGACTGACAGCCTCTATCTCCTTATATAAGACAAGTGGCAGGGGACGAGTGAAGCAGAGTGAGCCACC
TTGGGAGTTCTCAACGCTCTGTGCTCTGGTTCTAAGAAATTCCTGGGGAAGTGGCCCTGGCCCTCTGTCCCA
CTATTGCTGGAGGCTGGACATGGTACATACTCATGCACATGACTCTCCCCATTTCCAGGTCTCTGGGTACCCC
AGCCTGGGCTGGGGGAGAATCTCTTCCCCCTTTTCTAATGTGCTCTGTGATGCACACCAAGTGGTAGGTCAAA
GGTCAGTATATCCCGGTGGTGTATTGTCTGTGCTAGACCCTGCTATTTTCCTGACCCCTAAATCCTCTTTAGGGA
CCCAGTCACTATACCCTGTCTATGCCCTGTGGGCTCCAGACCCCTGAGCTTTGAGTCAGTGGCATCACAGTTTG
TAGCCTCAGGGGGTCTGGCTGGGGGCTGGTCCATGCTTGTGGTTAGTGGACAGCAGCCACCCCTTGACAGCTACC
TCTGGGCATCTCAAGGGCTTGACGCCCCACTGCTCCTTCTAACATTTTGTGTTGTTTGTAGATGGAGTCTCGCTC
TGTGCCCCAGGCTGGAATGCTGTAGCAAGATTTCCGGCTCACTGCAACCCCGTCTCCCGGGTTCAAGCGAATCTC
CTGCCTCAGCCTTCCAGTAGCTGGGATTACAGGCAAGCACCACCATGCCTGCTAATTTTTTATTTTATAGTAGAG
ATGGGGTTTTCATCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAGTGATCCACCTGCCTTGGCCTTTCAA
AGTGTGTTGGATTACAGGCATGAGCCACCGCACCTGGCCCTTCTAACGTTTTTTCATCATAGTCCCAAAAACCAAT
ACTTTACAAGTGGTTTTGGAAAGGCACCACTTTTGTGGCATGTTCTGGTTGGGAGAGGGAGTCAAGTTTCTACT
CCCCCACCAGCTATGCTTCTGCTCTGAGAAGGTGGTTATTTATACAAACATGGACATACTCACTCCCAAGGGCT
GATGAGATGCTGAATTTTCTTTGGGGGCATTCAATTAATTGTCCAGCTGCAGCGACTGGAGCAAGTCTGGAAGCT
GCCTGTGCTAAGACCACCCAGCTGTCCCTGGGTTCTCATCTAGGGCCTTCTTTGCTTCCAGGTGAGGGGACCTG
CTTCAATGAGAAAGCAACTGAATTGAGGCTAGGAGAGGTAGGGAGAGCTGAGTTCTGACTTCACCTGTGCAGAAC
TCTCTGCCCCCATGTTACCTGGACTGGAACAGACTGTGAATATAGCAGAAGGTTCCAAGAAGTCTGGTGTCTGAC

WO 2004/030615

PCT/US2003/028547

623/6881

FIGURE 580B

CTAGAAGAGGCACAGTTCTCTCTACTGGAAAGAAAACGATGTAGCCGATTGCACAAGGGTGCCAAGGGAAGACCC
AGGATGGCCCATCAAAGGAACCTGGGGGAGGATGCAGGAGGCTGAAGGGATGCACCTGGCATTCTCTCACTGTG
CTCTTACCGCATCAGCAACCCCCAACTTTTGGGCCTACTCTGCCCCCATGCGTGAATACCCTGCTTGGATGCTG
TGCTTTTCCGGTTTGTCTCTAAGCCCCCTTCTCCAGGGCATGTTGGTTTCCCTGGCCTCTCAGTGTCTTAAGTGG
AGCCCAGAGTGCTTGTCTGAGCCAGGAGACGGCTGAGCACTGGCCCTCCACACCTAAGCGTCCTTTACATTAA
CTTATTGGTCTTGTATAACACCTGGTGCCATTGCCAAGTGGCTGTGTCCTCAGCTACAGAGCTGGAATTGTGTGG
GGTTTAGTGCTAAATACTTCAATAAAGTCTGTTTTTTGTGATTGGCTG

WO 2004/030615

PCT/US2003/028547

624/6881
FIGURE 581

TCCCCGGGCCGGGAGCCAGCAGGCCGGGAGCGGCTGAGGCCACACCCCGCGGGCCGGGCGCTTCCCTCCGGTGA
ATCATCGCTCGCAGCGGGCGGCCGAGTGGCCGAGCAGCGCGCCGGGCCCTGGCCGCGCCCCAGCCGAGCGC
AGCGCGGAGTCGCCCCGACCTTTCTCTGCGCAGTACGGCCGCCGGGACCGCAGCATGGCGGGCATCGCGGCCAAG
CTGGCGAAGGACCGGGAGGCGGCCGAGGGGCTGGGCTCCCACGACAGGGCCATCAAGTACCTCAACCAGGACTAC
GAGGCGCTGCGGAACGAGTGCCTGGAGGCCGGGACGCTCTTCCAGGACCCGTCCTTCCCGGCCATCCCCTCGGCC
CTGGGCTTCAAGGAGTTGGGGCCCTACTCCAGCAAAACCCGGGGCATCGAGTGAAGCGCCCCACGGAGATCTGC
GCTGACCCCCAGTTTATCATTGGAGGAGCCACCCGCACAGACATCTGCCAAGGAGCCCTGGGTGACTGCTGGCTG
CTGGCAGCCATTGCCTCCCTCACCTTGAATGAAGAAATCCTGGCTCGAGTCGTCCCCCTAAACCAGAGCTTCCAG
GAAACTATGCAGGGATCTTTCACTTCCAGTTCTGGCAATACGGCGAGTGGGTGGAGGTGGTGGTGGATGACAGG
CTGCCCCACCAAGGACGGGGAGCTGCTCTTTGTGCATTACGCCGAAGGGAGCGAGTTCTGGAGCGCCCTGCTGGAG
AAGGCATACGCCAAGATCAACGGATGCTATGAAGCGCTATCAGGGGGTGCCACCACTGAGGGCTTCAAGACTTC
ACCGGAGGCATTGCTGAGTGGTATGAGTTGAAGAAGCCCCCTCCCAACCTGTTCAAGATCATCCAGAAGCTCTG
CAAAAAGGCTCTCTCCTTGGCTGCTCCATCGACATCACCAGCGCCGCGGACTCGGAGGCCATCACGTTTCAAGAG
CTGGTGAAGGGGCACGCGTACTCGGTACCCGAGCCGAGGAGGTTGAAAGTAACGGAAGCCTACAGAACTGATC
CGCATCCGAAATCCCTGGGGAGAAAGTGGAGTGGACAGGGCGGTGGAATGACAACTGCCCAAGCTGGAACACTATA
GACCCAGAGGAGAGGGAAAGGCTGACCAGACGGCATGAAGATGGAGAATTCTGGATGTCTTTTCACTGACTTCCTG
AGGCACTATTCCCGCTGGAGATCTGTAACCTGACCCAGACACTCTCACCAGCGATACCTACAAGAAGTGGAAA
CTCACCAAAATGGATGGGAACCTGGAGGCGGGGCTCCACCGCGGGAGGTTGCAGGAACCTACCCGAACACATTCTGG
ATGAACCTCAGTACCTGATCAAGCTGGAGGAGGAGGATGAGGACGAGGAGGATGGGGAGAGCGGCTGCACCTTC
CTGGTGGGGCTCATTGAGAAGCACCGACGGCGGCAGAGGAAGATGGGCGAGGACATGCACACCATCGGCTTTGGC
ATCTATGAGGTTCCAGAGGAGTTAAGTGGGCAGACCAACATCCACCTCAGCAAAAACCTTCTTCTGACGAATCGC
GCCAGGGAGCGCTCAGACACCTTCATCAACCTCCGGGAGGTTGCTCAACCGCTTCAAGCTGCCGCCAGGAGAGTAC
ATTCTCGTGCCCTCCACCTTCGAACCCAAACAAGATGGGGATTCTGTCATCCGGGTCTTTTCTGAAAAGAAAGCT
GACTACCAAGCTGTGATGATGAAATCGAGGCCAATCTTGAAGAGTTGACATCAGCGAGGATGACATTGATGAT
GGATTGAGGAGACTGTTTGCCAGTTGGCAGGAGAGGATGCGGAGATCTCTGCCTTTGAGCTGCAGACCATCCTG
AGAAGGGTTCTAGCAAAGCGCCAAGATATCAAGTCAGATGGCTTCAGCATCGAGACATGCAAAATTATGGTTGAC
ATGCTAGATTGCGACGGGAGTGGCAAGCTGGGGCTGAAGGAGTTCTACATTCTCTGGACGAAGATTCAAAAATAC
CAAAAATTTACCGAGAAATCGACGTTGACAGGTCTGGTACCATGAATTCCTATGAAATGCGGAAGGCATTAGAA
GAAGCAGGTTTCAAGATGCCCTGTCAACTCCACCAAGTCATCGTTGCTCGGTTTGCAGATGACCAGCTCATCATC
GATTTTGATAATTTTGTTCGGTGTGTTGGTTTCGGCTGGAAACGCTATTCAAGATATTTAAGCAGCTGGATCCCGAG
AATACTGGAACAAATGAGCTCGACCTTATCTCTTGGCTCTGTTTCTCAGTACTTTGAAGTTATAACTAATCTGCC
TGAAGACTTCTCATGATGGAATAATCAGCCAAGGACTAAGCTTCCATAGAAATACACTTTGTATCTGGACCTCAA
ATTATGGGAACATTTACTTAAACGGATGATCATAGCTGAAAATAATGATACTGTCAATTTGAGATAGCAGAAGTT
TCACACATCAAAGTAAAAGATTTGCATATCATTATACTAAATGCAAATGAGTCGCTTAACCTTGACAAGGTCAA
AGAAAGCTTTAAATCTGTAAATAGTATACACTTTTACTTTTACACACTTTCTGTTTCATAGCAATATTAAATCA
GGAAAAAAAATGCAGGGAGGTATTTAACAGCTGAGCAAAAACATTGAGTCACTCTCAAAGGACACGAGGCCCTT
GGCAGGGAATATTTAAAGCAACTTCAAGTTTAAATGCAGCTGTTGATTCTACCAAACAACAGTCCAAGATTACC
ATTTCCCATGAGCCAACCTGGGAAACATGGTATATCATGAAGTAATCTTGTCAAGGCATCTGGAGAGTCCAGGAGA
GAAGACTCACCTCTGTCGCTTGGGTAAACAAGAGACAGGTTTGTAGAATATTGATTGGTAATAGTAAATCGTT
CTCCTTACAATCAAGTTCTTGACCCTATTTCGGCCTTATACATCTGGTCTTACAAAGACCAAGGGATCCTGCGCT
TGATCAACTGAACAGTATGCCAAAACAGGCATCCAATTTGTAAACCAATTATGATAAAGGACAAAATAAGCTG
TTTGCCACCTCAAACTTTATGAACCTCACCACCACTAGTGTCTGTCCATGGAGTTAGAGGGGACATCACTTAGA
AGTTCTTATAGAAAGGACACAAGTTTGTTCCTGGCTTTACCTTGGGAAAATGCTAGCAACATTATAGAAATTTT
GCCTTGTTCCTTATCTTCTCCAAATGTAAGTTTAAATAAAAATAAAGGGTTACCCCATGCAATCACACCATGC
CATGTTTTCTTCTTGGAGGGCAGCCCCACAGGACGGTTTATGAGCACACAATTATAGCTTGTCTTACTTTAAC
AAGGTATGCTGCCTCTGTAAATTCATGTATTCAAAGGAAAAGACACCTTGCTATAATTAATGTGGAACATA
AAATTTTTTAAATCC

WO 2004/030615

PCT/US2003/028547

625/6881
FIGURE 582

TCTAATACCTATTGATCTGTTACTTTCTCCCATCACGCTCAGGTGGGAACATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCTGATTCTACATTATGGTGAGTTCCATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCTCAATGGCCTATTTAGGCCCATAACCTACGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTTGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATTCTTCACGCCCAGCTTCTACCTCACTTGGACCCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCAGCCTCTGC
CTCACAGCGGACTCTC

WO 2004/030615

PCT/US2003/028547

626/6881
FIGURE 583

GGTATTTTCAGGACAGCCAGGAGGGGGCGCACATCCGCCGAGAACTGTGAGCAAGAGCGTCTGTGCTGAACCATG
GCGCCACCAGAGGGCGCGCATCCCCGCCCAACCAACTTCCCCTGAGGTGCCAGAAGCAGCGAGGAGCTTCAGC
TTCCCTCAGGGCAGCACGAGGGTCGTGTTAACTTGGTGTTCTTCATTGATGATGATTATTTCCACCTTCTAAGAG
ACAAAGACCAACGAGCCACCACAGCCACCAGTCCCGAAGCTGCCAATGCTGGGGAACGGAAAATGAGGGAGTTT
AACTCTGGCCCTCACAATCCAGTGGAGGAGACGAAACTCATCTGCCTCTGTCCCTCTGGGCACGCCTCATGCCAG
GTGCATCTGTGGACAGGGGCCATGCCCTGGGCTTCCAAAGTTGGAGAGAGCTGCCAGGCTCAGGTCTGAAGGCC
AGAATTCTACAGTAAGTCTTACTGAGTCAAGGTGGGAGCAGGGTCCGGTAGCTTCCGAGGCTCTGCGGGAGAATCC
GTTTCCTGGCCGTAGAGGTGGCTGCACTCCCGCAGCTTGTGCTGCCCCGTCTCGAATGACTGGAGTTTCTGCTTC
TGTCATAACCTCCACCTCTCCATCACCTGCTCTGCTCTTACAAGGATCCGAAGAAATGGAATCATCGTATC
GCTGATCTACGTAAACAACTGAAGAATTGTCTGAAAGAAAATATGACATGAACCTTATGAATTCAACAGGTGAAG
ATTTACAACCTTGATAAATCAACTTTGTGAGCTCGAGCTGTAAAGCCAAAGGTCCGGTGATGATCCCATACCTT
TTTTCCAGTCTCATGTTGAAGATTTTTATGTAGAAGGCCTTCCCAAAGGAATTTTTTTTTTTTTTTTTTTGA
GATGGAGTTTTCACTCTTATCGCCAGGCTGGGGTGCAATGGCGCAACCTTGCTGGTCACTGCAACCTCTGCCTC
CTGGGTTCAAGAAATTCCTGCCCTAGCCTCCCAAGTCACTGGGATTACAGGTGCCACCACCATAACAGGCTA
ATTTTTGTATTTTAGTGGAGATGCGGTTTACCATGTTGGCCGGGCCAGTCTCGAACTCCTGACGTCAAGTGAT
CTTCCCGCTCGACTCCTGATATCAAGTGATCTTCCCGCTCGGCCCTCCAGAGTGCTGAGATTACAGAGCTGAA
CCCATGCCCTGGCCAGGAATTTTGTTTTTTAGGAAGGCTTCTACTAATGGAATTCCTGGCCTTGAGAGGATGTTA
CTTTAGAAGGAAAGGATTTTTTGTATTAAAAGCTGGACCTACCATGAAAGACTTCTGAATCCAGGAAGAGAAA
CTGACTGGGCAACATGTTATTACAGAAACAGGACCTTGCCCTGTCACTCAGGATGGAGTTGAGGATGTTA
GCTCATTATAGCCTCAAACCTCCAGGCTCAAGCAATCTACCATGTGAGCTTCCAGCTTCCAGTAGCTGGGACTACAGAT
ACCGGGTCTCACACTGTACCCAGGCTGGAGTACAGTGGCACAACCTCTGCTCACTGCAGCCTCCACCTGCCAGG
CTCAAGCAATTCCTGCTCAGCCTCCCGAGTAGCTGGTGATTCCAGGATGTGAGCTCACAATGACTCAAGCT
GCCACATACTGTTGATTGTGAAATGCCAGTTGAAGCATATGTCTCGAGCTTAGGGGTGCTACAAGTTGACCAC
TGCAGCAGTAAAGATGACTCTGAAGAATGGCGTGGGTGGTTCTTCTCAAATGCACCTTGAGCAGCGGTCTCCAAC
CACAGGGCCACAGAGCTGGAGCTGGATCTACCATGAAAGACTTGTGATTCAGGAAGAGAGACTGACTGGGCAAC
ATGTTATTACAGAACTTCTGTGCCATCCAGGCTGGAGTGCAGTGATGTGATCATAGCTCACTATAGCTTTGGCC
TTCTGAGATCAAGCAATCTCCATCTCAAGCTCCCAAGTAGCTAGGACTACACACGCATGTACCCATGCCAG
ATCATTTTTGTAGAGTACAGATTTTACCGTGGTGGCCAGGTTGGCCATGTTGGCCAGATGGGGTCTTCTTTTGT
GCCAGGCTGGCCACAAATTCCTGGGCTCAAGTGATCTTCCACCTCGTCTTGTAGAGATGAGATTTAGTTATG
TCTCCAGGCTGATCTCAAACCTCCTGGGCTAAATCGATTGTCTCACCTCAGCCTCTCAAGTATGTTATGAAGGTT
ATATGTTAGGAAGGTTCCAGGAGGTAAACCCACACAGATGGGATTTGGGCATAGGTTGGTTTCCAGGGGGCA
GTGCTGAGCTCTTTGCCAGTGGGAAATGGGATGCTGGTGATTCCAGTAGGTGACCTCACAGTCAAGCTAC
CACTTACTGTTGATTGTGACGAAATGCCAGCTGAGGCACATGCCTTGGGAGCTAAGTGGTTGCTGCCCTTGACCA
CTGTGAAGACTGGTGTGGGAAGGGTCGTTTTGGATGCACTTGAGCAGGGGTCCCCAACCCCTGAGCCATGGAGCC
GCAAGGAGCCACACAGCAGGAGGTGGGAACATCCAGTTGCAGGAAAACAAGCTTAACACGCCCAGTATTCTACA
TTATGCTCCTACCTCCCGGCAGCCTCTCCAGGCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGA
CTCTCAATGGCCTATTTAGGCCATACCCTACGTACGGCAGCCTCCGAGATGAGGCTACTGCCTCACACAGC
CTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCAGCCTTCTCTCCAGGCC
CTGAACCTTCTCAAGTTGACCTCACCAGGCCAGCTCATGCTTCTTGCAGCCTCTCCAGGCCAGCTCCTGCAT
CTTGGTGGCCCCCTCCAGGCCAGCCTCTGCCTCCCGTCAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATT
CTTCACGCCCAGCTTCTACCTCACTGTGGACCCCCAAGCCAAGCTCCCAACCTTTCAGCAGCTTCTACACACC
AGCTCCTGCCACCCAGTGGCCTCTTTAGGCCAAGCTCATGCTTACAAGGGCCTTTCAGGCCCAACTTTTGTCT
CATGGCAACCTTCCCTGGCCAGATTCTGCTGTCTCCAGCAGCCTAGACAGGCCAGGTCTTGCTCACACTG
GCCTCTCTACATCCAGCTTATGCCTCACGGTGGCCTCTCCA

WO 2004/030615

PCT/US2003/028547

627/6881
FIGURE 584

MMIIPHLLRDKDQRATTATSPRTRQCWGTENEGVLWPSQSSGGDETHLPLSLWARLMPGASVDRGHAPGLPKLE
KAARLRSEGQNSTVSPTESRWEQGR

WO 2004/030615

PCT/US2003/028547

628/6881
FIGURE 585

GGACGGAAGGAGCGGCGGCGACGGAGGAGGAGGATCGAGGCGGTGGTGTTCGTCTTCTCTCTCCTCGATTGTTGC
GCGCTCATCTTCCTCTCGGTCTACTTCATAATTACATTGTCTGATTTAGAAATGTGATTACATTAATGCTAGATCA
TGTTGCTCAAAATTAAACAAGTGGGTAATTCCAGAATTGATTGGCCATACCATTGTCACTGTATTACTGCTCATG
TCATTGCACTGGTTTCATCTTCCTTCTCAACTTACCTGTTGCCACTTGGAATATATATCGATACATTATGGTGCCG
AGTGGTAACATGGGAGTGTGTTGATCCAACAGAAATACACAATCGAGGGCAGCTGAAGTCACACATGAAAGAAGCC
ATGATCAAGCTTGGTTTCCACTTGCTCTGCTTCTTCATGTATCTTTATAGTATGATCTTAGCTTTGATAAATGAC
TGAAGCTGGAGAAGCCGTGGTTGAAGTCAGCCTACACTACAGTGCACAGTTGAGGAGCCAGAGACTTCTTAAATC
ATCCTTAGAACCGTGACCATAGCAGTATATATTTTCCTCTTGGAACAAAAAACTATTTTGTGTATTTTACCA
TATAAAGTATTTAAAAAACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

629/6881
FIGURE 586

MEAVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWWIPELIGHTIVTVLLLSLHWFIFLLNL
PVATWNIYRYIMVPSGNMGVFDPTTEIHNRGQLKSHMKEAMIKLGFHLLCFFMYLYSMILALIND

WO 2004/030615

PCT/US2003/028547

630/6881
FIGURE 587

CCCTAATCAAGTACCCCTCTCTCCACCACCTCCTGCCCCACCCCTCCCTGCATCTGGATTCTTTTTGGCATC
CATGTCAGAAGACAATCGCCCTTTAACTGGACTTGCAGCTGCAATTGCCGGAGCAAACTTAGGAAAGTGTCACG
GATGGAGGATACCTCTTTCCCAAGTGGAGGGAATGCTATTGGTGTGAAGTCCGCCTCATCTAAAAACAGATACAGG
CCGTGGAAATGGACCCCTTCTTTAGGGGGTAGTGGTTTAAATGGAAGAAATGAGTGCCCTGCTGGCCAGGAGGAG
AAGAATTGCTGAAAAGGGATCAACAATAGAAACAGAACAAAAAGAGGACAAAGGTGAAGATTGAGAGCCTGTAAAC
TTCTAAGGCCTCTTCAACAAGTACACCTGAACCAACAAGAAAACCTTGGGAAAGAACAAATACAATGAATGGCAG
CAAGTCACCTGTTATCTCCAGACCAAAATCCACACCCCTTATCACAGCCCAAGTGCCAATGGAGTCCAGACGGAAGG
ACTTGACTATGACAGGCTGAAGCAGGACATTTTAGATGAAATGAGAAAAGAAATTAACAAAGCTAAAAAGAGAGCT
CATTGATGCAATCAGGCAGGAAGTGAAGTCAAACTAGCA**TAG**AGGAACAGACTAAGGAGAGATAGGACTTT
AATCTGGAGGAAAAATATCCTACAAACAACAAGTTCACAAACAGCAAACCCCTACATTTATGAGCTGTAAAGAG
AAAATGGAGACAAACAGAGGAGGAGGAAAAACCAACCTACTCTGAAAGCCTTCAGACATTATGACTCTGGTGATAA
GCTCTTTCCCTCTCCGTTTGTCTGCTTTTTTCTGGCCTTTACAACAGAAATGGAAGAGAAATCATTTAAGAGTTCTTG
TAACAGTTATGCAGAAAATACTAAAACCCATCAGGCAAGATCACCACGCATTGAAATATTTTCATATCAAGATAA
AGTCGCACATTTTCCACAATACATTGCTAAAATAAGAGGAGAAAGGCTTAGGAAGTTTTCTGCAGAGAGTGCT
GGTAAAGAATTGAGCAAGTTTGTCTATTGTATTGTAATGTTTCTCTCAGGTTTGTCTTCTCATATGTTTGATAT
TCCATGAATAATTGAGATCAGCCCTATGTAAGTTAAGATCATAATATGTGGAACAAATGGAATTGTAAGTGCTTT
CAAAGGGTAATATTTATAAGAAAGTGTCCGAAAAATGTTTCTTCAGCTTGAGAAATTTAGAAATGATAGGAAGTT
TCTCGAGTTAGCCTTCATGCAATTTTGTAGATTTAAACATAAAATTTGTCCAGAACTTAAAGATTAGATGCCTT
CCTAAATTGTTACAATGCTTTACCAATCTATGACTTCTACATAACACAAACCAGTGGTCAAATGTAAACACTAT
ATTGTAGATTTACTGTAGGTTTTCAACCTTTTTTAGATTTATGCATGTGGACATTTTATAATGTAATTACAATC
ACCACAAGGTTAGCTTTTTTAATTGCAGACAGTAATGCATGTCACACTAATATGTAGTGGCCTTTTCAAGGCCTA
GTCCCAGGGAACATTTTGTAGAGTATAGGGGAGTGGGAGGAAGGGAGGAATAATTTTATTAAAGTTGAT
TTCTGCACATCTTTTTCTCAGTTACCTGCATGAATAAATAATGAGAAATATTTGTGACTTTAATTGGTAAATA
TGTTACAAAACCAAGTACTTAATCTTTTACATCATGCTTTCAGCTATTTGTATTTTAAACAGTAATTTCAATGGT
CTGAAACATGATTCTGAGCTTCACATAATATCTTAAGTGTGGAACCTAAAAGTTTGATCACTGAATTTGGCAGTT
ATTATTACCTAGGTACCCCGCTGTTTACACAGGTGTTTAGATACGTGTTTCTGAAATGAAGCTGCTTTTGAATTTT
GTTATGTTGAAATGCAAGAAATAACAATGATGGCAGCAATTAAGGTCACAGAAATCATTAGGTAAAGGAAAAACCA
ATGAGGAGTTCTGCAGTTTTCTTTTAATAAGTAAAGTGAGACTTGGGTGGTGGGAAGGAAGGTGGGAAGAAG
GAATTAGACACTCTGCCTGCCACTCTGCGTGTGTGCTCTCGCGCACGTGCTGTCTATATGGAAGCCACTCCCT
TTTCTTTCCCTTTGAAACTGGTAAGGTTAAATAGGGGAGAAATCCTACATGTTGGAATGATAGCTTTTTGGAAAA
TTTAAGAAACTCTCCAGGCTCTCCATCTTGATTTATGCTTGAGTTGTTATGTGCCATATTTGCTTTGAACTCTGA
TTATCAGAAGTTTTACTAAACTTTGAAATAATTCATTTTCTAGATTTTGTACATCTCAGTCCAT
AAAGCAAAGCTTGTTGATAGTGTAGTTTTCTAAACGCTGCAATTTGCAGCCTTTACCACTACAAAGAAGTTTGG
ATGAGGGATTTTTTTTTTCTTTGTCAAATAGTTCTGTTTCTGTAGAAATTTTCAATTTTATAGATTAAACTGTGAT
GGATGGGCTATCATAATTCAAGTATACATTTCTTTTTCTATCAGATATTCATTGTGCATGCAGTAGTAGTAAAAA
CATCAAAGATGCAGCAAGCTTATTAAGTATTATTTTCTAAAAGAAATAGGAGGCATTTTATCTTTATTATTGTA
CTTTTGGTTATGCAACACTTTGATAATATAAACAGTTATGTCCCTATAAATCTGGTCAGCAACCTCTTTTGAT
TTTGTGGGTAAGTTAAATAGTCTGTAGTAGGTAGGTACTGGGTACAAGTGGTCCAACTAAGATAAGAGACTA
AAATAAAATGCTAAATCTTAAAGAACTGGGTTTATGCACTAAACGTTTTGTGCTTGGTCTAATATTAAACATG
ATGTATGTGTAACCTGAC

WO 2004/030615

PCT/US2003/028547

631/6881
FIGURE 588

MSEDNRPLTGLAAAIAGAKLRKVS RMEDTSFPSSGNAIGVNSASSKTD TGRGNGPLPLGG SGLMEEMSALLARRR
RIA EKGSTIETE QKEDKGEDSEPVTSKASSTSTPEPTRKP WERTNTMNGSKSPVISRPKSTPLSQPSANGVQTEG
LDYDRLKQDILDEM RKELTKLKEELIDAIRQELSKSNTA

WO 2004/030615

PCT/US2003/028547

632/6881
FIGURE 589

GGGGCTGCTGGGACTCGCGTCGGTTGGCGACTCCCGGACGTAGGTAGTTTGTGGGCCGGGTTCTGAGGCCTTGC
TTCTCTTTACTTTTCCACTCTAGGCCACGATGCCGCGAGTACCAGACCTGGGAGGAGTTCAGCCGCGCTGCCGAGA
AGCTTTACCTCGCTGACCCTATGAAGGCACGTGTGGTTCTCAAATATAGGCATTCTGATGGGAACCTGTGTGTTA
AAGTAACAGATGATTTAGTTTGTGGTGTATAAAACAGACCAAGCTCAAGATGTAAAGAAGATTGAGAAATTC
ACAGTCAACTAATGCGACTTATGGTAGCCAAGGAAGCCCGCAATGTTACCATGGAACTGAGTGAATGGTTTGAA
ATGAAGACTTTGTCTGTACTTAGGAAGTAAATATCTTTGAATTAGAGAAAGTGTGGGACAGAAAGTACTTTA
TGTAACCTAAGTGGGCTGTTCAGAAGCTTAGAGGTCATTTTTGTAAATTTCTTTTAATTACTTTAGAGAGCTAG
GGATGCAAAATGTTTTAGTTAGAAAGCCTTTATTTACTTTTGGAATTTGAACAAGAAATGCATCTGTCTTAGAAA
CTGGAGATTATTTGATGTTAGGTAAAACATGTAATTGTTTCTCTGGCAAATTTGTATCAGTAATTTGAAAATGAG
ATATTAGGAAAAACCAATTCCTTCTTAAATTTAGTTTCATCTTTCTTTAAAAGAACATTAAATGTAACCATTTTGT
AGATCCATGTATTTTGGAGCATAAAATGTATGCTGTTGTGACCAATAAATATAAAATATGGTAATTGGAATTAAC
TCCACACCATAGTATGCATTGTTATACATACTGTGTACCTAATTATGTATAGCAGTGTAGTCTCAATTATATCTG
AAAGTAATTGTGACTAACAAGTATGCTTTGCCTTATTTCCACATTTAAACTACCTGTTAATATAAGGGATTTGTA
GTATCAGCTTGTTGAGCAATGACTTTGAATCTAGTTTTAGTGATCAGAAGCAGCAGTTATTTGAGTGTATGAAT
GGAATGATGATCACTGTGCTATAATGTACTGAAACCACCATATTACAGAAATATTTACTACATATTTCCATCTG
TAGTTTCTCAGAAGGGCTATGGATTAGTTTGAAGTGTCAAATCCTTGCACTTCTGTGACACCCCTGCCCATTT
TCTGTCTTTAATTAACCAAGGTGTTAGGTGTGACTGTCAAACTGTTATGTTTTCCAGTAACTAGAAGTACGAT
ATTTGATAATTATATTTGTATTTACCACCTAAATGTAATGTTGATTCTCAAGAATGAAATGAAGGCACTACAT
TGAAATATGTTTTGTATAAATTTGTCATGTTGAACAGCATTTTAGCATGGTAAGTTCCCTTAGCTATATGAATTT
TGGCATGTTTCAGAGAGATCAGTAAATAAAATATTAGAT

WO 2004/030615

PCT/US2003/028547

633/6881
FIGURE 590

MPQYQTWEEFSRAAEKLYLADPMKARVVLKYRHSDGNLCVKVTDDLVLVYKTDQAQDVKKIEKFHSQMLRMVA
KEARNVTMETE

WO 2004/030615

PCT/US2003/028547

634/6881
FIGURE 591

GCGGCTCCCAGGAGGCGTGAACCGCGGACCATGAGCGTGGGCTTCATCGGGGCCGGCCAGCTGGCCTATGCTCTG
GCGCGGGGCTTCACGGCCGCAGGCATCCTGTGCGGCTCACAAGATAATAGCCAGCTCCCCAGAAATGAACCTGCCC
ACGGTGTCCGCGCTCAGGAAGATGGGTGTGAACCTGACACGCAGCAACAAGGAGACGGTGAAGCACAGCGACGTC
CTGTTTCTGGCTGTGAAGCCACATATCATCCCCTTCATCCTGGATGAGATTGGGGCCGACGTGCAAGCCAGACAC
ATCGTGGTCTCCTGTGCGGCTGGTGTACCATCAGCTCTGTGGAGAAGAAGCTGATGGCATTCCAGCCAGCCCC
AAAGTGATTGCTGTCATGACCAACACACCTGTGGTAGTGCAGGAAGGCGCTACAGTGTACGCCACGGGCACCCAT
GCCCTGGTGGAGGATGGGCAGCTCCTGGAGCAGCTCATGAGCAGCGTGGGCTTCTGCACTGAGGTGGAAGAGGAC
CTCATCGATGCCGTCACGGGGCTCAGTGGCAGCGGGCCTGCCTATGCATTTCATGGCTCTGGACGCATTGGCTGAT
GGTGGGGTGAAGATGGGTTTGCCACGGCGCCTGGCAATCCAACTCGGGGGCCAGGCTTTGCTGGGAGCTGCCAAG
ATGCTGCTGGACTCGGAGCAGCATCCATGCCAGCTTAAGGACAATGTCTGCTCCCCTGGGGGAGCCACCATCCAC
GCCCTGCACTTTCTAGAGAGTGGGGGCTTCCGCTCTCTGCTCATCAATGCAGTTGAGGCCTCCTGTATCCGAACA
CGAGAGCTACAGTCCATGGCCGACCAAGAAAAGATCTCCCAGCTGCCCTTAAGAAGACCCTCTTAGACAGAGTG
AAGCTGGAATCCCCACAGTCTCCACACTGACCCCTCCAGCCCAGGAAGCTCCTCACAAGAAGCCTGGCCCTG
GGAGGCAAGAAGGACTAAGGCAGCATC

WO 2004/030615

PCT/US2003/028547

635/6881
FIGURE 592

TTTTCTTTTGAAGGCGTTTCGAGGTATTTTGTGTTTGCCGTTTGTTCGCTCAGAAATGGCATTGAGAGGTGATTGATACTGCT
AACAAATTTCTAGTACTCTAGTTTGTTCGAAGAAGAGATTTGGGTAGACGTAATCTTCACCCCTTCAAATTATA
TAACAATACGAACATTATTTTTTATACTGATCATAATTTCCAGATTGGGGAGGGGGTGATCGTGCCAGGAAAAG
TTGTATGTTTGGTAGTTGCATATGGTGATTTTGTATTTTCAATGCTGGTAGGTAAGTAAGGAGGTCTCTGTACC
ATGGCTCGTACAAAGCAGACTGCCCCGAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCC
GCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAACTCATCGTTACAGGCCTGGTACTGTGGCGCTCCGT
GAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTTCGCAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATT
GCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTAT
CTGGTTGGCCTTTTTGAAGACACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATC
CAGCTAGCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTCAATCTCAAAAAA
AAAAAAAATTTCTCTTCTTCTGTTATTGGTAGTTCTGAACGTTAGATATTTTTTTTCCATGGGGTCAAAGG
TACCTAAGTATATGATTGCGAGTGGAATAAGGGGACAGAAATCAGGTATTGGCAGTTTTTCCATTTTCATTG
TGTGTGAATTTTAAATATAAATGCGGAGACGTAAAGCATTAATGCAAGTTAAATGTTTCAGTGAACAAGTTTCA
GCGGTTCAACTTTATAATAATTATAAATAAACCTGTAAATTTTCTGGACAATGCCAGCATTGGATTTTTTTA
AAACAAGTAAATTTCTTATTGATGGCAACTAAATGGTGTGTTGTAGCATTTTATCATACAGTAGATTCCATCCAT
TCACTATACTTTTCTAACTGAGTTGTCCTACATGCAAGTACATGTTTTTAATGTTGTCTGTCTTCTGTGCTGTTT
CTGTAAGTTTGCTATTAAAATACATTAAACTAT

WO 2004/030615

PCT/US2003/028547

636/6881
FIGURE 593A

AATCTATCAGGGAACGGCGGTGGCCGGTGCGGCGTGTTCCGGTGGCGGCTCTGGCCGCTCAGGCGCCTGCGGCTGG
GTGAGCGCACGCGAGGCGGCGAGGCGGCAGCGTGTTTCTAGGTCGTGGCGTCGGGCTTCCGGAGCTTTGGCGGCA
GCTAGGGGAGGATGGCGGAGTCTTCGGATAAGCTCTATCGAGTCGAGTACGCCAAGAGCGGGCGCGCCTCTTGCA
AGAAATGCAGCGAGAGCATCCCCAAGGACTCGCTCCGGATGGCCATCATGGTGCAGTCGCCCATGTTTGATGGAA
AAGTCCCACACTGGTACCACCTTCTCCTGCTTCTGGAAGGTGGGCCACTCCATCCGGCACCTGACGTTGAGGTGG
ATGGGTTCTCTGAGCTTCGGTGGGATGACCAGCAGAAAGTCAAGAAGACAGCGGAAGCTGGAGGAGTGACAGGCA
AAGGCCAGGATGGAATTGGTAGCAAGGCAGAGAAGACTCTGGGTGACTTTGCAGCAGAGTATGCCAAGTCCAACA
GAAGTACGTGCAAGGGGTGTATGGAGAAGATAGAAAAGGGCCAGGTGCGCCTGTCCAAGAAGATGGTGGACCCGG
AGAAGCCACAGCTAGGCATGATTGACCGCTGGTACCATCCAGGCTGCTTTGTCAAGAACAGGGAGGAGCTGGGTT
TCCGGCCCGAGTACAGTGCGAGTCAGCTCAAGGGCTTCAGCCTCCTTGCTACAGAGGATAAAGAAGCCCTGAAGA
AGCAGCTCCCAGGAGTCAAGAGTGAAGGAAAGAGAAAAGCGATGAGGTGGATGGAGTGGATGAAGTGGCGAAGA
AGAAATCTAAAAAAGAAAAAGACAAGGATAGTAAGCTTGAAAAAGCCCTAAAGGCTCAGAACGACCTGATCTGGA
ACATCAAGGACGAGCTAAAGAAAGTGTGTTCAACTAATGACCTGAAGGAGCTACTCATCTTCAACAAGCAGCAAG
TGCCTTCTGGGGAGTCGGCGATCTTGACCGAGTAGCTGATGGCATGGTGTTCGGTGGCCTCCTTCCCTGCGAGG
AATGCTCGGGTCAGCTGGTCTTCAAGAGCGATGCCTATTACTGCAGTGGGGACGTCAGTGCCTGGACCAAGTGTA
TGGTCAAGACACAGACACCCAACCGGAAGGAGTGGGTAAACCCAAAGGAATTCCGAGAAATCTCTTACCTCAAGA
AATTGAAGGTTAAAAACAGGACCGTATATTCCCCCAGAAACCAGCGCCTCCGTGGCGGCCACGCTCCGCCCT
CCACAGCCTCGGCTCCTGTGCTGTGAACCTCTGCTTCAGCAGATAAGCCATTATCCAACATGAAGATCCTGA
CTCTCGGGAAGCTGTCCCGGAACAAGGATGAAGGCAAGGCCATGATTGAGAACTCGGGGGGAAGTTGACGGGGA
CGGCCAACAAAGGCTTCCCTGTGCATCAGCACCAAAAAGGAGGTGGAAGATGAATAAGAAGATGGAGGAAGTAA
AGGAAGCCAACATCCGAGTTGTGTCTGAGGACTTCCCTCCAGGACGCTCTCCGCTCCACCAAGAGCCTTCAGGAGT
TGTTCTTAGCGCACATCTTGTCCTTGGGGGCGAGAGGTGAAGGCAGAGCCTGTTGAAGTTGTGGCCCCAAGAG
GGAAGTCAGGGGCTCGCCTCTCCAAAAAAGCAAGGGCCAGGTCAAGGAGGAAGGTATCAACAAATCTGAAAAGA
GAAAGTAAATTAACCTCTTAAAGGAGGAGCAGCTGTGGATCCTGATTCTGGACTGGAACACTCTGCGCATGTCTGG
AGAAAGGTGGGAAGGTCTTCAGTGCCACCCTTGGCCTGGTGGACATCGTTAAAGGAACCAACTCCTACTACAAGC
TGCAGCTTCTGGAGGACGACAAGGAAAAACAGGTATTGGATATTAGGTCCTGGGGCCGTGTGGGTACGGTGATCG
GTAGCAACAAACTGGAACAGATGCCGTCCAAGGAGGATGCCATTGAGCACTTCATGAAATTATATGAAGAAAAAA
CCGGGAACGCTTGGCACTCCAAAAATTTACGAAAGTATCCCCAAAAGTTCTACCCCTGGAGATTGACTATGGCC
AGGATGAAGAGGCAGTGAAGAAGCTGACAGTAAATCCTGGCACCAAGTCCAAGCTCCCCAAGCCAGTTTCAAGACC
TCATCAAGATGATCTTTGATGTGGAAAAGTATGAAGAAAGCCATGGTGGAGTATGAGATCGACCTTCAGAAGATGC
CCTTGGGGAAGCTGAGCAAAAAGGCAGATCCAGGCCGCATACTCCATCCTCAGTGAGGTCCAGCAGGCGGTGTCTC
AGGGCAGCAGCGACTCTCAGATCCTGGATCTCTCAAATCGCTTTTACACCCTGATCCCCACGACTTTGGGATGA
AGAAGCCTCCGCTCCTGAACAATGCAGACAGTGTGCAGGCCAAGGTGGAAATGCTTGACAACCTGCTGGACATCG
AGGTGGCCTACAGTCTGCTCAGGGGAGGGTCTGATGATAGCAGCAAGGATCCCATCGATGTCAACTATGAGAAGC
TCAAAACTGACATTAAGGTGGTTGACAGAGATTCTGAAGAAGCCGAGATCATCAGGAAGTATGTTAAGAACACTC
ATGCAACCACACACAATGCGTATGACTTGGAAGTCATCGATATCTTTAAGATAGAGCGTGAAGGCGAATGCCAGC
GTTACAAGCCCTTTAAGCAGCTTCATAACCGAAGATTGCTGTGGCACGGGTCCAGGACCACCAACTTTGCTGGGA
TCCTGTCCCAGGGTCTTCGGATAGCCCCGCTGAAGCGCCCGTGACAGGCTACATGTTTGGTAAAGGGATCTATT
TCGCTGACATGGTCTCCAAGAGTGCCAACTACTGCCATACGTCTCAGGGAGACCCAATAGGCTTAATCCTGTTGG
GAGAAGTTGCCCTTGGAACATGTATGAAGTGAAGCACGCTTCACATATCAGCAAGTTACCCAAGGGCAAGCACA
GTGTCAAAGGTTTGGGCAAAACTACCCCTGATCCTTCAGCTAACATTAGTCTGGATGGTGTAGACGTTTCTCTTG
GGACCGGGATTTCATCTGGTGTGAATGACACCTCTCTACTATATAACGAGTACATTGTCTATGATATTGCTCAGG
TAAATCTGAAGTATCTGCTGAAACTGAAATTCATTTTAAGACCTCCCTGTGGTAATTGGGAGAGGTAGCCGAGT
CACACCCGGTGGCTCTGGTATGAATTCACCCGAAGCGCTTCTGCACCAACTCACCTGGCCGCTAAGTTGCTGATG
GGTAGTACCTGTACTAAACCACCTCAGAAAGGATTTTACAGAAACGTGTTAAAGGTTTTCTCTAAGTTCTCAAGT
CCCTTGTTTTGTGTTGTGTCTGTGGGAGGGGTGTTTTGGGGTGTGTTTTGTTTTTCTTGCCAGGTAGATAAA
ACTGACATAGAGAAAAGGCTGGAGAGAGATTCTGTTGCATAGACTAGTCCTATGGAAAAACCAAGCTTCGTTAG
AATGTCTGCCTTACTGGTTTCCCCAGGGAAGGAAAAATACACTTCCACCCTTTTTTCTAAGTGTTCTGCTTTTAGT

WO 2004/030615

PCT/US2003/028547

637/6881
FIGURE 593B

TTTGATTTTGGAAAGATGTTAAGCATTTATTTTGTAGTTAAAAATAAAAACTAATTTTCATACTATTTAGATTTTCT
TTTTTATCTTGCACTTATTGTCCCTTTTTAGTTTTTTTTGTTTGCCTCTTGTGGTGAGGGGTGTGGGAAGACCA
AAGGAAGGAACGCTAACAATTTCTCATACTTAGAAACAAAAAGAGCTTTCCTTCTCCAGGAATACTGAACATGGG
AGCTCTTGAAATATGTAGTATTAAAAGTTGCATTTG

WO 2004/030615

PCT/US2003/028547

638/6881
FIGURE 594

CGAGCGGCGGGCGGAGCAGGCATTTCCAGCAGTGAGGAGACAGCCAGAAGCAAGCTATTGGAGCTGAAGGAACCTG
AGACAGAAGCTAGTCCCCCTCTGAATTTTACTGATGAAGAACTGAGGCCACAGAGCTAAAGTGAATTTTCCCA
AGGTCGCCCAGCGAGGACGTGGGACTTCTCAGACGTCAGGAGAGTGATGTGAGGGAGCTGTGTGACCATAGAAAG
TGACGTGTTAAAAACCAGCGCTGCCCTCTTTGAAAGCCAGGGAGCATCATTCAATTTAGCCTGCTGAGAAGAAGAA
ACCAAGTGTCGGGATTACAGACCTCTCTGCGGCCCAAGTGTTCTGTGGTGCTTCCAGAGGCAGGGCTATGCTCAC
ATTCATGGCCTCTGACAGCGAGGAAGAAGTGTTGATGAGCGGACGTCCCTAATGTGCGCCGAGAGCCCCACGCC
GCGCTCCTGCCAGGAGGGCAGGCAGGGCCCAGAGGATGGAGAGAACACTGCCAGTGGAGAAGCCAGGAGAAGCA
GGAGGACGGTGAGGAGGACCTGACCGCTATGTCTGTAGTGGGGTTCCCGGGCGGCCGAGGCCTGGAGGAAGA
GCTGACCCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTGTCACTCTGTGCATGATCGTGGTGCT
AGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAGCTCATCTACACGACATTCAGTGAGGACAC
ACCCTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACACCCCTCATCATGATCAGCGTCATCGTGGTTATGAC
CATCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTTCATCCATGGCTGGTTGATCATGTCTTCACTGAT
GCTGCTGTTCCCTTACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGACTACCCAC
CCTCTTGCTGACTGTCTGGAACCTTCGGGGCAGTGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGCTGTGCA
GCAGGCCACCTCATCATGATCAGTGCGCTCATGGCCCTAGTGTTTCATCAAGTACCTCCAGAGTGGTCCGCGTG
GGTCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTGCCAAAGGGCCCTCTGAGAATGCTGGT
AGAACTGCCCAGGAGAGAAATGAGCCCATATTCCTGCCCCTGATATACTCATCTGCCATGGTGTGGACGGTTGG
CATGGCGAAGCTGGACCCCTCCTCTCAGGGTGCCCTCCAGCTCCCCTACGACCCGAGATGGAAGAAGACTCCTA
TGACAGTTTTGGGGAGCCTTCATACCCCGAAGTCTTTGAGCCTCCCTTGACTGGCTACCCAGGGGAGGAGCTGGA
GGAAGAGGAGGAAAGGGGCGTGAACTTGCCCTCGGGGACTTCATCTTCTACAGTGTGCTGGTGGGCAAGGCGGC
TGCCACGGGCAGCGGGGACTGGAATACCACGCTGGCCTGCTTCGTGGCCATCCTCATTGGCTTGTGTCTGACCCCT
CCTGCTGCTTGCTGTGTTCAAGAAGGCGCTGCCCGCCCTCCCCATCTCCATCACGTTTCGGGCTCATCTTTTACTT
CTCCACGGACAACCTGGTGCGGCCGTTTCATGGACACCCTGGCCTCCCATCAGCTCTACATCTGAGGGACATGGTG
TGCCACAGGCTGCAAGCTGCAGGGAATTTTCATTGGATGCAGTTGTATAGTTTTTACACTCTAGTGCCATATATTT
TTAAGACTTTTCTTTCTTAAAAAATAAAGTACGTGTTTACTTGGTGAGGAGGAGGCAGAACCAGCTCTTTGGTG
CCAGCTGTTTCATCACAGACTTTGGCTCCCGCTTTGGGGAGCGCCTCGCTTCACGGACAGGAAGCACAGCAGGT
TTATCCAGATGAACTGAGAAGGTCAGATTAGGGCGGGGAGAAGAGCATCCGGCATGAGGGCTGAGATGCGCAAAG
AGTGTGCTCGGGAGTGGCCCTGGCACCTGGGTGCTCTGGCTGGAGAGGAAAAGCCAGTTCCCTACGAGGAGTGT
TCCCAATGCTTTGTCCATGATGTCCTTGTTATTTTATTGCCTTTAGAACTGAGTCCTGTTCTTGTACGGCAGT
CACACTGCTGGGAAGTGGCTTAATAGTAATATCAATAAATAGATGAGTCCTGTTAGAAAAA

WO 2004/030615

PCT/US2003/028547

639/6881
FIGURE 595

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEEDGEEDPDRYVCSGVPGRPPGL
EEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTEDTPSVGQRLNLSVLNTLIMISVIV
VMTIFLVVLYKYRCYKFIHGWLIMSSIMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTWNFGAVGMVCIHWKGPL
VLQQAYLIMISALMALVFIKYLPEWSAWILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVW
TVGMAKLDPSSQALQLPYDPEMEEDSYDSFGEPSYPEVFEPLTGYPGEELEEEEEEERGVKLGLGDFIFYSVLVG
KAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI

WO 2004/030615

PCT/US2003/028547

640/6881
FIGURE 596

CGAGCGGCGGCGGAGCAGGCATTTCCAGCAGTGAGGAGACAGCCAGAAGCAAGCTATTGGAGCTGAAGGAACCTG
AGACAGAAGCTAGTCCCCCTCTGAATTTTACTGATGAAGAACTGAGGCCACAGAGCTAAAGTGACTTTTCCCA
AGGTGCGCCAGCGAGGACGTGGGACTTCTCAGACGTCAGGAGAGTGATGTGAGGGAGCTGTGTGACCATAGAAAG
TGACGTGTTAAAAACCAGCGCTGCCCTCTTTGAAAGCCAGGGAGCATCATTCAATTTAGCCTGCTGAGAAGAAGAA
ACCAAGTGTCGGGATTTCAGACCTCTCTGCGGCCCAAGTGTTTCGTGGTGCTTCCAGAGGCAGGGCTATGCTCAC
ATTCATGGCCTCTGACAGCGAGGAAGAAGTGTTGATGAGCGGACGTCCCTAATGTGCGCCGAGAGCCCCACGCC
GCGCTCCTGCCAGGAGGGCAGGCAGGGCCCAGAGGATGGAGAGAACACTGCCAGTGGAAGCCAGGAGAACGA
GGAGGACGGTGAGGAGGACCCTGACCGCTATGTCGTAGTGCGGTTCCCGGGCGGCCGAGGCCTGGAGGAAGA
GCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCTGTCACTCTGTGCATGATCGTGGTGGT
AGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAGCTCATCTACACGACATTCAGTGAGGACAC
ACCCTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACACCCCTCATCATGATCAGCGTCATCGTGGTTATGAC
CATCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACTGAT
GCTGCTGTTCTCTTACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGACTACCCAC
CCTCTTGCTGACTGTCTGGAACCTCGGGGCAGTGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCA
GCAGGCCTACCTCATCATGATCAGTGCGCTCATGGCCCTAGTGTTTCATCAAGTACCTCCCAGAGTGGTCCGCGTG
GGTCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTCTGAGAATGCTGGT
AGAAACTGCCAGGAGAGAAATGAGCCCATATTCCTGCCCTGATATACTCATCTGCCATGGTGTGGACGGTTGG
CATGGCGAAGCTGGACCCCTCCTCTCAGGGTGCCCTCCAGCTCCCTACGACCCGGAGATGGAAGACTCCTATGA
CAGTTTTGGGGAGCCTTCATACCCCGAAGTCTTTGAGCCTCCCTTGACTGGCTACCCAGGGGAGGAGCTGGAGGA
AGAGGAGGAAAGGGGCGTGAAGCTTGGCCTCGGGGACTTCATCTTCTACAGTGTGCTGGTGGGCAAGGCGGCTGC
CACGGGCAGCGGGGACTGGAATACCACGCTGGCCTGCTTCGTGGCCATCCTCATTGGCTTGTGTCTGACCCTCCT
GCTGCTTGCTGTGTTCAAGAAGGCGCTGCGCGCCCTCCCATCTCCATCAGTTTCGGGCTCATCTTTTACTTCTC
CACGGACAACCTGGTGCGGCCGTTTCATGGACACCCCTGGCCTCCCATCAGCTCTACATCTGAGGGACATGGTGTGC
CACAGGCTGCAAGCTGCAGGGAATTTTCATTGGATGCAGTTGTATAGTTTTTACACTCTAGTGCCATATATTTTAA
AGACTTTTCTTTCCTTAAAAAATAAAGTACGTGTTTACTTGGTGAGGAGGAGGCAGAACCAGCTCTTTGGTGCCA
GCTGTTTTCATCACCAGACTTTGGCTCCCGCTTTGGGGAGCGCCTCGCTTCACGGACAGGAAGCACAGCAGGTTTA
TCCAGATGAACTGAGAAGGTCAGATTAGGGCGGGGAGAAGAGCATCCGGCATGAGGGCTGAGATGCGCAAAGAGT
GTGCTCGGGAGTGCCCTGGCACCTGGGTGCTCTGGCTGGAGAGGAAAAGCCAGTTCCCTACGAGGAGTGTTCC
CAATGCTTTGTCCATGATGTCTTGTATTTTATTGCCTTTAGAACTGAGTCCTGTTCTTGTACGGCAGTCAC
ACTGCTGGGAAGTGGCTTAATAGTAATATCAATAAATAGATGAGTCCTGTTAGAAAAA

WO 2004/030615

PCT/US2003/028547

641/6881
FIGURE 597

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVPGRPPGL
EEELTLKYGAKHVIMLFVPVTLMIIVVATIKSVRFYTEKNGQLIYTTFTEDTPSVGQRLNLSVLNTLIMISVIV
VMTIFLVVLYKYRCYKF IHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPL
VLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVW
TVGMAKLDPSSQALQLPYDPEMEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEERGVKLGDFIFYSVLVGK
AAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI

WO 2004/030615

PCT/US2003/028547

642/6881
FIGURE 598A

TATACTTCGCTACTTGGCTAGAGTTGCAACTACAGCTGGGTTATATGGCTCTAATCTGATGGAACATACTGAGAT
TGATCACTGGTTGGAGTTCAGTGCTACAAAATTATCTTCATGTGATTCTTTACTTCTACAATTAATGAACCTCAA
TCATTGCCTGTCTCTGAGAACATACTTAGTTGGAACTCCTTGAGTTTAGCAGATTTATGTGTTTGGGCCACCT
AAAAGGAAATGCTGCCTGGCAAGAACAGTTGAAACAGAAGAAAGCTCCAGTTCATGTAAACGTTGGTTTGGCTT
TCTTGAAGCCCAGCAGGCCTTCCAGTCAGTAGGTACCAAGTGGGATGTTTCAACAACCAAGCTCGAGTGGCACC
TGAGAAAAAGCAAGATGTTGGGAAATTTGTTGAGCTTCCAGGTGCGGAGATGGGAAAGGTTACCGTCAGATTTCC
TCCAGAGGCCAGTGGTTACTTACACATTGGGCATGCAAAAGCTGCTCTTCTGAACCAGCACTACCAGGTTAACTT
TAAAGGGAAACTGATCATGAGATTTGATGACACAAATCCTGAAAAAGAAAGGATTTTGAAGGTTATCTT
GGAAGATGTTGCAATGTTGCATATCAAACCAGATCAATTTACTTATACTTCGGATCATTTTGAACTATAATGAA
GTATGCAGAGAAGCTAATTCAAGAAGGGAAGGCTTATGTGGATGATACTCCTGCTGAACAGATGAAAGCAGAACG
TGAGCAGAGGATAGAATCTAAACATAGAAAAACCCTATTGAGAAGAATCTACAAATGTGGGAAGAAATGAAAA
AGGGAGCCAGTTTGGTCAGTCTGTTGTTTGCAGCAAAAATTGACATGAGTAGTAACAATGGATGCATGAGAGA
TCCAACCTTTTATCGCTGCAAAATTCAACCACATCCAAGAAGTGGAAATAAATACAATGTTTATCCAACATATGA
TTTTGCCTGCCCCATAGTTGACAGCATCGAAGGTGTTACACATGCCCTGAGAACAACAGAATACCATGACAGAGA
TGAGCAGTTTACTGGATTATTGAAGCTTTAGGCATAAGAAAACCATATATTTGGGAATATAGTCGGCTAAATCT
CAACAACACAGTGCTATCCAAAAGAAAACCTCACATGGTTTGTCAATGAAGGACTAGTAGATGGATGGGATGACCC
AAGATTTCTACGGTTCGTGGTGTACTGAGAAGAGGGATGACAGTTGAAGGACTGAAACAGTTTATTGCTGCTCA
GGGCTCCTCACGTTTCAGTCGTGAACATGGAGTGGGACAAAATCTGGGCGTTTAAACAAAAGGTTATTGACCCAGT
GGCTCCACGATATGTTGCATTACTGAAGAAAGAAGTGATCCCAGTGAATGTACCTGAAGCTCAGGAGGAGATGAA
AGAAGTAGCCAAACACCCAAAGAATCCTGAGGTTGGCTTGAAGCCTGTGTGGTATAGTCCCAAAGTTTTCATTGA
AGGTGCTGATGCAGAGACTTTTTCGGAGGGTGAGATGGTTACATTTATAAATTGGGGCAACCTCAACATTACAAA
AATACACAAAAATGCAGATGGAAAAATCATATCTCTTGATGCAAGTTGAATTTGGAAAAACAAAGACTACAAGAA
AACCATAAGGTCATTGGCTTGACAGAGACTACACATGCTCTTCTTATTCCAGTAATCTGTGTCACTTATGAGCA
CTTGATCACAAAGCCAGTGCTAGGAAAAGACGAGGACTTTAAGCAGTATGTCAACAAGAACAGTAAGCATGAAGA
GCTAATGCTAGGGGATCCCTGCCTTAAGGATTTGAAAAAGGAGATATTATACAACCTCCAGAGAAGAGGATTCTT
CATATGTGATCAACCTTATGAACCTGTTAGCCCATATAGTTGCAAGGAAGCCCCGTGTGTTTTGATATACATTCC
TGATGGGCACACAAAGGAAATGCCAACATCAGGGTCAAAGGAAAAGACCAAAGTAGAAGCCACAAAAAATGAGAC
CTCTGCTCCTTTTAAGGAAAGACCAACACCTTCTCTGAATAATAATTGTACTACATCTGAGGATTCTTGGTCTCT
TTACAATAGAGTGGCTGTTCAAGGAGATGTGGTTCGTGAATTAAGGCAAGAAAGCACCAGGAAGATGTAGA
TGCAGCTGTAAACAGCTTTTGTCTTTGAAAGCTGAATATAAGGAGAAAACCTGGCCAGGAATATAAACCTGGAAA
CCCTCCTGCTGAAATAGGACAGAATATTTCTTCTAATTCTCAGCAAGTATTCTGGAAAGTAAATCTCTGTATGA
TGAAGTTGCTGCACAAGGGGAGGTGGTTCGTAAAGCTAAAAGCTGAAAAATCCCTAAGXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXCTTCTCAAGGGGAAGTAGTTCGGAACTTAAACTGAAAAAGCCCTAAGGATCAAGT
AGATATAGCTGTTCAAGAACTCCTTCAGCTAAAGGCACAGTACAAGTCTTTGATAGGAGTAGAGTATAAGCCTGT
GTCGGCCACTGGAGCTGAGGACAAAGATAAGAAGAAGAAAGAAAAAGAAAATAAATCTGAAAAGCAGAATAAGCC
TCAGAAACAAAATGATGGCCAAAGGAAAGACCCCTTCTAAAAACCAAGGAGGTGGGCTCTCATCAAGTGGAGCAGG
AGAAGGGCAGGGGCCTAAGAAAACAGACCAGGTGGGTCTTGAGGCAAAAAAGAAAGAAAATCTTGCTGATTGGTA
TTCTCAGGTCATCACAAAGTCAGAAATGATTGAATACCATGACATAAGTGGCTGTTATATTCTTCGTCCCTGGGC
CTATGCCATTTGGGAAGCCATCAAGGACTTTTTTGATGCTGAGATCAAGAACTTGGTGTGAAAACCTGCTACTT
CCCCATGTTTGTGTCTCAAAGTGCATTAGAGAAAGAGAAGACTCATGTTGCTGACTTTGCCCCAGAGGTTGCTTG
GGTTACAAGATCTGGCAAAACCGAGCTGGCAGAACCAATTGCCATTCTGCTCTACTAGTGAAACAGTAATGTATCC
TGATATGCAAAATGGGTACAATCACACAGAGACCTGCCCATCAAGCTCAATCAGTGGTGCAATGTGGTGCGTTG
GGAATTCAAGCATCCTCAGCCTTTCCTACGTACTCGTGAATTTCTTTGGCAGGAAGGGCACAGTGCTTTTGCTAC
CATGGAAGAGGCAGCGGAAGAGGTCTTGAGATACTTGACTTATATGCTCAGGTATATGAAGAACTCCTGGCAAT
TCCTGTGTGTTAAAGGAAGAAAGACGGAAGGAAAAATTTGCAGGAGGAGACTATACAACCTACAATAGAAGCATT
TATATCTGCTAGTGGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAATTTTCCAAAATGTTTGA

WO 2004/030615

PCT/US2003/028547

643/6881
FIGURE 598B

AATCGTTTTTGAAGATCCAAAGATACCAGGAGAGAAGCAATTTGCCTATCAAAACTCCTGGGGCCTGACAACTCG
AACTATTGGTGTTATGACCATGGTTCATGGGGACAACATGGGTTTAGTATTACCACCCCGTGTAGCATGTGTTCA
GGTGGTGATTATTCCTTGTGGCATTACCAATGCACTTTCTGAAGAAGACAAAGAAGCGCTGATTGCAAAATGCAA
TGATTATCGAAGGCGATTACTCAGTGTTAACATCCGCGTTAGAGCTGATTTACGAGATAATTATTCTCCAGGTTG
GAAATTCAATCACTGGGAGCTCAAGGGAGTTCCCATTAGACTTGAAGTTGGGCCACGTGATATGAAGAGCTGTCA
GTTTGTAGCCGTCAGACGAGATACTGGAGAAAAGCTGACAGTTGCTGAAAATGAGGCAGAGACTAAACTTCAAGC
TATTTTGAAGACATCCAGGTCACCCTTTTCAAGGGCTTCTGAAGACCTTAAGACTCATATGGTTGTGGCTAA
TACAATGGAAGACTTTCAGAAGATACTAGATTCTGGAAAGATTGTTTCAAGATTCCATTCTGTGGGAAATTGACTG
TGAGGACTGGATCAAAAAGACCACTGCCAGGGATCAAGATCTTGAACCTGGTGCTCCATCCATGGGAGCTAAAAG
CCTTTGCATCCCCTTCAAACCACTCTGTGAACTGCAGCCTGGAGCCAAATGTGTCTGTGGCAAGAACCCTGCCAA
GTACTACACCTTATTTGGTCGCAGCTACTGAGGGATGAACGAAAGCCCCCTCTTCAACTCCTCTCACTTTTTAAA
GCATTGATATTAGTATCTTCTCAGATACAGACCGTTTTATGATTTTTTAAAAAGTAAAAGTTCTAAAATGAAGTC
ACACAGGACAATTATTCTTATGCCTAAGTTAACAGTGGATAAAAGACTTTTCTGTAAACAACTCCAGTAATAAAT
ATCATGAACTA

WO 2004/030615

PCT/US2003/028547

644/6881
FIGURE 599A

AGTAGCTGCGGCGCAGGGGCGGAGCGAAGGCTGCGGCGGCGTGGGTACGCGCACACGTTGCATCTTCTTCCTTT
CGCGGGGTCTCCGTAGTTCTGGCACGAGCCAGGCGTACTGACAGGTGGACCAGCGGACTGGTGGAGATGGCGAC
GCTCTCTCTGACCGTGAATTCAGGAGACCCCTCCGCTAGGAGCTTTTGCTGGCAGTAGAACACGTGAAAGACGATGT
CAGCATTTCGGTTGAAGAAGGGAAAGAGAATATTCTTCATGTTTCTGAAAATGTGATATTCACAGATGTGAATTC
TATACTTCGCTACTTGGCTAGAGTTGCAACTACAGCTGGGTATATGGCTCTAATCTGATGGAACATACTGAGAT
TGATCACTGGTTGGAGTTCAGTGCTACAAAATTATCTTCATGTGATTCTTTACTTCTACAATTAATGAACTCAA
TCATTGCCTGTCTCTGAGAACATACTTAGTTGGAACTCCTTGAGTTTAGCAGATTTATGTGTTTGGGCCACCCCT
AAAAGGAAATGCTGCCTGGCAAGAACAGTTGAAACAGAAAGCTCCAGTTCATGTAAAACGTTGGTTTGGCTT
TCTTGAAGCCCAGCAGGCCCTCCAGTCAGTAGGTACCAAGTGGGATGTTTCAACAACCAAAGCTCGAGTGGCACC
TGAGAAAAAGCAAGATGTTGGGAAATTTGTTGAGCTTCCAGGTGCGGAGATGGGAAAGGTTACCGTCAGATTTCC
TCCAGAGGCCAGTGGTTACTTACACATTGGGCGATGCAAAAGCTGCTCTTCTGAACCAGCACTACCAGGTTAACTT
TAAAGGGAACTGATCATGAGATTTGATGACACAAATCCTGAAAAAGAAAGGAAGATTTTGAGAAGGTTATCTT
GGAAGATGTTGCAATGTTGCAATACAAACCAGATCAATTTACTTATACTTCGGATCATTTTGAAACTATAATGAA
GTATGCAGAGAAGCTAATTCAGAAGGGGAAGGCTTATGTGGATGATACTCCTGCTGAACAGATGAAAGCAGAACG
TGAGCAGAGGATAGACTCTAAACATAGAAAAACCCCTATTGAGAAGAATCTACAAATGTGGGAAGAAATGAAAA
AGGGAGCCAGTTTGGTCAGTCCTGTTGTTGCGAGCAAAATTGACATGAGTAGTAACAATGGATGCATGAGAGA
TCCAACCCCTTTATCGCTGCAAAATTC AACCATCCAAGAACTGGAAATAAATACAATGTTTATCCAACATATGA
TTTTGCTGCCCCATAGTTGACAGCATCGAAGGTGTTACACATGCCCTGAGAACAAACAGAATACCATGACAGAGA
TGAGCAGTTTTACTGGATTATTGAAGCTTTAGGCATAAGAAAACCATATATTTGGGAATATAGTCGGCTAAATCT
CAACAACACAGTGCTATCCAAAAGAAAACCTCACATGGTTTGTCAATGAAGGACTAGTAGATGGATGGGATGACCC
AAGATTTCTACGGTTTCGTGGTGTACTGAGAAGAGGGATGACAGTTGAAGGACTGAAACAGTTTATTGCTGCTCA
GGGCTCCTCACGTTTCAGTCGTGAACATGGAGTGGGACAAAATCTGGGCGTTTAACAAAAAGGTTATTGACCCAGT
GGCTCCACGATATGTTGCATTACTGAAGAAAGAAAGTATCCAGTGAATGTACCTGAAGCTCAGGAGGAGATGAA
AGAAGTAGCCAAACACCCAAAGAATCCTGAGGTTGGCTTGAAGCCTGTGTGGTATAGTCCCAAGTTTTTCATTGA
AGGTGCTGATGACAGACTTTTTTCGGAGGGTGAGATGGTTACATTTATAAATTGGGGCAACCTCAACATTACAAA
AATACACAAAAATGCAGATGGAAAAATCATATCTTTGATGCAAAAGTTGAATTTGGAAAACAAAGACTACAAGAA
AACCCTAAGGTCACTTGGCTTGACAGACTACACATGCTCTTCTTATTCCAGTAATCTGTGTCACTTATGAGCA
CTTGATCACAAAGCCAGTCTAGGAAAAGACGAGGACTTTAAGCAGTATGTCAACAAGAACAGTAAGCATGAAGA
GCTAATGCTAGGGGATCCCTGCTTAAGGATTTGAAAAAAGGAGATATTATACAACCTCCAGAGAAGAGGATTCTT
CATATGTGATGAACCTTATGAACCTGTTAGCCCATATAGTTGCAAGGAAGCCCCGTGTGTTTTGATATACATTCC
TGATGGGCACACAAAGGAAATGCCAACATCAGGGTCAAAGGAAAAGACCAAGTAGAAGCCACAAAAATGAGAC
CTCTGCTCCTTTTAAAGGAAAGACCAACACCTTCTCTGAATAATAATTGTACTACATCTGAGGATTCCTTGGTCCT
TTACAATAGAGTGGCTGTTCAAGGAGATGTGGTTTCGTGAATTAAGGCAAGAAAGCACCAGGAAGATGTAGA
TGCAGCTGTAAAACAGCTTTTGTCTTTGAAAAGCTGAATATAAGGAGAAAACTGGCCAGGAATATAAACCTGGAAA
CCCTCCTGCTGAAATAGGACAGAATATTTCTTCTAATTCCTCAGCAAGTATTCTGGAAAGTAAATCTCTGTATGA
TGAAGTTGCTGCACAAGGGGAGGTGGTTTCGTAAGCTAAAAGCTGAAAAATCCCCTAAGGCTAAAATAAATGAAGC
TGTAAGATGCTTACTGTCCCTGAAGGCTCAGTATAAAGAAAAAACTGGGAAGGAGTACATACCTGGTCAGCCCCC
ATTATCTCAAAGTTTCGGATTCAAGCCCCAACAGAAATTCGAACCTGCTGGTTTAGAAACACCAGAAGCGAAAGT
ACTTTTTGACAAAAGTAGCTTCTCAAGGGGAAGTAGTTCGGAAAACCTAAAAGCTGAAAAAGCCCTAAGGATCAAGT
AGATATAGCTGTTCAAGAACTCCTTCAGCTAAAGGCACAGTACAAGTCTTTGATAGGAGTAGAGTATAAGCCTGT
GTCGGCCACTGGAGCTGAGGACAAAAGATAAGAAGAAGAAAGAAAAAGAAATAAATCTGAAAAGCAGAATAAGCC
TCAGAAAACAAAATGATGGCCAAAGGAAAGACCTTCTAAAAACCAAGGAGGTGGGCTCTCATCAAGTGGAGCAGG
AGAAGGGCAGGGGCTAAGAAACAGACCAGGTGGGTCTTGAGGCAAAAAAAGAAGAAATCTTGCTGATTGGTA
TTCTCAGGTCAACAAAGTCAGAAATGATTGAATACCATGACATAAGTGGCTGTTATATTCTTCGTCCTGGGC
CTATGCCATTTGGGAAGCCATCAAGGACTTTTTTGATGCTGAGATCAAGAACTTGGTGTGAAAAGCTGCTACTT
CCCCATGTTTGTGTCTCAAAGTGCATTAGAGAAAGAGAAGACTCATGTTGCTGACTTTGCCCCAGAGGTTGCTTG
GGTTACAAGATCTGGCAAAACCGAGCTGGCAGAACCAATTGCCATTCTGCTCTACTAGTGAACAGTAATGTATCC
TGCATATGCAAAATGGGTACAGTCACACAGAGACCTGCCCATCAAGCTCAATCAGTGGTGCAATGTGGTGCGTTG

WO 2004/030615

PCT/US2003/028547

645/6881
FIGURE 599B

GGAATTCAAGCATCCTCAGCCTTTCTTACGTACTCGTGAATTTCTTTGGCAGGAAGGGCACAGTGCTTTTGCTAC
CATGGAAGAGGCAGCGGAAGAGGTCTTGCAGATACTTGACTTATATGCTCAGGTATATGAAGAACTCCTGGCAAT
TCCTGTTGTTAAAGGAAGAAAGACGGAAAAGGAAAAATTTGCAGGAGGAGACTATACAACTACAATAGAAGCATT
TATATCTGCTAGTGGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAATTTTCCAAAATGTTTGA
AATCGTTTTTGAAGATCCAAAGATAACCAGGAGAGAAGCAATTTGCCTATCAAACTCCTGGGGCCTGACAACTCG
AACTATTGGTGTTATGACCATGGTTTCATGGGGACAACATGGGTTTAGTATTACCACCCCGTGTAGCATGTGTTCA
GGTGGTGATTATTCCTTGTGGCATTACCAATGCACTTTCTGAAGAAGACAAAGAAGCGCTGATTGCAAAATGCAA
TGATTATCGAAGGCGATTACTCAGTGTTAACATCCGCGTTAGAGCTGATTTACGAGATAATTATTCTCCAGGTTG
GAAATTCAATCACTGGGAGCTCAAGGGAGTTCCCATAGACTTGAAGTTGGGCCACGTGATATGAAGAGCTGTCA
GTTTGTAGCCGTCAGACGAGATACTGGAGAAAAGCTGACAGTTGCTGAAAATGAGGCAGAGACTAACTTCAAGC
TATTTTGAAGACATCCAGGTCACCCTTTTTACAAGGGCTTCTGAAGACCTTAAGACTCATATGGTTGTGGCTAA
TACAATGGAAGACTTTTCAAGATACTAGATTCTGGAAAGATTGTTTCAAGATTCCATTCTGTGGGAAATTGACTG
TGAGGACTGGATCAAAAAGACCACTGCCAGGGATCAAGATCTTGAACCTGGTGCTCCATCCATGGGAGCTAAAAG
CCTTTGCATCCCCTTCAAACCACTCTGTGAAGTGCAGCCTGGAGCCAAATGTGTCTGTGGCAAGAACCCTGCCAA
GTACTACACCTTATTTGGTTCGAGCTACTGAGGGATGAACGAAAGCCCCCTCTTCAACTCCTCTCACTTTTTAAA
GCATTGATATTAGTATCTTCTCAGATACAGACCGTTTTATGATTTTTTAAAAAGTAAAAGTTCTAAAATGAAGTC
ACACAGGACAATTATTCTTATGCCTAAGTTAACAGTGGATAAAAGACTTTTCTGTAAACAACCTCCAGTAATAAAT
ATCATGAACTAATATGGTTTAAAAAAAAAAAAAAAAAAAAAGG

WO 2004/030615

PCT/US2003/028547

646/6881
FIGURE 600

CCCAGGATGTAGAGCTGGCAGTGCCTGACGGCGCTCTGACGCGGAGTTGGGTGGGGTAGAGAGTAGGGGGCGGT
AGTCGGGGGTGGTGGGAGAAGGAGGAGGCGGCAAAATCACTTATAAAATGGCGCGGAAGCAGGACCCGAAGCCTAAA
TTCCAGGAGGGTGAGCGAGTGCTGTGCTTTTCATGGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATA
AAGGACAAACAAGTGAAATACCTTCATACATTACAGTGGTTGGAATAAAAAATTGGGATGAGTGGGTTCCGGAGAGC
AGAGTACTCAAATACGTGGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCA
GAGGGGAAGATGAGAGGGGCTGCCCCAGGAAAGAAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTGAAAACG
AAAAAGAACAACAGAAAACACCTGGAAATGGAGATGGTGGCAGTACCAGTGAGACCCCTCAGCCTCCTTGGAAG
AAAAGGGCCCCGGGTAGATCCTACTGTTGAAAATGAGGAAACATTTCATGAACAGAGTTGAAGTTAAAGTAAAGATT
CCTGAATAGCTAAAACCGTGGCTTGTGTGATGACTGGGACTTAATTACCAGGCAAAAACAGCTCTTTTATCTTCCT
GCCAAGAAGATGTGGATTCCATTCTTGAGGATTATGCAAATTACAAGAAATCTCGTGGAACACAGATAATAAG
GAGTATGCGGTTAATGAAGTTGTGGCAGGGATAAAAGAATACTTCAACGTAATGTTGGGTACCCAGCTACTCTAT
AAATTTGAGAGACCACAGTATGCCGAAATTCCTGCAGATCATCCCGATGCACCCATGTCCCAGGTGTATGGAGCG
CCACATCTCCTGAGATTATTTGTACGAATTGGAGCAATGTTGGCCTATACACCTCTGGATGAGAAGAGCCTTGCT
TTATTACTCAATTATCTTCACGATTTCTTAAAGTACCTGGCAAAGAATTCTGCAACTTTGTTTAGTGCCAGCGAT
TATGAAGTGGCTCCTCCTGAGTACCATCGGAAAGCTGTGTGAGAGGCACTCTCACTCACTTATGTTTGGATCTCC
GTAAACACATTTTTGTCTTAGTCTATCTCTGTACAAACAATGTGCTTTGAAGATGTTAGTGTATAACAATTGA
TGTTTGTTTTCTGTTGATTTTAAACAGAGAAAATAAAAGGGGTAATAGCTCCTTTTTTCTTTTCTTTTTTTTT
TCATTTCAAAGTTGCTGCCAGTGTTTTCAATGATGGACAACAGAGGGATATGCTGTAGAGTGTTTTATTGCCTAG
TTGACAAAGCTGCTTTTGAATGCTGGTGGTTCTATTCTTTTGACACTATGCACTTTTATAATACATGTTAATGCT
ATATGACAAAATGCTCTGATTCCTAGTGCCAAAGGTTCAATTCAGTGTATATACTGAACACACTCATCCATTTG
TGCTTTTTTTTTTTTTTTTATGGTGCTTAAAGTAAAGAGCCCATCCTTTGCAAGGCATCCATGTTGTTACTTAGG
CATTTTATCTTGGCTCAAATGTTGAAGAATGGTGGCTTGTTTCATGGTTTTTGTATTTGTGTCTAATGCACGTT
TTAACATGATAGATGCAATGCACTGTGTAGCTAGTTTTCTGGAAAAGTCAATCTTTTAGGAATTGTTTTTCAGAT
CTTCAATAAATTTTTCTTTAAATTC

WO 2004/030615

PCT/US2003/028547

647/6881
FIGURE 601

GAGGAGGCGGCAAAATCACTTATAAAATGGCGCGGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCGAGTG
CTGTGCTTTTCATGGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATAAAGGACAAACAAGTGAAATAC
TTCATACATTACAGTGGTTGGAATAAAAAATTGGGATGAGTGGGTTCCGGAGAGCAGAGTACTCAAATACGTGGAC
ACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCAGAGGGGAAGATGAGAGGGGCT
GCCCCAGGAAAGAAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTGAAAACGAAAAAGAACAAACAGAAAACA
CCTGGAAATGGAGATGGTGGCAGTACCAGTGAGACCCCTCAGCCTCCTTGGAAGAAAAGGGCCCGGTAGATCCT
ACTGTTGAAAAATGAGGAAACATTCATGAACAGAGTTGAAGTTAAAGTAAAGATTCCTGAATAGCTAAAACCGTGG
CTTGTTGATGACTGGGACTTAATTACCAGGCATTATGCAAATTACAAGAAATCTCGTGGAACACAGATAATAAG
G

WO 2004/030615

PCT/US2003/028547

648/6881
FIGURE 602

AATCACTTATAAATGGCGCGGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCGAGTGCTGTGCTTTTCAT
GGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATAAAGGACAAACAAGTGAAATACTTCATACATTAC
AGTGGTTGGAATAAAAATTGGGATGAGTGGGTTCCGGAGAGCAGAGTACTCAAATACGTGGACACCAATTTGCAG
AAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCAGAGGGGAAGATGAGAGGGGCTGCCCCAGGAAAG
AAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTTACGAATTGGAGCAATGTTGGCCTATACACCTCTGGATGA
GAAGAGCCTTGCTTTATTACTCAATTATCTTCACGATTCCTAAAGTACCTGGCAAAGAATTCTGCAACTTTGTT
TAGTGCCAGCGATTATGAAGTGGCTCCTCCTGAGTACCATCGGAAAGCTGTGTGAGAGGCACTCTCACTCACTTA
TGTTTGATCTCCGTAAACACATTTTGTTCCTTAGTCTATCTCTGTACAAACAATGTGCTTTGAAGATGTTAGT
GTATAACAATTGATGTTTGTTCCTGTTTGATTTTAAACAGAGAAAATAAAAGGGTAATAGCTCCTTTTTTCTT

WO 2004/030615

PCT/US2003/028547

649/6881
FIGURE 603

TTTTGCGCTCGGACCTTCGCCAGAGGGGCCGGGACATC**ATG**ACGGTGGGAGCCAGGCTCCGAAGCAAGGCGGAGA
GCAGCCTCCTGCGCCGCGGGCCCCGAGGGCGAGGGCGAACCAGGGGGACGAGGAGGCGGCCCATCCTGGAGC
ACCTGGAGTACGCGGACGAGGCGGAGGCGGCGGCCGAGAGCGGGACGAGCGGGCGGACGAGCGGGCCCCGGGA
CCCCGGGCGCGCGGAGGGTGCACCTTCGCCCTCCTGCCCGAGCGCTACGAGCCACTGGAGGAGCCGGCGCCGAGCG
AGCAGCCCAGGAAGAGGTACCGGAGGAAGCTGAAGAAGTACGGCAAGAATGTCGGGAAGGTCAATCAAAAGGAT
GCCGCTACGTGGTCAATCGGCCTGCAAGGCTTCGCTGCAGCCTACTCCGCCCGTTTGGGGTAGCCACCAGCGTGG
TATCCTTCGTGCGCT**TAA**TGGGAGCTGCTGTGGCAGGTGCCCCAGAGTGAACGGGAGCCCCGTGTGTGGGAACCT
TGTGAATCCTGGAGCATCTCAGACTTGAACACACAGCATATTTGGAAGAGAAAACATGCCTTTCTTTGTTGAATC
ACATTAGTATGATGAGTGAGTCATCCCTGCCCATCTGCTGAGCTTCTCACATCTCTCAGTACACAGTGGACCCAG
TGGTCAATCCTGCAGAGAATTCGGCGGAGGTTAGGTTTGGGAGTGGAGCTAGCGTGAAGCAGAGCCTTCAC
GTGAAGGTGGCAGGCACTGGGGCGGAAGCCAACACTCAACAGATGCAAGCAGTGTGGGTGTGCAGCAGAACAGTG
ATCTTGGGGGAGGAAGAGGATGTTACTAGAGTCAGATGATTTGCTGTATTCTCCTGAAAGGTGCTAGGCTGACAG
GCGCTCACATTCCTTGGCTGCCTCGGTTCTGAGGGCAGCTAAGGAGCTGTTTATTCTCAAGTCATGCTCCCCGA
TCTCCTTCTCTACCACTCTGTCAACAGGAGTTTAAATTACAGGCTTGAGGAGAAGAAAGGAAGAAAAGATATCTT
GATGCTTTGAAAACCTGTGTTGGCAGTGTGGCATGACTGTTTAAAGTAGATAAAACCTTGTCATTTTACCCCATCC
CTGCATGACTGTGAAGCTGGCGAGGAAGGAGGAAGAAGGGCAAGTTTCAGATGCAGGCTGGGTGGCTGGGACAGGT
TGGCTAAGGGACTACTCTGGAGGGCTCTTCTGCCTGGCATTGCCACTTCGGCCCAGCCACGTGTTTGCAGCGAC
CAGAGTCCCTGCAAAGGTGTGGCTGGCTGTGGTCAGGGTGTACTAGCACCATCAGCGCACTCCCGCCATTGGCT
CAGCTCCTCTCTGCCAGTCCAACCTAAGAGTGCTTTGTCTGGGTGGGACATAGGGGCTGAGAGAGATGGGGGGAG
ACATAACACCCAGGAATGAAAATACAGATTTAGAGAAGGAACCAGTAAGTAGGAGACAGATGTGAAGGAAATGGA
AATGAGGCAAGAGGACATTGGAAGAGAGAAGTTTGTCTGTCCAGGAGCCAGGTCTGGAGCATCAGTGTGAGGGAGT
TCAGGTAGGCTGGGCCTGTGCCTCTAGGTAGGGACAAGGGAGGCTGGGTAGCCAGGGCTGGTGCTTAAACCCCT
GAGGCCATGAGCTCATTGGCTGCCTTTGTAGCATCCTGTCTTCTTCTGTGCTGCCTGGTTTGATCTCATCTCACC
TGGATTCAAAGGGTAAGGTGGGCATGGGTCTTGGGCCTGACACCCACCAAGGATGACCTGTGGACTGCCATCGGA
TGCTGAACAGGGAGATGAAAGGAGGTCTCTTACCATAACCCCTCTGCCAACCCCCCAGTAGGCCACTGTTCTGAC
TTTGTCTCCAGAATATCCAGAAATCCAAAGGGGCTGTTGCTGAACAGTCTGCAGGACCAGTGACAGCACCTACCT
GTTGTCCCAAGGCATACAAAGGAGGCCTCAACGCTCATGCTTCTCTAATCAAGCCCTACCAAGACAGACAGAAAG
ACAGACAGAAAAAAGGAAGGGGTAGAGGAGAAGGTTGAAGCTGTGGAGCTAGACTCTGCTTCACTTCCTGAAGCT
TCAACTTCATGTCGAAGATTCACTGGGACCCAATTCTGTCATTGTTAATATTTGTGAGGAAAAGTGAAACAAGTG
ATCTGGTTTTAGCCCAGATGATGAAAGTGATATGGCACATTTTACACACGTGAGATAATTACAGCTTGCCCCA
CAACACTGGGTGTTGGAGAAAAGGGAGAGATAGTCATAAGTGGAAGAAAAAGCCAAGCATAGTGAGTGGGAAGGAG
AGTGAGAGCCTGTGCAGGCTGCTGACGAGCCCCAGGCAGCCACAAGTTTCTCGTGGGGAGATGGAGGCAGAGCC
CAGGGTAGGGGACAGAGCTGCTGGGGCCTTTCTTGCCTGGGAATCTGTCCAGGAAGAGCTTCCCCACTCCCAT
CCCCCAAATTGGAAAAACCGTACATTCAAGCCTGTTTGGCCCTGAAATTCTTAAGAATCTGGTTAAGAATTA
CACTAATGTCAAAAGTCAAAACCTCCTAGGGGTGTCTTGGGAGTCAGGTTACGGGTACAGAAGATGAATCTCA
GATGTCACTCAACCTGAGCCGTCACTCTGTGTGGCAGGGCTGCCCTGGGTTTCTTACTCAATCCCTGGAGTGT
AAGCATTTGGATTGTGTACAGATTACCTTTTTACCTTTTCTTTCTTTTTTTTTCTTTTTTCAATATCAGTGCC
CACACCTTACTGAGTATTGAGTTTTAGAGCTTTCGCTTGATGTGCTTGACCAAGAGACTTCTTTTGTATCCTTTT
CTTGTCTATGATGTAAATAAAAGCCTCGATTTATGT

WO 2004/030615

PCT/US2003/028547

650/6881
FIGURE 604

MTVGARLRSKAESSLLRRGPRGRGRTEGDEEAAAILEHLEYADEAEAAAESGTSAADERGPGTRGARRVHFALLP
ERYEPLLEPPAPSEQPRKRYRRKLKKYGKNVGKVIKGCYVVIGLQGFAAAYSAPFAVATSVVSFVR

WO 2004/030615

PCT/US2003/028547

651/6881
FIGURE 605

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACATGCCCAGTATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGCACCTAATAAATGTAAATGTGCTTAAATCTTTTGTCCTCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATAACCTACCTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCTCACAAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGTCTCTGCCTCCAGCCTTCTCTCCAGGCCCTGAACCTTCTCAAGTCGACCTCACCAGGCCCAGTTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTCACTGTGGACCCCCCA
GACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCTGCAGCCTCTCCAGGCCCAGCTCC
TCCTGCCTCCAGTGGCCTCTTTCAGCCCAGCCCAGCTCATGCCTCCTGGCGGCCTTCCCAGGCCCTGCTTTTGA
CTTTTGGTGGCCTCTGCAGGCCTCGACAAGGCCCGGCCTCCTGCCTCCCGAA

WO 2004/030615

PCT/US2003/028547

652/6881
FIGURE 606

GGCACGAGGGCTCTGTGGAGCTGCGCCTGCCAACTCATTGCTTTCTGCTGTGCTGTGATCCTGCAGTCAGTTGCC
GCTGTTGCTACTGCAATCATTTGCACCAAAGTGGAGCCAGAGAAGTTCCCTCTTTTAACATAAAGAGTCAAGAAAT
TGGAGCATGGCTATGAGCAATGGAAACAATGATTTTGTGGTTCTGAGCAACAGCAGCATCGCAACCAGTGCTGCT
AACCCGAGTCCCCTCACCCCTGTGATGGAGACCATGCAGCCAGCAGCTCACACCCAAAGAAGCAACAAGAACA
AAAGTGAGTCCAAATGGATGCCTGCAACTTAATGGCACGGTCAAATCATCCTTTCTGCCTTTAGACAACCAAAGA
ATGCCTCAGATGTTACCCCAATGCTGCCATCCTTGCCCATACCATCACCTTTGACTAGCCATAGCAGTCACCAA
GAGTGCCATCCCGAGGCTGGCCCTGCAGCACCTCTGCTTTGGCCCTCGTGTTCATGCAGCCACACTCCGAGTAT
TCTGCATCTCTTTGTCCAAATCATTCACCTGTGTATCAGACTACGTGCTGTCTTCAGCCCTCTCCATCCTTCTGC
CTGCATCATCCGTGGCCTGACCATTTTCAGCATCAGCCTGTGCAACAGCACATAGCCAACATAAGACCATCCAGA
CCTTTCAAGTTGCCAAAAGTTATGCAGCCCTGATAGCCGACTGGCCGGTGGTGGTCTTGGGCATGTGCACCATG
TTCATCGTAGTCTGTGCCTTGGTTGGAGTATTAGTGCCAGAGCTCCCTGACTTCTCTGATCCATTGCTGGGTTTT
GAACCAAGAGGAACAGCAATAGGCCAGAGATTGGTCACATGGAATAATATGGTGAAAAATACAGGATACAAAGCA
ACATTAGCAAATTATCCCTTTAAATATGCAGATGAACAAGCCAAAAGCCATCGGGATGATAGATGGTCAGATGAT
CATTATGAAAGAGAGAAAAGAGAAGTTGACTGGAACCTCCACAAGGACAGCTTTTTCTGCGACGTTCCAAGTGAC
CGATATTCCAGAGTGGTATTTACTTCATCTGGAGGGGAGACATTATGGAATTTACCTGCAATTAATCAATGTGC
AATGTAGATAATTCCAGGATCAGATCTCATCCCCAGTTTGGTGATCTCTGCCAGAGGACCACTGCTGCCTCCTGC
TGCCCCAGCTGGACACTGGGAAACTACATCGCCATTCTGAACAATAGATCGTCCTGTCAGAAAATAGTTGAGCGA
GACGTTTCTCATACCTTGAAGCTGCTTCGGACTTGTGCCAAACACTACCAAATGGCACTCTGGGGCCAGACTGC
TGGGACATGGCAGCCAGAAGAAAGGACCAGCTCAAGTGACCAATGTGCCACGCAAATGTACCAAGTACAATGCT
GTGTACCAGATCCTCCATTACTTGGTGGACAAAGACTTTATGACCCAAAGACGGCTGACTATGCCACGCCAGCT
TTAAAATACAGCATGCTCTTCTCTCCACAGAGAAAGGGGAGAGCATGATGAACATTTACTTGGACAACCTTTGAA
AACTGGAACCTCTTCTGACGGCGTGACTACCATCACCAGGATTGAGTTTGGTATCAAACACAGTTTGTTCAGGAT
TATCTTCTAATGGATACTGTGTATCCTGCCATAGCCATTGTGATTGTCCTTTTAGTTATGTGTGTCTACACCAAG
TCCATGTTTATCACTCTGATGACAATGTTTGCAATAATCAGTTCTTTGATTGTTTCCTAAAAAAAAAAAAAAAAAAAA
A

WO 2004/030615

PCT/US2003/028547

653/6881

FIGURE 607

MAMSNNGNDFVVLNSSSIATSAANPSPLTPCDGDHAAQQLTPKEATRTKVSPNGCLQLNGTVKSSFLPLDNQRM
QMLPQCCHPCPYHHPLTSHSSHQECHPEAGPAAPSALASCCMQPHSEYSASLCPNHSPVYQTTCCCLQPSPSFCLH
HPWPDHFQHQPVQQHIANIRPSRPFKLPKSYAALIADWPVVVLGMCTMFIVVCALVGVLVPELPDFSDPLLGFEP
RGTAIGQRLVTWNNMVKNLTGYKATLANYPFKYADEQAKSHRDDRWSDDHYEREKREVDWNFHKDSFFCDVPSDRY
SRVFTSSGGETLWNLPAIKSMCNVDNSRIRSHPOFGDLCQRTTAASCCPSWTLGNYIAILNNRSSCQKIVERDV
SHTLKLRLCAKHYQNGTLGPDWCWMAARRKDQLKCTNVPRKCTKYNAVYQILHYLVKDFMTPKTADYATPALK
YSMLFSPTEKGESMMNIYLDNFENWNSSDGVTTITGIEFGIKHSLFQDYLLMDTVYPAIAIVIVLLVMCVYTKSM
FITLMTMFAISSLIVS

WO 2004/030615

PCT/US2003/028547

654/6881
FIGURE 608

GCTTCCGCCTCGGCTCCTCTTCCCTGCCGGCATCCGGGATCCCTACGTCCCGCGTCCCCGAGCGCTCGGAGCCTA
CGCGCCCAGCGCTACCGAAACCCAGAGTCCTGCGCCCTGGAGTCCCCGCGCCCCGGAGCCCCGAGCACCCGGGAGT
CCCCGAGCCTCGCGCCCCGGAGTGCCCCGAGCCTGCGCCGCCGCACCCGGATACCCCGGGTCCCCGCGAGCTGCCGA
GGCCGCCCGCCGCCGCCCGCGGGACAGTACCGCCTTCCCTCCCTCTGTCCGCGCCATGGCCGCCCGGACCTGTC
CACCAACCTCCAGGAGGAGGCCACCTGCGCCATCTGCCTCGACTACTTCACGGATCCGGTGATGACCGACTGCGG
CCACAACCTTCTGCCGCGAGTGTCATCCGGCGCTGCTGGGGGCCAGCCCGAGGCCCGTACGCGTGCCCCGAGTGCCGC
GAGCTGTCCCCGAGAGGAACCTGCGGCCCAACCGCCCGCTTGCTAAGATGGCCGAGATGGCGCGGCGCCTGCAC
CCGCCGTGCGCGGTCCCGCAGGCGTGTGCCCGCGCACCGCGAGCCACTGGCCGCTTCTGTGGCGACGAGCTGCG
CCTCCTGTGTGCGGCCTGCGAGCGCTCTGGGGAGCACTGGGCGCACCGCGTTGGCCGCTGCAGGACGCGGCCGAA
GACCTCAAGGCGAAGCTGGAGAAGTCACTGGAGCATCTCCGGAAGCAGATGCAGGATGCGTTGCTGTTCCAAGCC
CAGGCGGATGAGACCTGCGTCTTGTGGCAGAAGATGGTGGAGAGCAGCGGCAGAACGTGCTGCGTGAGTTTCGAGC
GTCTTCGCCGTTTGTGTCAGAGGGAGGGACAGCAGCTGCTGCAGAGGCTGGAGAGGAGGAGCTGAAGGTGCTGC
CCCGGTGCGGGAGGCGCAGCCACCTAGGCCAGCAGAGCGCCACCTAGCTGAGCTCATCGCCGAGCTCGAGAG
GCCGCTGCCAGCTGCCTGCGCTGGGGCTGCTGCAGGACATCAAGGACGCCCTGCGCAGGGTCCAGGATGTGAAGC
TGCAGCCCCCAGAAGTTGTGCCTATGGAGCTGAGGACCGTGTGCAGGGTCCCGGGACTGGTAGAGACACTGCGGA
GGTTTCGAGGGGACGTGACCTTGGACCCGGACACCGCCAACCTGAGCTGATCCTGTCTGAAGACAGGCGGAGCG
TGCAGCGGGGGGACCTACGGCAGGCCCTGCCGGACAGCCAGAGCGCTTTGACCCCGGCCCTGCGTGCTGGGCC
AGGAGCGCTTCACCTCAGGCCGCCACTACTGGGAGGTGGAGGTGGGGACCGCACAGCTGGGCCCTGGGGGTGT
GCAGGGAGAAGCTGAACAGGAAGGAGAAGGGCGAGCTGTCCGCGGGCAACGGCTTCTGGATCCTGGTCTTCTTG
GGAGCTATTACAATTCTCGGAACGGGCCCTTGCTCCACTCCGGGACCCACCCAGGCGCGTGGGGATCTTCTTG
ACTACGAGGCTGGACATCTCTTTCTACAGTGCCACCGATGGGTCACTGCTATTTCATCTTTCCCGAGATCCCT
TCTCGGGGACGCTGCGGCCCTCTTCTCACCCCTGTCCAGCAGCCCGACCCGATGACTATCTGCCGGCCGAAAG
GTGGGTCCGGGGACACCTGGCTCCCCAGTGACTCGGGCCCTCCTGGAGGAGTCTGTGCTCTCTGCCCCTC
CAGGCCACTGAGTGTTTTGGCCACTTGGAGGACCTGGGAGGAGGGAGTGTGTCCTTTGAGCAAGAGGAGGAATC
CTGGTGCCTTTCTGAGCCTGCGTGGGAGAACCCCAATTCTAGCACTCCAGGAACTGTGGGAGAGTGTGGGGCAG
GCTCCGTCCCTCCCTGGGAGACCCCTCCAGCCACCGGTGCCACTTAATGCCAACAGCCCTTACCAAGCTGGGAG
CCCCATTGCCCCGGCAGCTCTGGCCTGTGGTTCCAGAAGCTGAGAAAACCTCCACTGGGGCTTGAGAATCCAGGG
TTCACCTAAGCTGCACAGTTCTGCACTTGTGTCAGCCCCCTGAAAGTCTTGTGTACCCACCTCTGAAGATGCT
GGGGAAGGCAGCTGGGATGGGAGCCAGCCCCATGCCTGTCTGTGACCCACAGTGGGTGAGAGCCCGTCACAGTC
CTGGGTGTGGCTGCTCTGGAAGAAATTAGGAGGCAGCCATAATAAGAGTCTTCAGAGAGATGATGGGAGGGGCCAG
TGAGGACAGGAACAGAGAGTAGATGTCCTATAATAAGGGGCTTCTGGGAGGTGCCTGGGCACAGATGCTGTTC
AGCAGGTGTGTGGCCTAGAGGAGAGAGCAGAGCCAGAAATGTCTTTTGAGGCCACGTTCTGACTTGAAGCT
TTCGTGGGCATGTTGCCATTGGGTTTGGCCCTTGCAAAGGCTTCCTAGGTCTCCAGTGGCCCTCAGGACCCAGG
GTCCAGCTGCTGCTTGGGGATGTGCACTGCTGCGCCGCCCTTGCACTCTCTCTACCCCTGGGAGGAACAGTGGC
TTCTCAGAGCCTGGGGCATAAGAAAGGCAGGAGTTGATTTTGTGTTGGGTTTGGGGTTTCTTTGTCTCAA
GGTACTGTTCTGTTCTCTTTACCCCTCTGCTTTATTTATTGTAAGCATTCCACGTTAAATAAACTTTGGCTGT
TGCTAC

WO 2004/030615

PCT/US2003/028547

655/6881
FIGURE 609

MELRTVCRVPGLVETLRRFRGDVTLDPDTANPELILSEDRRSVQRGDLRQALPDSPERFDPGPCVLGQERFTSGR
HYWEVEVGDAAGPWGCAGRT

WO 2004/030615

PCT/US2003/028547

656/6881
FIGURE 610

CCGCAGGCAGTAGAGTGAAGCGCGCAGCTGCCAGGACTTGCGCGGTGACGTGCGCCGCTGCCAGGACCTTG CAGG
TGGAGAGCATAGTTGCCAAAATCAAGGCGGAGGAGCGCACCGCCGCTAGGATCCAGGCGGAGAAGCCCACCGCGG
CCAGGACCTAAGGATGCAGTACACTGCTGCCAGGATCTTGTCTGTGGAGCGCAGCGCGGCCAGGACCTCCGGCTG
CAGCACACCGCTGCCAGGATCTTATCGGCAGAGCGCTCCGCGGTCCGGACCCCGCCCCGTGCGCGTCCCCGACCC
CGCCCCGTGCGCGTCCCCGGCGTTGGCGTCTTCGTCTGTGCTGGTCTCCGTCCGGTCGCGCGCCGTCTAGGTC
TCCGGCCCTCCCCAGCGCTCCTGCGCCCTTGCCGGCCCCCGCCCGCCGAGCCCTGGCGCTCCCTGCGGGCCCCG
CCGAGGCCCGCTGCGCCCTGTGCCAGCGCGCGCCCCGGGAACCGGTGCGCGCCGACTGCGGCCACCGCTTCTGTC
GGGCGTGCGTGGTGCGCTTCTGGGCGGAGGAGGACGGGCCCTTCCCGTGCCCCGAGTGCGCCGACGACTGCTGGC
AGCGCGCCGTGGAGCCCGGCAGGCCCCGCTCAGCCGCGCCTTCTGGCGCTCGAGGAGGCGGCCGCGCGGCCCG
CGCGCGACGGCCCGGCCAGCGAGGCCGCGCTGCAGCTGCTGTGCCGCGCCGACGCCGGCCCGCTCTGCGCCGCT
GCCGTATGGCTGCGGGCCCCGAGCCGCCGAGTGGGAACCGCGCTGGAGGAAGGCGCTGCGCGGCAAGGAGAACA
AGGGGTCTGTGGAATCATGAGAAAGGACTTGAAATGACGCCCCGGGACCTGCATGGCCAGGCAGAGTCAGCAGCTG
CAGTGTGGAAGGGACACGTGATGGACCGTAGGAAGAAGGCACTGACCGACTACAAGAAGCTGCGGGCCTTCTTTG
TGGAGGAGGAGGAGCATTTCCTGCAGGAGGCTGAGAAGGAGGAGGGGCTCCCTGAGGACGAGCTGGCTGACCCCA
CTGAGCGGTTCAAGTCACTGCTGCAGGCGGTCTCGGAGCTGGAGAAGAAGCATCGCAACCTGGGCCTCAGCATGC
TGCTGCAGTGATGGCGCCAACCCGTGGCAGTCCCAGAGCTGGAGGCAGGAGGATGGATCCTCATCTCCATGGGAA
GTGTCAGCGTGTGGCTGCCAGGGAAGCGTGGCAGGCGCCTGGCCTTGGGTCCATCTACATAGTTGCGTGTTTCAA
CAATGTCCATTTATCCTTCACCCCGAGGCGTGTTTTGGGGGCTGCAAACACCTCCCTGTGCTCCACCTGCCTCCG
CAGAAGGAAGCCTCTTTCTCTGTTTCCCTGGGTGAGGGGGCTGGCAGGTGGCTAACCCCATTTAGCATCTCCAGG
CCCTGCCATCGTGCTCATCTTGCTGTTATCTCTAGCTCTTTCCCTCCTCCCATTTTCTTTAGTAGTTGAATTTT
GCAAAGCTTGTAGCAGTAGCTCAGTTGCCTGCAGCATCCTTGTGTGTAGATAAATTAGTCGACAGAACTCAGCA
CTGGGGACAGGATTGCAAAGTCGGGGACATAGATGCAGACAGTTGTTGAGATTTGGGGATAGCCGGGCTTGTGAG
CGGTGCCCATTTCCAGATGAAGCCTTTCAGCCCTTCTGAGTCCCCGGCCCTTGGTGCGATGTCTGTGAGTTTGAC
CTGCCCAGCGTGTGGGCTGGCTCAATGCTGAATAAAGTGGGTTTGTGTGAGCTCGTTTGCTTCTCGTGTGT
CCACCTGGCCTCTTCCCCCTGCCCTGGCCACCCTCCAGTGTCAAAGGAACTTCCCTCGTGACACGTGCTAAAGCA
TGGTGAGGAGGACTTTGATTGGGACCATTTGAGATGGGTGTGGGACCTTTTCTTGGGGCCTGGGGGGAGATGGGG
CTCCACCCCGACGTAGCAGGGCAGGGTTGGAGGAGCGAGGAGCAGTATAGGGTCCATGGGTGGGAATGACTGTG
AGGAGACATCAGGGCTGAGGGGGCTCTGGCTAAACCCACCTCACAGAGTCCTTGCTGCAGGCAGGCAGGGCGATC
AGA

WO 2004/030615

PCT/US2003/028547

657/6881
FIGURE 611

MQYTAARILSVERSAARTSGCSTPLPGSYRQSAPRSGFRPVVPDPAPCASPALASSSCCWSPSGRRPSRSPALP
SRSCALAGPAARSPGAPCGPRRGRLRPVPARAPGTGARRLRPPLLSGVRGALLGRGGRALVPRVRRRLLAARRG
ARQAPAQPPPSGARGGGRGARARRPGQRGAAAAVPRRRRPPALRRLPYGCGPRAARVGTALEEGAARQGEQGVCG
NHEKGLE

WO 2004/030615

PCT/US2003/028547

658/6881
FIGURE 612

GGCACGAGGCGCTGGCCGGGCTGGCTGCGGCCGCCCTGGGCCGGGCCCCACCGGACGGCTTGCTCTGCTCTTTAC
CTGGGGTTGCTGTCGAGGACCCCTGTGCAAGACTCGGCCGGTTTTTCTTTCTCCCTGATGGACAGACCCAAACATA
GCCGCGCAGCATCGTGAAGGGCTGGGGCCTTCACTCCTCTGTGGCTCTGGAAGAGCCCGATTTCTCAGGAGGCA
TGTCGGGCCCCAGGCCTGTGGTGTGAGCGGGCCTTCGGGAGCTGGGAAGAGCACCCCTGCTGAAGAGGCTGCTCC
AGGAGCACAGCGGCATCTTTGGCTTCAGCGTGTCCCATACACGAGGAACCCGAGGCCCGGCGAGGAGAACGGCA
AAGATTACTACTTTGTAACCAGGGAGGTGATGCAGCGTGACATAGCAGCCGGCGACTTCATCGAGCATGCCGAGT
TCTCGGGGAACCTGTATGGCACGAGCAAGGTGGCGGTGCAGGCCGTGCAGGCCATGAACCGCATCTGTGTGCTGG
ACGTGGACCTGCAGGGTGTGCGGAACATCAAGGCCACCGATCTGCGGCCCATCTACATCTCTGTGCAGCCGCCTT
CACTGCACGTGCTGGAGCAGCGGCTGCGGCAGCGCAACTGAAACCGAGGAGAGCCTGGTGAAGCGGCTGGCTG
CTGCCCAGGCCGACATGGAGAGCAGCAAGGAGCCCGGCCTGTTTGATGTGGTCATCATTAAACGACAGCCTGGACC
AGGCCCTACGCAGAGCTGAAGGAGGCGCTCTCTGAGGAAATCAAGAAAGCTCAAAGGACCGGCGCCTGAGGCCTTGC
TGTCTGTTCTCGGCACCCCGGGCCCATAACAGGACCAGGGCAGCAGCATTGAGCCACCCCTTGGCAGGCGATACG
GCAGCTCTGTGCCCTTGGCCAGCATGTGGAGTGGAGGAGATGCTGCCCCTGTGGTTGGAACATCCTGGGGTGACC
CCCGACCCAGCCTCGCTGGGCTGTCCCCTGTCCCTATCTCTCACTCTGGACCCAGGGCTGACATCCTAATAAAAT
AACTGTTGGATTAGAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

659/6881
FIGURE 613

MSGPRPVVLSGPSGAGKSTLLKRLQLQEHSGIFGFSVSHHTTRNPRPGEENGKDYYFVTREVMQRDIAAGDFIEHAE
FSGNLYGTSKVAVQAVQAMNRCVLDVDLQGVNRNIKATDLRPIYISVQPPSLHVLEQRLRQNTETEEESLVKRLA
AAQADMESKEPGLFDVVIINDSLDQAYAEALKEALSEEIKKAQRTGA

WO 2004/030615

PCT/US2003/028547

660/6881
FIGURE 614

GGCACGAGGTCTGGGCTGGGTCCGACGGTAGTGGGTAGCGGGTCTCGGGTTGCGGGTTGCAGGTTGCAAGCCGCA
GGCCCCAGGCAACTGCCTTCCCGGCGCCATGTTTCGGCTCCAGTCGTGGAGGCGTGCGCGGCGGGCAGGACCAGTT
CAACTGGGAGGACGTGAAGACTGACAAGCAGCGGGAGAACTACCTGGGCAACTCGCTGATGGCGCCGGTAGGCCG
CTGGCAGAAGGGCCGCGACCTCACCTGGTACGCCAAGGGCCGGGCGCCATGCGCGGGCCCGAGCCGCGAGGAGGA
ACTGGCAGCCGTGCGGGAGGCGGAGCGCGAGGCGCTGCTGGCCGCCCTTGGCTACAAGAACGTGAAGAAGCAGCC
CACGGGCCTGAGCAAGGAGGACTTCGCGGAGGTCTGCAAGCGGGAAGGAGGCGACCCCGAGGAGAAGGGCGTGGA
CCGGCTGCTGGGGCTGGGGAGCGCAAGTGGCTCCGTGGGCCGCGTGGCGATGTCCCGAGAGGACAAGGAGGCCGC
CAAACTGGGGCTGTCTGTGTTACGCATCACCGCGTAGAGAGCGGCGGGCCCGGGACCTCGGCAGCCTCGGCCAG
GAGGAAGCCGCGGGCGGAGGATCAGACGGAAAGCAGTTGTGAGAGCCACAGGAAAAGCAAGAAGGAGAAGAAGAA
AAAGAAAAAGAGGAAACACAAGAAAGAGAAGAAGAAGAAAGACAAAGAGCACAGGCGGCCAGCTGAGGCCACCTC
CTCTCCACATCTCCTGAGAGGCCCAGGCACCAACCACCATGACTCCGACTCCAACCTCCCCCTGCTGTAAGAGGAG
GAAGCGGGGACACAGTGGGGACAGGAGGAGCCCGTCTCGCAGGTGGCATGACAGAGGCTCTGAGGCCTGATGGCT
GGACCCTGCTCACTGCTGTTGTGGGACCCTGAACCCTCCCTTACCTTGCTTGCTCCTGCCTCGGAAGCTCCTT
GGGTGTGGGTGAAGCCCGAGGCTGCTCCTGTGGAAGTGGCTCTGGGCACCAGCCTGTGGGGCTAAAGACTTGACA
GCTAGCTCTGGAGCAGCCGGCTTCCCTGGAAAACCTCCAGGTTTCGCATACCAGGGATGGCCCTGGCTTGGCCTG
CGAAGGTGAACCTGCCCAGATTTATCAGTAGAGGCTGGACTCCCTCTGTGTCCTGCCCATGGTTGCAGCAGCCAT
GGGCCTATGAGCGGTCTAACTGTGGCCAAGTATGGTGACCTCTATTTTCTTTATATTGACTCTTTGTATTTCAA
TAAATATATTTTAAAAGGAAGGTAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

661/6881
FIGURE 615

MFGSSRGGVRGGQDQFNWEDVKTDKQRENYLGNSLMAVGRWQKGRDLTWYAKGRAPCAGPSREEELAAVREAER
EALLAALGYKNVKKQPTGLSKEDFAEVCKREGGDPEEKGVDRLLGLGSASGSVGRVAMSREDKEAAKLGLSVFTH
HRVESGGPGTSAASARRKPRAEDQTESSCESHRKSKKEKKKKKKRKHKKKEKKKKDKEHRRPAEATSSPTSPERPR
HHHHDSDSNSPCCCKRRKRGHSGDRRSPSRRWHD RGSEA

WO 2004/030615

PCT/US2003/028547

662/6881
FIGURE 616

AGGAAGCCCTGCTTGATGAGCATGAGGCTCCACGGGGGCAGTGGCTGTGACGGTGAGTGCCACACAGAGCTGCCC
ACACTGGTGGAGGGAAGGCAGGGAGATACCAGGACCATCCGGAAGGGGCTGAGTGTCATTTGACAGGTGCCATGT
GAGCAGAGATGTGAAGGAGTGGCCCCGGGACAATCAGGGCAGAATCCCTGAGGTGTCCCTGGCCAGTGTCTTTCCA
CCTGTCCACAAGCATGGGGAACATCTTCGCCAACCTCTTCAAGGGCCTTTTGGCAAAAAGAAATGCGCATCCT
CATGGTGGGCCTGGATGCTGCAGGGAAGACCACGATCCTCTACAAGCTTAAGCTGGGTGAGATCGTGACCACCAT
TCCCACCATAGGCTTCAACGTGGAAACCGTGGAGTACAAGAACATCAGCTTCACTGTGTGGGACGTGGGTGGCCA
GGACAAGATCCGGCCCCCTGTGGCGCCACTACTTCCAGAACACACAAGGCCTGATCTTCGTGGTGGACAGCAATGA
CAGAGAGCGTGTGAACGAGGCCCCGTGAGGAGCTCATGAGGATGTGTGGCCGAGGACGAGCTCCGGGATGTGTCTCT
CCTGGTGTTCGCCAACAAAGCAGGACCTCCCCAACGCCATGAATGCGGCCGAGATCACAGACAAGCTGGGGCTGCA
CTCACTACGCCACAGGAACCTGGTACATTACAGGCCACCTGCGCCACCAGCGCGACGGGCTCTATGAAGGACTGGA
CTGGCTGTCCAATCAGCTCCGGAACCAGAAAGTGAACGCGACCCCCCTCCCTCTCACTCCTCTTGCCCTCTGCTTT
ACTCTCATGTGGCAAACGTGCGGCTCGTGGTGTGAGTGCCAGAAGCTGCCTCCGTGGTTTGGTCACCGTGTGCAT
CGCACCGTGTGTAAATGTGGCAGACGCAGCCTGCGGCCAGGCTTTTTATTTAATGTAAATAGTTTTTGTTCCTCA
ATGAGGCAGTTTCTGGTACTCCTATGCAATATTACTCAGCTTTTTTTATTTGTAAGAAAGAAAAATCAACTCACTGT
TCAGTGCTGAGAGGGGATGTAGGCCCATGGGCACCTGGCCTCCAGGAGTCGCTGTGTGGGAGAGCCGGCCACGC
CCTTGGCTTTAGAGCTGTGTTGAAATCCATTTTGGTGGTGGTTTTTAACCCAACTCAGTGCATTTTTTAAAT
AGTTAAGAATCCAAGTCGAGAACCTTGAACACACAGAAGGGAGACCCCGCCTAGCATAGATTGTCAGTTACGGC
CTGGATGCCAGTCGCCAGCCAGCTGTTCCCCTCGGGAACATGAGGTGGTGGTGGCGCAGCAGACTGCCATCAAT
TCTGCATGGTCACAGTAGAGATCCCCGCAACTCGCTTGTCTTGGGTACCCCTGCATTCCATAGCCATGTGCTTG
TCCCTGTGCTCCCACGGTTCCCAGGGGCCAGGCTGGGAGCCACAGCCACCCCACTATGCCGACAGCCGCCCTAC
CCACCTTCAGGCAGCCTATGGGACGCAGGGCCCCATCTGTCCCTCGGTGCGCGTGTGGCCAGAGTGGGTCCGTG
TCCCCAACACTCGTGCTCGCTCAGACACTTTGGCAGGATGTCTGGGGCCTCACCAGCAGGAGCGGTGCAAGCCG
GGCAGGCGGTCCACCTAGACCCACAGCCCCCTCGGGAGCACCCCACTCTGTGTGTGATGTAGCTTTCTCTCCCTC
AGCCTGCAAGGGTCCGATTTGCCATCGAAAAAGACAACCTCTACTTTTTCTTTGTATTTTGATAAACTGAA
GCTGGAGCTGTAAATTTATCTTGGGGAACCTCAGAACTGGTCTATTTGGTGTGCGTGAACCTCTTACTGCTTT
CAATACACGATTAGTAATCAACTGTTTTGTATACTTGTTTTCAGTTTTTCATTTCGACAAACAAGCACTGTAATTA
TAGCTATTAGAATAAAATCTCTTAATATT

WO 2004/030615

PCT/US2003/028547

663/6881
FIGURE 617

MGNIFANLFGKLGKKEMRIIMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIR
PLWRHYFQNTQGLIFVVDSDNRERVNEAREELMRMLAEDELRDVLLVFANKQDLPNAMNAEITDKLGLHSLRH
RNWYIQATCATSGDGLYEGLDWLSNQLRNQK

WO 2004/030615

PCT/US2003/028547

664/6881
FIGURE 618A

GTGGGACCATCCAGTTGCAGGAAAACAAGCTTAACACGCCCACTGATTCTACATTATGCTCCTACCTCCCAGCAG
CCTCTCCAGGCCCAGAAGCTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAAATGGCCTATTTAGGCC
CATACCTACCTCACGGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCG
TTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCT
CACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCAGCTCCTGCATCTTGGTGGCACCTCCAGGCCCA
GCCTCTGCCTCCCGTCGGCCTCTACAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCAGCATCTGCCTC
ACTGTGGACCCCCCAAGCCAAGCTCCCAACCTTTTCAGCAGCTTCTACACACCCAACTCCTGCCACCCAGTGGCCT
CTTTAGGCCAAGCTCATGCTTACAAAGGGCCTTTCCAGGCTCAACTTTTGTCTCATGGCAACCTTTCCCTGGCCAG
ATTCTGCCTGTCTCCAGCAGCCTAGACAGGCCAGGTCTTGCCTCACACTGGCCTCTCTACATCCAGCTCATG
CCTCACGGTGGCCTCTCCAGGCCCAACTCCTGTCCCAGGACGTATCTCCGGGCCAAAACCTTACTCAAGTCAGA
CTCTCTAGTCCCAACTGCTGCCTCCTGGTGGCCTATGAAGGCCAAAATCTCCTCAAGTGGACCTCTCCAGGCC
AGCTCCTGCCTCCTGTGCAGCCTCTACAGGCCCAACCTCTGCCTCATGGGGCTTCTCCAGGCCACCTCTTCCCTC
TTGGCTGGGTCTACAGGCACAACCTGCTGCCTCACAACAGCCTTTTTTGGCCAGTTCTGTCCAGCTCATGGCGG
CCAATGTAGGCCCAAACTTCTCTCAAGTCAAACTCTCCAGGCCACCTTCTGCTTCCGGTGGCATGAACAGGCC
CAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTGCTCTTGCCTCCCAGGGGCTTTTTCCAGACCCAGCTCCTGC
CTCATGGCAGCTGCCCCAGGCCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAG
TGGCCCATTTAGGCCCAACTCATGACTGTGGGCCATTTCCAGGCCCTAGTGCCTGCCTCGTGGCTGACTCTTGAA
GCCCCAAACTTCTCTCAAAATCAGCCTTTTGGCCAACTTCTGTCTACTGTCTCGACTCTACAGGCCAGCTCTGCCTC
ACAGTGGACCCCTCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCCGCAGCCTC
TACAGGCCAGCTCCTGCCTTGCACTGGCCTCTTTAGGCCAAGCTCATGCCCCATGGCGACTTTTCCAGGCACAG
CTTTTGCTTTTGCAGCCTGTGCAGGCCCAGAAATGTCTTAACCTCGGCATCTCCAGGATGAGCTCATCCTCCAG
TGCGTCTACAGGCCCGTCTCCTGCCTCACAACAACCTCCTTTGGCCCAACTCCTGCTGCTGAGCTGCTGGCAGCCTCT
GTAGGCCACAGAATTCTTAAGGTAAAGCTTTCCAGGCCACCTTTGGCCTCCCGGCAGGCTCAGCAATCAAACTA
TTCCCTCACTGCGGCCACCGAAAGCCAAGTTTCTCCCTGCCTCAGGCATCCTCCGAAAACCTGAGCATTGTGCTC
ACGGTGGCCTCCCCAGGCCATGAATCTGCCTGCCTCCCAGGCAGCTGCTGCCTCACAATGGTCTCTTTAGGCCCA
GCTCATGCTAAAAGATGGACTCTCCAGGCACAGCTCTTGCCTCCTGGCAGCCTCTGCAGGCCCAAAATTCTCCAA
AGTTGGCCTCTCCTAACTCAGCTCCTGCCTCATGTCTGCCTACACAGGCCAGACTCTTACCACACAGTAGACCC
TCCAGGCCACCACTTGCCCTGATCATAGCCTCCTAAGGCCAAGCTCCTGCCTTTCCGGCAGCCTCTACAGGCCAAG
CTCCTGCCTCGCAATTGCCTCTGTAGGCCAAGATCATGCCGTGAAGTGGCCTTCCCTAGCCTAACTTTTGTCTTT
TGACGCATACTCCAGTCCCAAACTTCTCCTCAGTCAGCCGGTCCAGGCCAAGCTCTTCCCTCCCAAGGCTTCTGC
AGGCCAAAATCATCCTGAAGTCACCTCTGCAGGCGCAGCTCCTGCCTCCAAGTGTGTGTAGGCCAAGCTAATG
CCTCACAGCACACTTTCCAGGCTGAGCATTTCTCTTTGTGCATCCTCTCCAAGCCCTGAACTTACTCCAGTTGGC
CTCTCCAGACCAAGCTCTCCCTCCAGTGGCCTCTACAGGCCAAAATTGTCTCAGGTGAGCCTCTCCAGGGCCA
ACTCCTAGCTACCGGTGGCTTCTGCAGGCCAAAATCGACCTCAAGTCAGCCTCTTACACCCAGCTCTTGCCTCT
GAGTGGCCTCTCCAGGAGCAAACTTTCTCAAGTCGGCCTCTCCAGGCCAGCCTCCTGCTTCCCGAGGGCATGT
ACAGGCCAGCCTCTGCCTCACAGCAGACTCTTACACCCAGCTCTTCCCTGTCTGCGGCCTCTCCAGTCCAAAG
CTGCTCCTGCCTTTTGGCAGCTTGTACAGGCCAGCTCCTCCCTCACGGTGGCCTCTTTCGGCCCAACTCATGCC
TCTTGCAACGTGCCCAAGTGTGAGCTCCTGCCTCACACTGGCCTGTTGAGGCCAGCTCATGCCTCTCGTGGCCT
CAACGGGCCCATCCCTGCCTGTGCGGCGCCTCTACAGGCCCGCCTCTACCTCACAGTGGGCTCTCCAGGCCCA
CCTCTTCTCCTACCGTGGCCTCCTGGGGCAATGCTCCTCCCTCTCGGGAGCCTCTGTGGGCCAGCTCCTGCCTCC
CAGTGGCCTCTGTGAGGCCAAGCCGTGCCTCAGGGCAGCCTTTCCAGGCCAGCGTTTGTGCTTTGCATCCTCT
CCAGGCCCTGGAATTCCTCCAGTCGGCCTCTCCAGGCCAGCTCTTCTCTCGGCGGCCTCTGCAGGCCAGACT
GTCGTCAAGTCGGCCTGTCCAGGGCCAGCTCCTGCCTCCCGCGGCCTCTGCAGGCCCAAGTCGTCTCAAGTTG
GCCTCCCCAGGCCAGCAACGGCCTCTCGGCGCCTTTCCGGGTGCAAAAGTTCTCGAGTCAGCCTCTCCAGGC
CCAGCTCCTCCTGCCTCCAGTGGCCTCTTTCGGGCCAGGCCAGCTCATGCCTCCCGGCGGCCTTCCAGGCCCT
GCTTTTGAATTTTGGTGGCCTCTGCAGGCCCTCGACAAGGCCAGGCCCTCCTGCCTCCCAAGGCTGACAGGCC
AGCCTCTGCCTCACAGCAGACTCTCCAGGCCAGCTAGCTCTGCCTCACTGCGGCTTCCCGAGTCCAAAGCTCC
TGCTCTCAGCCGCTTCGGCAGGCCAGCTCCCGCCTGCCAGTGGCCTCTCAGGCCCATGGGGCTCATTCTCA

WO 2004/030615

PCT/US2003/028547

665/6881

FIGURE 618B

CAACGGCCTTTCCAGGCCAGTTTTCCCTTCGGCGGCCTCTTGGCCTCTAATTTGTTTATCTTTGGGTATAA
ATCCCAAAATATTGAATTTTGAATATTTCCACCATT

WO 2004/030615

PCT/US2003/028547

666/6881
FIGURE 619

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGTAAATGTGCTTAAATCTTTTGGCCCAGCTCCTACCTCCCAGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATAACCCTACCTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCACCTCCAGGCCCAGCCTCTGCCTCCCGT
CGGCCTCTACAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTCACTGTGGACCCCCCA
GACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCCGCAGCCTCTCCAGGCCCAGCTCC
TCCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGGCTCTCGGCGGCCTTCCCAGGCCCCGCTTTTGA
CTTTTGGCGGCCTCTTCAGGCC

WO 2004/030615

PCT/US2003/028547

667/6881
FIGURE 620

TTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGAACATGCTGAGAACTGATGAAGCTG
CAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTG
AATGCGATGGAGTGTGCATTACATTTGGAAAAAAGTGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACT
GACAAAAATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATAAGCAGGTGAAAGCCATCAAAGAA
TTGGGTGAGCACGTGACCAACTTGTGCAAGATGGGAGCGCCCGAATCTGGCTCGGCGGAATACCTCTTAGACAAG
CACACCCTGGGGGACAGTGATAATGAAAGCTTAAGCCTCAGGCTAATTTCCACATAGCCGTGGGAGTGACTTCCCT
GGTCACCAAG

WO 2004/030615

PCT/US2003/028547

668/6881
FIGURE 621

MKLQNQRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKSVNQSLLELHKLATDKNDPHLCDFIETHYLNKQVKA
IKELGEHVTNLCKMGAPESGSAEYLLDKHTLGDSDNES

WO 2004/030615

PCT/US2003/028547

669/6881
FIGURE 622

ATGGCCGGCACAAGATGGGGCGGGAGGACAGCGTGCTGGATACGGCGTGGGGCGGGTCCGCGGCCCGGGAGACC
CATGCTGGGGCGGCCCTGTCACTCGTCTCGCTGCCAAGCACAGGGCTGAGGTGCGGAGGGACCACTGAGAGGACT
TCGCTGCGTGTCTAGCTCAGCTCTGGACGGCGTGGAGGAGCCCTGGAACTTTATTTACAAAACTGACAGCAGCT
GCCCTTAGTTTGGCAGCTGGAAAAATGGGAAAGAGAAAGTAAGAGGAAGGGTGGCAAAGGAGGGAGCCCATGTGGA
CAGCAGGAACGGGTACACGATAGCACAGAATCAAAACAAAGGCTCTCTGGTCGGAGTTTAGAAAGGCTGAAGGG
GATACTAAAGGAGGAGATAAAGCCCAGGTGAAGGACGAACCACAGAATAGATCCGCGAGGTTGTCTGCTAAACCT
GCTCCTCCAAAACCAGAGCCCAAGCCTAAAAAGGCCCTGCAGAGACAGTACCCAAAGGGAAAAAGGGAAAAGCT
GTTGCTGGCAAGGAGGGGAAATAACCTGACAGAAAATGGAGATGCCAAAACAGACCAGGCACAGAAAGCTGAAGGT
GCTGGAGATGCCAAGGCAAACTGTCTGCCACGGTGTGGCAGCAAAGAAATGAAAGGAAGTGTCTGGCAGCGCAGG
GGAGAAATTGTGTTTCCTCCTTCTCCAAAGGTTACCTTTTCTATTTACCTTCATCATTATAAGAAGGTGAAA
GGATGCCAGGAGCAAGGCGGATCTACGGGACTTTTGAAAAGAAATGTACTGACCTTTGGCTGTAAAACTGTGTC
ATGAGAACAGAAAGCCCTGAGAGAAGAAGACAGCCATTCATGGGATCTATGGCGCACTCTGTGCTAGGGCAGAAT
GCCAGGGAAGAGCTGCCTGTCTTCAGCGCCCTTGCTGGGAACCACACGCCAGAACCCGACCCTGCCATGCTTTGT
GCTTCAGGCAGCAGGACCCACCCCTAACAGAGTCTCAAGTCAGACACTTAA

WO 2004/030615

PCT/US2003/028547

670/6881
FIGURE 623

MAGTKMGREDSVLDTAWGGSAAARETHAGAALSLVSLPSTGLRCGGTTERTSLRVSSALDGVEEPWKLYLQKLTAA
ALSLAAGKWERESKRKGGKGGSPCGQQERVHDSTRIKTKALWSEFRKAEGDTKGGDKAQVKDEPQNR SARLSAKP
APPKPEPKPKKAPAETVPKGKKKGKAVAGKEGNNPAENGDAKTDQAQKAEGAGDAKANLLPRCGSKEMKGSVWQRR
GEIVFPPSPKVHLFYFTFIHKKVKGCQEQQGSTGLLKRNVLTFGCKNCVMRTESPERRRQPFMGSMHSLV LGQN
AREELPVFSALAGNHTPEPDPAMLCASGSRTPLTESQVRH

WO 2004/030615

PCT/US2003/028547

671/6881
FIGURE 624

AAGAAGCTGCCGTTGTTCTGGGTACTACAGCAGAAGGGTATCGGGAAGCGAGCACCCCAGTCTGAGATGGCTCCT
GCCGGTGTGAGCCTGAGGGGCCACCATCCTCTGCCTCCTGGCCTGGGCTGGCCTGGCTGCAGGTGACCGGGTGTAC
ATACACCCCTTCCACCTCGTCATCCACAATGAGAGTACCTGTGAGCAGCTGGCAAAGGCCAATGCCGGGAAGCCC
AAAGACCCACCTTCATACCTGCTCCAATTCAGGCCAAGACATCCCCTGTGGATGAAAAGGCCCTACAGGACCAG
CTGGTGCTAGTCGCTGCAAACTTGACACCGAAGACAAGTTGAGGGCCGCAATGGTTCGGGATGCTGGCCAACTTC
TTGGGCTTCCGTATATATGGCATGCACAGTGAGCTATGGGGCGTGGTCCATGGGGCCACCGTCCTCTCCCCAACG
GCTGTCTTTGGCACCCCTGGCCTCTCTCTATCTGGGAGCCTTGGACCACACAGCTGACAGGCTACAGGCAATCCTG
GGTGTTCCTTGGAAGGACAAGAACTGCACCTCCCGGCTGGATGCGCACAAGGTCCTGTCTGCCCTGCAGGCTGTA
CAGGGCCTGCTAGTGGCCAGGGCAGGGCTGATAGCCAGGCCCAGCTGCTGCTGTCCACGGTGGTGGGCGTGTTT
ACAGCCCCAGGCCTGCACCTGAAGCAGCCGTTTGTGCAGGGCCTGGCTCTCTATACCCCTGTGGTCTCTCCACGC
TCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAAGATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAG
ACTGGCTGCTCCCTGATGGGAGCCAGTGTTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGGAAG
ATGAAGGGCTTCTCCCTGCTGGCCGAGCCCCAGGAGTTCTGGGTGGACAACAGCACCTCAGTGTCTGTTCCCATG
CTCTCTGGCATGGGCACCTTCCAGCACTGGAGTGACATCCAGGACAACCTTCTCGGTGACTCAAGTGCCCTTCACT
GAGAGCGCCTGCCTGCTGCTGATCCAGCCTCACTATGCCTCTGACCTGGACAAGGTGGAGGGTCTCACTTTCCAG
CAAACTCCCTCAACTGGATGAAGAACTGTCTCCCGGACCATCCACCTGACCATGCCCCAACTGGTGTGCAA
GGATCTTATGACCTGCAGGACCTGCTCGCCAGGCTGAGCTGCCCGCCATTCTGCACACCGAGCTGAACCTGCAA
AAATTGAGCAATGACCGCATCAGGGTGGGGGAGGTGCTGAACAGCATTTTTTTTGTAGCTTGAAGCGSATGAGAGA
GAGCCACAGAGTCTACCCAACAGCTTAACAAGCCTGAGGTCTTGGAGGTGACCCTGAACCGCCATTCTGTGTTT
GCTGTGTATGATCAAAGCGCCACTGCCCTGCACTTCTTGGGCCGCGTGGCCAACCCGCTGAGCACAGCATGAGGC
CAGGGCCCCAGAACACAGTGCCCTGGCAAGGCCTCTGCCCCCTGGCCTTTGAGGCAAAGGCCAGCAGATAACAA
CCCCGGACAAATCAGCGATGTGTCACCCCCAGTCTCCACCTTTTCTTCTAATGAGTCGACTTTGAGCTGGAAAG
CAGCCGTTTCTCCTTGGTCTAAGTGTGCTGCATGGAGTGAGCAGTAGAAGCCTGCAGCGGCACAAATGCACCTCC
CAGTTTGCTGGGTTTATTTTAGAGAATGGGGGTGGGGAGGCAAGAACCAGTGTGTTAGCGCGGGACTACTGTTCCA
AAAAGAATTCCAACCGACCAGCTTGTTTGTGAACAAAAAAGTGTTCCTTTTCAAGTTGAGAACAAAAATTGGG
TTTTAAATTAAAGTATACATTTTGCATTGCCTTCGGTTTGTATTTAGTGTCTTGAATGTAAGAACATGACCTC
CGTGTAGTGTCTGTAATACCTTAGTTTTTCCACAGATGCTTGTGATTTTTGAACAATACGTGAAAGATGCAAGC
ACCTGAATTTCTGTTTGAATGCGGAACAATAGCTGGTTATTTCTCCTTGTGTTAGTAATAAACGTCTTGCCAC

WO 2004/030615

PCT/US2003/028547

672/6881
FIGURE 625

MRKRAPQSEMAPAGVSLRATILCLLAWAGLAAGDRVYIHPFHLVIHNESTCEQLAKANAGKPKDPTFIPAPIQAK
TSPVDEKALQDQLVLVAAKLDTEKLRAMVGMLANFLGFRIYGMHSELWGVVHGATVLSPTAVFGTLASLYLGA
LDHTADRLQAILGVPWKDKNCTSRDAHKVLSALQAVQGLLVAQGRADSQAQLLLSTVVGFTAPGLHLKQPFVQ
GLALYTPVVLPRSLDFTELDVAAEKIDRFMQAVTGWKTGCSLMGASVDSTLAFNTYVHFQGMKGFSLLAEPQEF
WVDNSTSVSVPMLSGMGTFQHWSIDIQDNFSVTQVPFTESACLLLIQPHYASDLKVEGLTFQQNSLNWMKKLSPR
TIHLTMPQLVLQGSYDLQDLLAQAEIPAILHTELNLQKLSNDRIRVGEVLNSIFFEADEREPTTESTQQLNKPE
VLEVTLNRPFLFAVYDQSATALHFLGRVANPLSTA

WO 2004/030615

PCT/US2003/028547

673/6881
FIGURE 626

GAATTTCGGCACGAGCCGGGATCCTGTGTAGCGGCTGCAGAGGGTGCCGCCGCCCTAGGCGAAGTAGGGCCGTCCT
GAGCGAAAAGAACCGCCCCCAGCAGGAGCACCACCACGGCTTAGCAAAGAATCCCAGACCCCGCCCGGGAAGGCAG
CCGCACCAATGGAGTCTTCCAGTTTCATCTAACTCTTATTTCTCCGTTGGCCCAACCAAGTCCCAGCGCTGTCTGTCT
CCTCTACTCGAAGGAGCTCAAAAAGTGGGATGAGTTTGAAGATATTTTAGAAGAGAGGAGGCATGTCAGTGACTT
GAAATTTGCAATGAAATGCTACACACCTCTTGTCTATAAGGGAATTACTCCATGTAAACCAATTGATATTAAATG
TAGTGTTCTCAATTCTGAGGAGATTCAATTATGTCAATAACAGCTTTCCAAGGAATCCCTTCAATCTGTGGATGT
CCTCCGAGAGGAAGTGAGTGAGATCTTAGATGAAATGAGTCACAACTGCGTCTTGGAGCCATTCGGTTTTGTGC
CTTCACCCCTGAGCAAAAGTATTTAAACAAATTTTCTCGAAGGTGTGTGTAAATGAAGAAGGTATTCAGAACTACA
AAGAGCCATCCAGGAGCATCCTGTTGTTCTGCTGCCTAGTCATCGAAGTTACATTGACTTCCTCATGTTGTCTTT
TCTTCTATACAATTATGATTTGCCTGTGCCAGTTATAGCAGCAGGAATGGACTTCCTGGGAATGAAAATGGTTGG
TGAGCTGCTACGAATGTGCGGTGCCTTTTTTCATGCGGCGTACCTTTGGTGGCAATAAACTCTACTGGGCTGTATT
CTCTGAATATGTAAAACTATGTTACGGAATGGTTATGCTCCTGTTGAATTTTCTCGAAGGGACAAGAAGCCG
CTCTGCCAAGACATTGACTCCTAAATTTGGTCTTCTGAATATTGTGATGGAGCCATTTTTTAAAGAGAAGTTTT
TGATACCTACCTTGTTCCCAATTAGTATCAGTTATGATAAGATCTTGGAAGAACTCTTTATGTGTATGAGCTTCT
AGGGGTTTCTAAACCAAAAGAGTCTACAACCTGGGTTGCTGAAAGCCAGAAAGATTCTCTCTGAAAATTTTGAAG
CATCCATGTGTACTTTGGAGATCCTGTGTCACTTCGATCTTTGGCAGCTGGGAGGATGAGTCGGAGCTCATATAA
CTTGGTTCCAAGATACATTCCTCAGAAACAGTCTGAGGACATGCATGCCTTTGTCACTGAAGTTGCCACAAAAT
GGAGCTTCTGCAAAATGAAAACATGGTTTTGAGCCCCCTGGACCCTAATAGTTGCTGTTCTGCTTCAGAACCGGCC
ATCCATGGACTTTGATGCTCTGGTGGAAAAGACTTTATGGCTAAAAGGCTTAACCCAGGCATTTGGAGGGTTTTCT
CATTTGGCCTGATAATAAACCTGCTGAAGAAGTTGTCCCGGCCAGCATTCTTCTGCATTCCAACATTGCCAGCCT
TGTCAAAGACCAGGTGATTCTGAAAGTGGAATCCGGAGACTCGGAAGTGGTCGATGGGCTTATGCTCCAGCACAT
CACTCTCCTCATGTGCTCAGCTTATAGGAACCAGCTGCTCAACATTTTTGTGCGCCCATCCTTAGTAGCAGTAGC
ATTGCAGATGACACCAGGGTTCAGGAAAGAGGATGTCTACAGTTGCTTTTCGCTTCTACGTGATGTTTTTGCAGA
TGAGTTCATCTTCTTCCAGGAAACACACTAAAGGACTTTGAAGAAGGCTGTTACCTGCTTTGTAAAAGTGAAGC
CATACAAGTGACTACGAAAGACATCCTAGTTACAGAGAAAGGAAATACTGTGTTAGAATTTTTAGTAGGACTCTT
TAAACCTTTTGTGGAAGCTATCAGATAATTTGCAAGTACCTTTTGAGTGAAGAAGAGGACCCTTCAGTGAGGA
ACAGTACTTGGCTGCAGTCAGAAAATTCACAAGTCAGCTTCTCGATCAAGGTACCTCTCAATGTTATGATGTATT
ATCTTCTGATGTGCAGAAAAACGCCTTAGCAGCCTGTGTGAGGCTCGGAGTAGTGGAGAAGAAGAAGATAAATAA
TAACTGTATATTTAATGTGAATGAACCTGCCACAACCAAATTAGAAGAAATGCTTGGTTGTAAGACACCAATAGG
AAAACCAGCCACTGCAAACTTTTAATAATCAACAAATAGTTATGGAAAATTCGGTCACGTAATTACTCTCATCGA
AGGACTCATTACAACAAACAGGAAGTAAAGGAAGAGACACATCCTCTCATACTCCCTGAGACTCTGAGAACAGT
GGACGCAGAGGGAAGAGATGATCATTGGAAGCAATCAGTTTACTCTTCCCCACCACAGTGTTAAAAGGCGTTTTG
TATCTGACACTATGTGTGTGTTTTAAATAAACCTTTTGGAAACATGAAAAAAAAAAAAAAAAAACTCGAG

WO 2004/030615

PCT/US2003/028547

674/6881
FIGURE 627

MESSSSSNSYFSVGPTSPSAVLLYSKELKKWDEFEDILEERRHVSDLKFAMKCYTPLVYKGITPCKPIDIKCSV
LNSEEIHYVIKQLSKESLQSVDLREEVSEILDEMSHKLRGAI RFCAFTLSKVFKQIFSKVCVNEEGIQKLQRA
IQEHPVLLPSHRSYIDFLMLSFLLYNYDLPVPVIAAGMDFLGMKMGELLRMSGAFFMRRTFGGNKLYWAVFSE
YVKTMLRNGYAPVEFFLEGTRSRSAKTLTPKFGLLNIVMEPFFKREVFDTYLPISISYDKILEETLYVYELLGV
PKPKESTTGLLKARKILSENFGSIHVYFGDPVSLRSLAAGRMSRSSYNLVPRYIPQKQSEDMHAFVTEVAYKMEL
LQIENMVLSPWTLIVAVLLQNRPSMDFDALVEKTLWLKGLTQAFGGFLIWPDNKPAEEVVPASILLHSNIASLVK
DQVILKVDSGDSEVVDGLMLQHITLLMCSAYRNQLLNIFVRPSLVAVALQMTPGFRKEDVYSCFRFLRDVFADEF
IFLPGNTLKDFEEGCYLLCKSEAIQVTTKDILVTEKNTVLEFLVGLFKPFVESYQICKYLLSEEDHFSEEQY
LAAVRKFTSQLLDQGTSQCYDVLSSDVQKNALAACVRLGVVEKKKINNNCIFNVNEPATTKLEEMLGCKTPIGKP
ATAKL

WO 2004/030615

PCT/US2003/028547

675/6881
FIGURE 628

CTCTTCCTAAGCCGGCGCTCGGCAAGTTCTCCCAGGAGAAGGCCATGTTTCAGTACGAGCGCCAAGATCGTGAAGC
CTAATGGCGAGAAGCCGGACGAGTTTCGAGTCCCGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTTGGACC
TCAAGGCTCAGCTCAGGGAGCTGAATATTATGGCAGCCAAGGAAATTGAGGTTGGTGGTGGTCAGAAAGCTATCA
TAATCTTTGTTCCCGTTCCTCAACTGAAATCTTTCCAGAAAATCCAAGTCCGGCTAGTATGTGAATTGGAGAAAA
AGTTCAGTGGGAAGCATGTTGTCTTTATCGCTTAAAGGAGAATCCTGCCTAAGCCAACCTTGAAAAAGCTGTACAA
AATATAAGCAAAAGCATCCCAGGAGCCATACTCTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCA
CAAGCAAAATTGTGGGCAAGAGAATCCGCGTGAAACTAGATGGCAGCCGGCTCATGAAGGTTTCAATTTGGACAAAG
CACAGCAGAACAATGTGGAACACAAGGTTGAAACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTA
ATTTTGAATTCACAGAGTTTCAATTGTAAACAAAAATGACTAAATAAAAAATATATATTCACAGT

WO 2004/030615

PCT/US2003/028547

676/6881
FIGURE 629

MFSTSAKIVKPNGEKPDEFESRISQALLELEMNLDLKAQLRELNIMAAKEIEVGGGQKAIIFVVPVQLKSFQKI
QVRLVCELEKKFSGKHVVFI AKRRILPKPTWKSCITKYKQKHPRSHLTAVHDAILEDLVFTSKIVGKRIRVKLDG
SRLMKVHLDKAQQNNVEHKVETFSGVYKKLMGKDVNFEPFQQL

WO 2004/030615

PCT/US2003/028547

677/6881
FIGURE 630

GTCGCGACCCCTGGTCCGGACCTGACCTGAATTGCGACCCCAACCTGGACTGCTCCCCTGACCGCAACCCCTACCC
CCGCCCACCAGTATGGCCCCGGGCACGTGTTCCCTAACGGGGCCCCCAGGAGTTGGAAAAACAACATTGATCCATAAA
GCCAGTGAGGTTTTAAATCCTCTGGTGTGCCTGTTGATGGATTTTATACCGAAGAAGTCAGACAGGGAGGGAGA
AGAATAGGATTTCGATGTCGTCACGTTGTCCGGCACCCGGGGGCCCTTTATCGAGAGTTGGGTAGAGCCTCCACCT
GGAAAACGTGAATGCCGAGTTGGGCAGTATGTGGTTCGACCTGACTTCTTTTGAGCAGTTGGCACTACCCGTCTTG
AGGAATGCCGACTGCAGCAGTGGCCCAGGGCAAAGAGTGTGCGTCATCGATGAGATTGGGAAGATGGAGCTCTTC
AGTCAGCTTTTCATTCAAGCTGTTTCGTCAGACGCTGTCTACCCCAGGGACTATAATCCTTGGCACAATCCAGTT
CCTAAAGGAAAGCCACTGGCTCTTGTTAGTAAGAAATCAGAAACAGAAAGGATGTGAAGGTGTTTAAATGTCACCAAG
GAAAACAGAAACCACCTTCTGCCAGATATCGTGACGTGCGTGCAGAGCAGCAGGAAGTGAAGACACGTGCATTCC
TGCCTTCCGTGAAGGAGTGGCCAGTTCAAGAGGAGCCTGATGGAGCCCTGCCTGTGAGGCTGTATGCCTATGGG
GTTATGGAACCTTGTGGGCTTTTCTAGAGAAACTCAACAGCTGTTTCCATAAAATGTTTAAAAGATCAAATTA
GCCTTAATGCTGGATTGTCTGTACAAGATTAACCTATCCATTGTGGCTTATCTATGCTTAAAGATTCTTGTATTAT
TTAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

678/6881
FIGURE 631

MARHVFLTGPPGVGKTTLIHKASEVLKSSGVPVDGFYTEEVROGGRRIGFDVVTLSGTRGPLSRVGLEPPPGKRE
CRVGQYVVDLTSFEQLALPVLNADCSSGPGQRVCFIDEIGKMEFSQLFIQAVRQTLSTPGTIILGTIPVPGK
PLALVEEIRNRKDVKFNVTKENRNHLLPDIVTCVQSSRK

WO 2004/030615

PCT/US2003/028547

679/6881
FIGURE 632

GCAAGATGGCAGAAAGTAGAGCAGAAGAAGAAGCGGACCTTCCGCAAGTTCACCTACCGCGGCGTGGACCTGGACC
AGCTGCTGGACATGTCCTACGAACAGCTGATGCAGCTGTACAGTGCGCGCCAGCGGCGGCGGCTGAACCGGGGCC
TGCGGCGGAAGCGGCACTACCTGCTGAAGCGCCTGCGCAAGGCCAAGAAGGAGGCGCCGCCCATGGAGAAGCCGG
AAGTGGTGAAGACGCACCTGAGGGACGTGATCATCCTGCCCGAGGTGGTGGGCAGCATGGTGGGCGTCCACAACG
GCAAGACCTTCACCTACAAGCCCGTAAAGCAATGCCGGTCCGGCATCGGCGCCACCCACTCCTTCTGCTTCATCC
CTCTCAAGTAGTGGCTCAGCTAATAAAGGCGCACATG

WO 2004/030615

PCT/US2003/028547

680/6881
FIGURE 633

MAEVEQKKKRTFRKFTYRGVDLDQLLDMSYEQLMOLYSARQRRRLNRGLRRKRHYLLKRLRKAKKEAPPMEKPEV
VKTHLRDVIIILPEVVGSMVGVHNGKTFTYKPVKQCRSGIGATHSFCFIPLK

WO 2004/030615

PCT/US2003/028547

681/6881
FIGURE 634

ACCATGTCTATTCTCAAGATCCATGCCAGGGAGCTCTTTGACTCTCGTGGGAATCCCAGTGTGAGGTTGATCTC
TTCACCTCAGAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCAACTGGTATCTATGAGGTCCTAGAGCTC
CAGGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGCCTGTTGAGCCCATCAATAAACTATTGCA
CCTGTCCTGGTTAGCAAGAACTGAACGTACAGAACTTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAG
CTCTAGCCCTTGCAAGTCATGTAATTGGCCCAAATCACCGGAGCCACGTGACCCTCCAGTGTATCTCCGGGGTGGC
CACAGGCAAGATCCCCAGTGATTTTGTGCTCAAAATAAAAAGCCTCATTGACCCATGAG

WO 2004/030615

PCT/US2003/028547

682/6881
FIGURE 635

MSILKIHARELFD SRGNPTVEVDLFTSEGLFRAAVPSGASTGIYEVLELQDNDKTRYMGKGVSKPVEPINKTIAP
VLVSKKLNVTPELLQKPSSLEPCWQL

WO 2004/030615

PCT/US2003/028547

683/6881
FIGURE 636

CCCAGAAATTCTACCCAAGCTCCCTCAGCACCAATGTACCGAGCACTTCGGCTCCTCGCGCGCTCGCGTCCCCCTCG
TGCGGGCTCCAGCCGAGCCTTAGCTTCGGCTCCCGGCTTGGGTGGCGCGGCCGTGCCCTCGTTTTGGCCTCCGA
ACGCGGCTCGAATGGCAAGCCAAAATTCCTTCCGGATAGAATATGATACCTTTGGTGAACATAAGGTGCCAAATG
ATAAGTATTATGGCGCCAGACCGTGAGATCTACGATGAACCTTAAAGATTGGAGGTGTGACAGAACGCATGCCAA
CCCCAGTTATTAAAGCTTTTGGCATCTTGAAGCGAGCGGCCGCTGAAGTAAACCAGGATTATGGTCTTGATCCAA
AGATTGCTAATGCAATAATGAAGGCAGCAGATGAGGTAGCTGAAGGTAAATTAATGATCATTTTCCTCTCGTGG
TATGGCAGACTGGATCAGGAATCAGACAAATATGAATGTAAATGAAGTCATTAGCAATAGAGCAATTGAAATGT
TAGGAGGTGAACCTTGGCAGCAAGATACCTGTGCATCCCAACGATCATGTTAATAAAAGCCAGAGCTCAAATGATA
CTTTTCCACAGCAATGCACATTGCTGCTGCAATAGAAGTTCATGAAGTACTGTTACCAGGACTACAGAAGTTAC
ATGATGCTCTTGATGCAAAATCCAAAGAGTTTGCACAGATCATCAAGATTGGACGTACTCATACTCAGGATGCTG
TTCCACTTACTCTTGGGCAGGAATTTAGTGTTATGTTCAACAAGTAAATATGCAATGACAAGAATAAAAGCTG
CCATGCCAAGAACTATGAGCTCGCAGCTGGAGGCACTGCTGTTGGTACAGGTTTAAATACTAGAATTGGCTTTG
CAGAAAAGGTTGCTGCAAAAGTGGCTGCACTTACAGGCTTGCCTTTTGTCACTGCTCCGAATAAATTTGAAGCTC
TGGCTGCTCATGACGCTCTGGTTGAGCTCAGTGGAGCCATGAACACTACTGCCTGCAGTCTGATGAAGATAGCAA
ATGATATTTCGATTTTGGGTTCTGGTCCCTCGGTACAGGTCTGGGAGAATTGATCTTGCCTGAAAATGAACCAGGAA
GCAGTATCATGCCAGGCAAGGTGAACCTACTCAGTGTGAAGCAATGACCATGGTTGCAGCCCAAGTCATGGGGA
ACCATGTTGCTGCTCACTGTCGGAGGCAGCAATGGACATTTTGAAGTTGAATGTTTTCAAGCCAATGATGATTAAAA
ATGTGTTACACTCAGCCAGGCTGCTGGGGGATGCTTCAGTTTCCTTTACAGAAAACCTGCGTGGTGGGAATCCAGG
CCAATACAGAAAGGATCAACAAGCTGATGAATGAGTCTCTAATGTTGGTGACAGCTCTCAATCCTCATATAGGGT
ATGACAAGGCAGCAAAGATTGCTAAGACAGCACAAAAATGGATCAACCTTAAAGGAACTGCTATCGAACTTG
GCTATCTCACAGCAGAGCAGTTTGACGAATGGGTAAAACCTAAGGACATGCTGGGTCCAAAGTGATTTACATAAA
TTTATAATGAAAATAAACATGTATAAAATTTAAAAAACAGACTCCCATTCTTAAAAACGGATAAGTTTGAAAG
GAACTGCTATTGAACCTAAGCATCTCTAGCAGAGCAATTTGATCAGTATATAAAACCTAGGATGTGCTAGGTC
TAAGATGGATTAAACAAGTATAAAATAAAATACATTTATAAAATAAAAAGGAAAACAGACTTAAAA

WO 2004/030615

PCT/US2003/028547

684/6881
FIGURE 637

MYRALRLLARSRLVRAPAAALASAPGLGGAAVPSFWPPNAARMASQNSFRIEYDTFGELKVPNDKYYGAQTVRS
TMNFKIGGVTERMPTPVIKAFGILKRAAAEVNQDYGLDPKIANAIMKAADEVAEGKLNDFPLVWQTGSGTQTN
MNVNEVISNRAIEMLGGEIGSKIPVHPNDHVNKSQSSNDTFPTAMHIAAAIEVHEVLLPGLQKLHDALDAKSKEF
AQIIKIGRTHTQDAVPLTLGQEFSGYVQVQVKYAMTRIKAAMPRIYELAAGGTAVGTGLNTRIGFAEKVAAKVAAL
TGLPFVTAPNKFEALAAHDALVELSGAMNTTACSLMKIANDIRFLGSGPRSGLGELILPENEPGSSIMPGKVNPT
QCEAMTMVAAQVMGNHVAVTVGGSNGHFELNVFKPMMIKNVLHSARLLGDASVSFTENCVVGIQANTERINKLMN
ESLMLVTALNPHIGYDKAAKIAKTAHKNGSTLKETAIELGYLTAEQFDEWVKPKDMLGPK

WO 2004/030615

PCT/US2003/028547

685/6881
FIGURE 638

GGGXTCGGCCCTCCCCCTCTTCTGCGCTCTCTTCGGGATACACGTGGGCTTCGGGCTGGGCCGCGCAGTTTTT
CTTTGGCTTTCTCGAATCATCGAGGAGACTGGCAAAATTAGTAATGTCTTTAGACTGCGTCACTAGCGCCAATCG
AATTCGTAGTTGATTGTTCTTTGAATTCACATTTGAGTCCTCGGTTAAACCTCAGTTAAAAAGCAGGATAAAGT
CGAGCTGCTTTGGTTCTCGGAACGGAAAAGCGTTTTTTTTGTTGTTTAGAGGCTTGGCCTTTATGGGGCTCGTGTG
TGTTTTAGGGGACGGCAAAACAGAACAGAAAGGCGGAGATAAAAAGAGGGGTGTTAAAGACCACGAGAAGATCA
TGGCCGTGGATATTTTGAGTACATTGAAGAGAACAAGTATAGCAGAGCCAAATCTCCTCAGCCACCTGTTGAAGA
AGAAGATGAACACTTCGATGACACAGTGGTTTTGCTTTGATACTTATAATTGTGATCTACATTTTAAATATCAAG
AGATCGTCTCAGTGCTTCTTCCCTTACAATGGAGAGTTTTGCTTTTTCTTTGGGCTGGAGGAAGAGCATCCTATGG
TGTGTCAAAGGCAAAGTGTGTTTTGAGATGAAGGTTACAGAGAAGATCCCAGTAAGGCATTTATATACAAAAGA
TATTGACATACATGAAGTTTCGTATTGGCTGGTCACTAACTACAAGTGAAGTGTACTTGGTGAAGAAGAATTTTC
TTATGGGTATTTCTTAAAAGGAATAAAAACATGCAACTGTGAGACTGAAGATTATGGAGAAAAGTTTGATGAAAA
TGATGTGATTACATGTTTTGCTAACTTTGAAAAGTGTGAAGTAGAACTCTCGTATGCTAAGAATGGACAAGATCT
TGGCGTTGCCCTTCAAATCAGTAAGGAAGTTCTTGCTGGACGGCCACTGTTCCCGCATGTTCTCTGCCACAACCTG
TGCAGTTGAATTTAATTTTGGTCAGAAGGAAAAGCCATATTTCCAATACCTGAAGAGTATACTTTTCATCCAGAA
CGTCCCTTAGAGGATCGAGTTAGAGGACCAAAGGGGCTGAAGAGAAGAAAGATTGTGAAGTTGTGATGATGAT
TGGCTTGCCAGGAGCTGGAAAACTACCTGGGTTACTAAACATGCAGCAGAAAATCCAGGGAAATATAACATTCT
TGGCACAAATACTATTATGGATAAGATGATGGTGGCAGGTTTTAAGAAGCAAATGGCAGATACTGGAAAACCTGAA
CACACTGTTGCAGAGAGCCCCCAGTGTCTTGGGAAATTTATTGAGATTGCTGCCCGAAAGAAGCGAAATTTTAT
TCTGGATCAGACAAATGTGTCTGCTGCTGCCCAGAGGAGAAAAATGTGCCTGTTTGCAGGCTTCCAGCGAAAAGC
TGTTGTAGTTTGCCCAAAAGATGAAGACTATAAGCAAAGAACACAGAAGAAAGCAGAAGTAGAGGGGAAAGACCT
ACCAGAACATGCGGTCTCAAATGAAAGGAACTTTACCCTCCAGAGGTAGCTGAGTGCTTTGATGAAATAAC
CTATGTTGAACTTCAGAAGGAAGAAGCCCCAAAACCTCTTGAGCAATATAAGGAAGAAAGCAAAAAGGCTCTTCC
ACCAGAAAAGAAACAGAACACTGGCTCAAAGAAAAGCAATAAAAATAAGAGTGGCAAGAACCAGTTTAACAGAGG
TGGTGGCCATAGAGGACGTGGAGGATTCAATATGCGTGGTGGAAATTCAGAGGAGGAGCCCCCTGGGAATCGTGG
CGGATATAATAGGAGGGGCAACATGCCACAGAGAGGTGGTGGCGGTGGAGGAAGTGGTGAATCGGCTATCCATA
CCCTCGTGCCCCGTGTTTTCTTGGCCGTGGTAGTTACTCAAACAGAGGGAACTACAACAGAGGTGGAATGCCCAA
CAGAGGGAACATAACCAGAACTTCAGAGGACGAGGAAACAATCGTGGCTACAAAAATCAATCTCAGGGCTACAA
CCAGTGGCAGCAGGTCATTTCTGGGTCAGAAGCCATGGAGTCAGCATTATCACCAAGGATATTATTGAATACC
CAAATAAAACGAACTGATACATATTTCTCCAAAACCTTCACAAGAAAGTCGACTGTTTTCTTTAGTAGGCTAACTT
TTTAAACATTCCACAAGAGGAAGTGCCTGCGGGTTCCTTTTTTAGAAGCTTTGTGGGTTGATTTTTTTCTTTTC
TTTTTGTACATTTTAAATTGCAGTTTAAAAGTGAATCGTAAGAGAACCTCAGCATTGTGCACGATAAGAGAATG
TGTCAGTATTTAGGGTTCTACATTTTATCTGTAAAATGTGACTTTTTTTTTTTTTATCACAAACAGAAGTAAAA
ATTGTCACAATATAATAGAAATGTTAGCAACCAGATTTCATGTAAGGACTAAGTGGTCCCTCATGAATTGCATTAAG
ACTCTGTACTGCTCATATTACACTCCATCCTCTCTGTAGTTTGTGGGTAGTGGAGGGGGTAAGCTAAATCATAG
TTTCTGACAATAACTGGGAAGGTTTTTTCTTAAAATAACAATGGAATTGGTATAATTGGGATTGAAAACATAAAC
TTGGAACATAAGATAGAGAAGATGGAGTGTATGTAGAAGGGCTGTTAAAAATGTAAAACCTGGTTCATTATTGT
GGAGGCTCAAACCTTGTGAAGGTTAATACCATAATTTTTCCATTGTTCTGCATTTTGATTCTGAAAAGAAAGCTG
GCTTTGGCCATTTCTTATTAATAAAAAAAGTTGTTGTAATCCAGTTGTCTAATGGGATCTATATGAAGTAGCCATG
TCTGTATGCCCTTCTCCACAAAATACTGTATAACTAGTGTGCTTGTAGTAGTTAACTCCACCATCTTTGTAAGC
TAATGAAATTGTGAGTCACCCATTTATATCTTAATTTTTAATCATGTGAGTTCTTGAATGGGTATCTCCTTAGCC
TGCTGATTTCTTTTTCTTTCTAAAGAAAGTGGGTGGAGAAATTAATTTAGACGTTTGTGCAATAAAAAGAATT
CATTTT

WO 2004/030615

PCT/US2003/028547

686/6881
FIGURE 639

GGCGTTGCCGGCCGTGGGTGCTCTGGCCACAGTGAGTTAGGGGCGTCGGAGCGGGTTTCTCCAACCGCAATCGGC
TCCGCTCAAGGGGAGGAGGAGAGTCCCTTCTCGGAAGGCCTAAGGAAACGTGTCGTCTGGAATGGGCTTGGGGGC
CACGCTGCACATCTCCGCGAGACAGAGGGATAAAGTGAAGATGGTGCTGTTATTGTTACCTCGAGTGCCACATG
CGACCTCTGAGATATGTACACAGTCATTCTTACTATCGCACTCAGCCATTCTTACTACGCTAAAGAAGAAATAAT
TATTCGAGGATATTTGCGCTGGCCCAGAAGAACTTATGTAAATTTTCATGAACTATTATATCCGTTTTCTCGGAG
TGAGAGAAAACCTCTTTTAGATATCATCTGAGAGAACTAGTGAATCCCAGTCACTGAGTGGAGTTGAGAGTCTAA
GAACCTCTGAAATTTGAGAACTGCTGGACCAGAGCCTTTAGAGCTCTGATAAGGTGTCAACAGGGTAGTTAATTT
GGCACCATGGGGATACAGGGATTGCTACAATTTATCAAAGAAGCTTCAGAACCCATCCATGTGAGGAAGTATAAA
GGGCAGGTAGTAGCTGTGGATACATATTGCTGGCTTCACAAAGGAGCTATTGCTTGTGCTGAAAACTAGCCAAA
GGTGAACCTACTGATAGGTATGTAGGATTTTGTATGAAATTTGTAAATATGTTACTATCTCATGGGATCAAGCCT
ATTCTCGTATTTGATGGATGTACTTTACCTTCTAAAAAGGAAGTAGAGAGATCTAGAAGAGAAAGACGACAAGCC
AATCTTCTTAAGGGAAAGCAACTTCTTCGTGAGGGGAAAGTCTCGGAAGCTCGAGAGTGTTCACCCGGTCTATC
AATATCACACATGCCATGGCCCCACAAAGTAATTAAGCTGCCCCGGTCTCAGGGGGTAGATTGCCTCGTGGCTCCC
TATGAAGCTGATGCGCAGTTGGCCTATCTTAACAAAGCGGGAATTTGTGCAAGCCATAATTACAGAGGACTCGGAT
CTCCTAGCTTTTGGCTGTAAAAAGGTAATTTTAAAGATGGACCAGTTTGGAAATGGACTTGAAATTGATCAAGCT
CGGCTAGGAATGTGCAGACAGCTTGGGGATGTATTACGGAAGAGAAGTTTCGTTACATGTGTATTCTTTCAGGT
TGTGACTACCTGTCTACTGCGTGGGATTGGATTAGCAAAGGCATGCAAAGTCTTAAGACTAGCCAATAATCCA
GATATAGTAAAGGTTATCAAGAAAAATTGGACATTATCTCAAGATGAATATCACGGTACCAGAGGATTACATCAAC
GGGTTTATTCGGGCCAACAAATACCTTCTCTATCAGCTAGTTTTTGATCCCATCAAAGGAACTTATTCCTCTG
AACGCCATGAAGATGATGTTGATCCTGAAACACTAAGCTACGCTGGGCAATATGTTGATGATTCCATAGCTCTT
CAAATAGCACTTGGAATAAAGATATAAATACTTTTGAACAGATCGATGACTACAATCCAGACACTGCTATGCCCT
GCCCATTCAAGAAGTCATAGTTGGGATGACAAAACATGTCAAAAGTCAGCTAATGTTAGCAGCACTTTGGCATAGG
AATTACTCTCCAGACCAGAGTCGGGTACTGTTTCAGATGCCCCACAATTGAAGGAAAAATCCAAGTACTGTGGGA
GTGGAACGAGTGATTAGTACTAAAGGGTTAAATCTCCCAAGGAAATCATCCATTGTGAAAAGACCAAGAAGTGCA
GAGCTGTGAGAAGATGACCTGTTGAGTCAGTATTCTCTTTCATTTACGAAGAAGACCAAGAAAAATAGCTCTGAA
GGCAATAAATCATTGAGCTTTTCTGAAGTGTTTGTGCCTGACCTGGTAAATGGACCTACTAACAATAAGAGTGTA
AGCACTCCACCTAGGACGAGAAATAAATTTGCAACATTTTACAAAGGAAAAATGAAGAAAGTGGTGAGTTGTG
GTTCCAGGGACCAGAAGCAGGTTTTTTTGAGTTCAGATTCTACTGACTGTGTATCAAAACAAAGTGAGCATCCAG
CCTCTGGATGAACTGCTGTACAGATAAAGAGAACAATCTGCATGAATCAGAGTATGGAGACCAAGAAGGCAAG
AGACTGGTTGACACAGATGTAGCACGTAATTCAAGTGATGACATTCCGAATAATCATATTCCAGGTGATCATATT
CCAGACAAGGCAACAGTGTTTACAGATGAAGAGTCCCTACTCTTTTGGAGAGCAGCAAATTTACAAGGACCATTTC
CCACCCACTTTGGGAACACTAAGAAGTTGTTTTAGTTGGTCTGGAGGTCTTGAGATTTTTCAAGAACGCCGAGC
CCCTCTCCAAGCACAGCATTGCAGCAGTTCCGAAGAAAGAGCGATTCCCCACCTCTTTGCCTGAGAATAATATG
TCTGATGTGTGCGAGTTAAAGAGCGAGGAGTCCAGTGACGATGAGTCTCATCCCTTACGAGAAGGGGCATGTTCT
TCACAGTCCCAGGAAAGTGGAGAATTCTCACTGCAGAGTTCAAATGCATCAAAGCTTTCTCAGTGCTCTAGTAAG
GACTCTGATTTCAGAGGAATCTGATTGCAATATTAAGTTACTTGACAGTCAAAGTGACCAGACCTCCAAGCTATGT
TTATCTCATTTTCTCAAAAAAGACACACCTCTAAGGAACAAGGTTTCTGGGCTATATAAGTCCAGTTCTGCAGAC
TCTCTTTCTACAACCAAGATCAAACCTCTAGGACCTGCCAGAGCCAGTGGGCTGAGCAAGAAGCCGGCAAGCATC
CAGAAGAGAAAGCATCATTAATGCCGAGAACAAGCCGGGTTACAGATCAAACCTCAATGAGCTCTGGAAAACTTT
GGATTTAAAAAAGATTCTGAAAAGCTTCTCTCTTGTAAAGAAACCCCTGTCCCCAGTCAGAGATAACATCCAATA
ACTCCAGAAGCGGAAGAGGATATATTTAACAACCTGAATGTGGCCGTGTTCAAAGAGCAATATTCCAGTAAATG
CAGACTGCTGCAAAGCTTTTGCCTGCAAGAGAATCTGATCAATTTGAAGTCCCTGTTTGGGAATGAGGCATTAT
CAGCATGAAGAATTTTTTCTATTCTGTGCCATTTAAAAATAGAATACATTTTGTATATTGACTTTAAAAAAA
AAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

687/6881
FIGURE 640

MGIQGLLQFIKEASEPIHVRKYKGQVAVD TYCWLHKGAIACAELAKGEPTDRYVGFCMKFVNMLLSHGIPIL
VFDGCTLP SKKEVERSRERRRQANLLKGKQLLREGKVSEARECFTRS INITHAMAHKVIKAARSQGVDCLVAPYE
ADAQLAYLNKAGIVQAIITEDSDLLAFGCKKVILKMDQFGNGLEIDQARLGMCRLGDVFTTEKF RYMCILSGCD
YLSSLRGIGLAKACKVLR LANNPDIVKVIKKIGHY LKMNITVPEDYINGFIRANNTFLYQLVFDPIKRKLIPLNA
YEDDVPETLSYAGQYVDDSI ALQIALGNKDINTFEQIDDYNPD TAMP AHSRSHWDDKTCQKSANVSSIWH RNY
SPRPESGTVSDAPQLKENPSTVGVERVISTKGLNLPRKSSIVKRPRSAELSEDDLLSQYSLSF TKKTKKNSSEGN
KSLSFSEVFVPDLVNGPTNKKSVSTPPRTRNK FATFLQRKNEESGAVVVPGTRSRFFC SSDSTDCVSNKVS IQPL
DETA VTDKENNLHESEYGDQEGKRLVD TDVARNSSDDIPNNHIPGDHIPDKATVFTDEESYSFESSKFTRTISP P
TLGTLRSCFSWSGGLGDFSRTPSPSPSTALQQFRRKSDSPTSLPENNMSDVSQLKSEESSDDESHPLREGACSSQ
SQESGEFSLQSSNASKLSQCSSKSDSEESDCNIKLLDSQSDQTSKLCLSHFSKKDTPLRNKVPGLYKSSSADSL
STTKIKPLGPARASGLSKKPASIQRKHHNAENK PGLQIKLNELWKNF GFKKDSEKLPPCKKPLSPVRDNIQLTP
EAEEDIFNKPECGRVQRAIFQ

WO 2004/030615

PCT/US2003/028547

688/6881
FIGURE 641

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCCACTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCTGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTACAATGGCCTATTTAGGCCCATAACCCTACGTCAC
GGCAGTCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGTCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCCACCGAAAGTCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCA

WO 2004/030615

PCT/US2003/028547

689/6881
FIGURE 642

GTCCACATGCAGAGGCTCGCTACAGAAGCTACAGAAGAAGATGGTTACATTTCAAGTGGGCAGGTGCCGTTTGCT
TATGAGCACCATCAGCCACATCAGCCACGGTTCTTTGAATTTTACCTAATTGTCTCTAATTCTTAACAATTCCTT
GAGGTGATCTGCAACTCTTTCACCATCTGTAATGCGGAGATGCAGGAAGTTGGTGTGGCCTATATCCCAGTATC
TCTTTGCTCAATCACAGCTGTGACCCCAACTGTTTCGATTGTGTTCAATGGGCCCCACCTCTTACTGCGAGCAGTC
CGAGACATCGAGGTGGGAGAGGAGCTCACCATCTGCTACCTGGATATGCTGATGACCAGTGAGGAGCGCCGGAAG
CAGCTGAGGGACCAGTACTGCTTTGAATGTGACTGTTTCCGTTGCCAAACCCAGGACAAGGATGCTGATATGCTA
ACTGGTGATGAGCAAGTATGGAAGGAAGTTCAAGAATCCCTGAAAAAAATTGAAGAAGTGAAGGCACACTGGAAG
TGGGAGCAGGTTCTGGCCATGTGCCAGGCAATCATAAGCAGCAATTCTGAACGGCTTCCCGATATCAACATCTAC
CAGCTGAAGGTGCTCGACTGCGCCATGGATGCCTGCATCAACCTCGGCCTGTTGGAGGAAGCCTTGTTCATGGT
ACTCGGACCATGGAGCCATACAGGATTTTTTTCCAGGAAGCCATCCCGTCAGAGGGGTTCAAGTGATGAAAGTT
GGCAAAGTGCAGCTACATCAAGGCATGTTTCCCAAGCAATGAAGAATCTGAGACTGGCTTTTGATATTATGAGA
GTGACACATGGCAGAGAACACAGCCTGATTGAAGATTTGATTCTACTTTTAGAAGAATGCGACGCCAACATCAGA
GCATCCTAAGGGAACGCAGTCAGAGGGAAATACGGCGTGIGTCTTTGTTGAATGCCTTATTGAGGTCACACACTC
TATGCTTTGTTAGCTGTGTGAACCTCTCCTATTGGAATTTCTGTTCCGTGTTTGTGTAGGTAAATAAAGGCAGAC
ATGGTTTGCAAACCACAAGAATCATTAGTTGTAGAGAAGCAGATTATAATAAATTCAAAACATTTGGTTGAGGA
TGCC

WO 2004/030615

PCT/US2003/028547

690/6881
FIGURE 643

CTTGCTTCGGACGCCGGATTTTGACGTGCTCTCGCGAGATTTGGGTCTCTTCCTAAGCCGGCGCTCGGCAAGTTC
TCCCAGGAGAAAAGCCATGTTCAGTTCGAGCGCCAAGATCGTGAAGCCCAATGGCGAGAAGCCGGACGAGTTCGAG
TCCGGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTCGGACCTCAAGGCTCAGCTCAGGGAGCTGAATATT
ACGGCAGCTAAGGAAATTGAAGTTGGTGGTGGTTCGGAAAGCTATCATAATCTTTGTTCCCGTTCCTCAACTGAAA
TCTTTCCAGAAAATCCAAGTCCGGCTAGTACGCGAATTGGAGAAAAAGTTCAAGTGGGAAGCATGTCGTCTTTATC
GCTCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCCGTACAAAAAATAAGCAAAAGCGTCCCAGGAGCCGT
ACTCTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCCCAAGCGAAATTGTGGGCAAGAGAATCCGC
GTCAAAC TAGATGGCAGCCGGCTCATAAAGGTTCAATTTGGACAAAGCACAGCAGAACAATGTGGAACACAAGGTT
GAAACTTTTTCTGGTGTCTATAAGAAGCTCACGGGCAAGGATGTTAATTTGAATTCCCAGAGTTTCAATTGTAA
ACAAAAATGACTAAATAAAAAAGTATATATTCACAGTAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

691/6881
FIGURE 644

MFSSSAKIVKPNGEKPDEFESGISQALLELEMNSDLKAQLRELNITAAKEIEVGGGRKAIIFVVPVQLKSFQKI
QVRLVRELEKKFSGKHVVFIAQRRILPKPTRKSRTKNKQKRPRSRTLTA VHDAILEDLVFPSEIVGKRIRVKLDG
SRLIKVHLDKAQQNNVEHKVETFSGVYKKLTGKDVNFEFPEFQL

692/6881

FIGURE 645

GGCACGAGGCGGGCCAGCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGC
GCTCAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTGCCATCTGG
ACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGGCCTCAAAGGGGATGCGGGAGA
GAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAA
AGGACAGAAAGGCAGTGTGGGTGCTCATGGAATAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGG
TGACATAGGACCCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGG
GGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCCGGTGTGCGCGA
GACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGACGCCAGCTGTCTGCCAGGGCCG
CGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCT
GGCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCG
GACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCTC
GGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGC
CTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTG
CCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATG
GCCTATGCTTAAGAGGAAAATGAAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATT
GTAGCCCCAATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATA
CAATAAAATCTTTAAGTAGTGCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

693/6881
FIGURE 646

MRGNLALVGVLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVGPTEGEKGDMDGDKGQ
KGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGEMDNQVSQLTSELKFIKNAVAGVRETE
SKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAANGLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTF
NKWRSGEPPNAYDEEDCVEMVASGGWNDVACHTTMYFMCEFDKENM

WO 2004/030615

PCT/US2003/028547

694/6881
FIGURE 647

GGCACGAGGGGCTTCTGTACCTTCCTCACGGACCTTGGTCACGGCCGACGGTGACCCCTTAGCCCAGCTCCAGT
GGGCGGGTGGCAGGGTCATGGAGGACGCTGGCGGCGGCGAGGAGACCCCGGCCCGGAGGGCCCCGACCCCCCTC
AGCTCGCGCCTCCGGAGGAGCAGGGGTTGCTCTTCCAGGAGGAAACCATCGATCTTGCGGAGATGAGTTTGGAT
CCGAAGAGAACGAGACCGCATCGGAAGGCTCGAGTCCTCTCGCGGACAAGCTGAACGAACACATGATGGAGAGCG
TCCTCATCTCTGACTCCCCAACAGCGAGGGCGACGCGGGCGACCTGGGCGGAGTGCGGGACGAAGCTGAGCCCCG
GAGGGGAAGGCGACCCAGGCCCGGAGCCCGCGGGCACCCGAGTCCCAGCGGCGAGGCCGACGGCGACTGTGCCC
CCGAGGACGCGGCACCCAGTAGCGGAGGGGCCCCGAGGCAGGACGCGGCCCGCGAGGTCCCAGGCAGCGAAGCCG
CGCGCCCGGAGCAGGAGCCTCCCGTTGCGGAGCCGGTCCCGGTGTGCACCATCTTCAGCCAGCGCGCGCCCCAG
CCTCCGGGGACGGCTTCGAGCCGAGATGGTGAAGTCGCCAGCTTCGGTGGCGCCAGCGAGGCCCTCGGCCAGGA
CACCGCCCCAGGTCTGTGAGCCAGCCCGAGCCTCAGCACGTTCTTCGGAGACACGGCCGCCAGCCACTCCTTGG
CCTCGGACTTCTTCGACTCCTTTACTACCTCCGCCTTCATTTCCGTGAGCAATCCCGGCGCGGGCTCCCCGCCCC
CCGCCAGCCCGCCTCCCTCGCTGTGCCGGGACCGAGGGGCGCCCCGAACCCGTGGCCATGCGAGGGCCCCAGG
CAGCTGCGCCCCCGGCGTCGCCAGAGCCTTTCGCGCACATCCAGGCAGTGTTCGAGGGAGTGACGACCCCTTGT
CCACCGCCCTGAGCATGAGCGAGATGGACCGGAGGAACGACGCCTGGCTTCCCGGCGAGGCTACGCGTGGAGTCC
TGCGGGCCGTGGCCACCCAGCAGCGCGGCGCGCTGTTCGTGGACAAGGAGAACCTCACCATGCCGGGCCTCAGGT
TCGACAACATCCAGGGAGATGCAGTTAAAGACTTGATGCTTCGCTTCTGGGTGAAAAAGCTGCAGCAAAGAGAC
AAGTCCTAAATGCCGACTCAGTGGAACAATCTTTTGTGGATTGAAACAGCTAATCAGCTGCAGAACTGGAGGG
CAGCAGTGGACCTGTGCGGACGTCTCTCACAGCCACGGCCAGGGCTACGGCAAGAGCGGGCTGCTCACCAGCC
ACACGACAGATTCACTGCAGCTCTGGTTTGTTCAGGCTGGCACTACTAGTGAAGTTGGGCCCTTTCCAGAATGCTG
AGATGGAATTTGAACCTTCGGAAATCTTGATCAGCCAGATCTTTATTACGAGTACTACCCGCACGTGTACCCCTG
GGCGCAGGGGCTCCATGGTCCCTTCTCGATGCGCATCTTGACGCGGAGCTTCAGCAGTACCTGGGGAACCCAC
AGGAGTCGCTGGATAGACTGCACAAGGTGAAGACTGTCTGCAGCAAGATCCTGGCCAATTTGGAGCAAGGCTTAG
CAGAAGACGGCGGCATGAGCAGCGTGACTCAGGAGGGCAGACAAGCCTCTATCCGGCTGTGGAGGTACGCTCTGG
GCCGGGTGATGTACTCCATGGCAAACGTGTCTGCTCCTGATGAAGGATTATGTGCTGGCCGTGGATGCGTATCATT
CGGTTATCAAGTATTACCCAGAGCAAGAGCCCCAGCTGCTCAGCGGCATCGGCCGGATTTCCTCCAGATTGGAG
ACATAAAAACAGCTGAAAAGTATTTTCAAGACGTTGAGAAAGTAACACAGAAATTAGACGGACTACAGGGTAAAA
TCATGGTTTTGATGAACAGCGCTTCCTTCACCTCGGGCAGAATAACTTTGCAGAAGCCACAGGTTCTTCACAG
AGATCTTAAGGATGGATCCAAGAAACGCACTGGCCAACAACAACGCTGCCGTGTGTCTGCTCTACCTGGGCAAGC
TCAAGGACTCCCTGCGGCAGCTGGAGGCCATGGTCCAGCAGGACCCAGGCACTACCTGCACGAGAGCGTGCTCT
TCAACCTGACCACCATGTACGAGCTGGAGTCTCACGGAGCATGCAGAAGAAACAGGCCCTGCTGGAGGCTGTGCG
CCGGCAAGGAGGGGGACAGCTTCAACACACAGTGCCCTCAAGCTGGCCCTAGCTGCCTCCAACACACTACGTAGAA
GGACCCGGGTCTTTGAAACTGTGTCTTGAAGCTAATGTATTAATGTGACATGGAGGAACTCAATAAACTCCTGC
TTCAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

695/6881
FIGURE 648

MLRFLGEKAAAKRQVLNADSVEQSFVGLKQLISCRNWRAAVDLCGRLLTAHGQGYGKSGLLTSHTTDSLQLWFVR
LALLVKLGFLQNAEMEFEPFGNLDQPDLYEYYPHVYPGRRGSMVPFSMRILHAELQQYLGNPQESLDR LHKVKT
VCSKILANLEQGLAEDGGMSSVTQEGRQASIRLWRSRLGRVMYSMANCLLLMKDYVLAVDAYHSVIKYYPEQEPQ
LLSGIGRISLQIGDIKTAEKYFQDVEKVTQKLDGLQGKIMVLMNSAFLHLGQNNFAEAHRFFTEILRMDPRNAVA
NNNAAVCLLYLGKLKDSLRLQLEAMVQDPRHYLHESVLFNLTMYELESSRSMQKKQALLEAVAGKEGDSFNTQC
LKLA

WO 2004/030615

PCT/US2003/028547

696/6881
FIGURE 649

AATTCGGCACGAGAAGACTTCCAGTTTGGAGTCGTTTGTGCGGGGAGGGAATGAATGGGCGCTGGGAACACGCC
CGCGAGGTGGGGACGCGCCGCGCGTAGCGAGGTCCCTAGCGTGTGAGTGGCCGGGGTCGGGTTCGCTTCCCCGCAG
CATGGGAGGACGATGCACCAGTGATCTACGGGCTGGAGTTCCAGGCACGTGCCTTAACACCTCAAACCTGCAGAAAC
AGATGCCATTTCGGTTTTTTGGTTGGGACGCAGTCTCTTAAATATGATAATCAGATCCATATCATAGATTTTGACGA
TGAAAACAACATTATAAAATAAAAAATGTCTCTCCATCAAGCGGGTGAAATCTGGCATATTAGCGCTAGCCCTGC
AGACAGAGGTGTGCTGACGACCTGCTACAACAGAACTTCAGACAGCAAAGTCCTGACATGTGCAGCCGTGTGGAG
GATGCCGAAGGAATTGGAATCAGGCAGCCACGAGTCCCTGATGATTTCATCCAGCACTGCACAGACCCTGGAGCT
GCTCTGTACCTTGACAACACAGCCCATGGCAACATGGCCTGTGTCTGTGGGAGCCAATGGGAGATGGGAAGAA
AATCATTTTCCTTGGCTGATAACCATATCCTGCTGTGGGATTTACAGGAAAGCTCGAGCCAGGCTGTGCTGGCCAG
CTCAGCGTCCCTGGAAGGGGAAGGGACAACCTGAAGTTACCTCAGGACGGTGGAGCCCACATCAACTGCACCCA
GGTGGCCACAGCGAACGACACCACCTCCGTGGCTGGGACACCCGGAGCATGAGCCAGATCTACTGCATAGAGAA
TGCCCACGGACAGCTGGTGCGGGACCTTGACTTTAATCCCAATAAGCAGTACTACTTGGCCAGCTGCGGAGACGA
CTGTAAGGTGAAGTTCTGGGACACCCGAAATGTCACCGAACCCGTGAAGACCCTGGAGGAGCACTCCCACTGGGT
GTGGAACGTCCGCTACAACCACTCTCATGACCAGCTGGTCCTCACGGGCAGCAGTGACAGCAGAGTCATCCTTTC
CAACATGGTGTCCATCTCGTCGGAGCCCTTCGGCCACTTGGTAGACGACGATGACATCAGTGACCAGGAGGACCA
CCGTTCTGAAGAGAAGAGCAAGGAGCCCTGCAGGACAACGTGATCGCCACCTACGAGGAGCACGAGGACAGCGT
CTATGCCGTGGACTGGTCTCGGCTGACCCGTGGCTGTTTGCTCCCTGAGCTATGACGGGAGGCTCGTGATCAA
CAGGGTGCCAGGGCCCTGAAGTACCACATCCTGCTATTGACTCCCGGGCCTGGGTATCCAGGTCCCATTGAGTG
GTTTTCTCTTGGCAGATTCTCAAACAGTCGCAGCTCTTTGGAGGTGACTCGTGTTCCAGGTGGATCCCTCTCTG
GGAGAGCCGCTGTTCCCTTCCTGTAGCAGCAGCATTATGAATGGGGTGAATGGGGCTATTGTGACGGCACAGC
TAATGCCCCGAACCCAGCCCTGTGCGGCAGAGACAGAGCCCACTATTATGTGAATAACAATGTTTTCTGTTTT
AAGGGTGTGAGGAGTTTCGCTTTTTAAAAAATGTCTGTTCTGTCAGTAGTAACCTCTTCTTCTTGTGAGAGTAA
AAAATGAAATAAAATAAATCCACGCTGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

697/6881
FIGURE 650

MEDDAPVIYGLEFQARALTPQTAETDAIRFLVGTQSLKYDNQIHIIDFDDENNIINKNVLLHQAGEIWHISASPA
DRGVLTTCYNRTSDSKVLTCAAVWRMPKELESGSHESPDDSSSTAQTLELLCHLDNTAHGNMACVVWEPMGDGKK
IISLADNHILLWDLQESSSQAVLASSASLEGKGQLKFTSGRWSPHHNCTQVATANDTTLRGWDTRSMSQIYCIEN
AHGQLVRDLDFNPNKQYYLASCDDCKVKFWDTNRNTEPVKTLEESHVWVNVRYNHSHDQLVLTGSSDSRVILS
NMVSISSSEPFGLVDDDDISDQEDHRSEEKSKEPLQDNVIATYEEHEDSVYAVDWSSADPWLFASLSYDGRVLIN
RVPRALKYHILL

WO 2004/030615

PCT/US2003/028547

698/6881
FIGURE 651

CCCAGGCGCAGCCAATGGGAAGGGTCGGAGGCATGGCACAGCCAATGGGAAGGGCCGGGGCACCAGCCAATGG
GAAGGGCCGGGAGCGCGCGGGCGGGAGATTTAAAGGCTGCTGGAGTGAGGGGTGCCCCGTGCACCCTGTCCCAG
CCGTCTGTCTGGCTGCTCGCTCTGCTTCGCTGCGCCTCCACTATGCTCTCCCTCCGTGTCCCGCTCGCGCCCA
TCACGGACCCGCAGCAGCTGCAGCTCTCGCCGCTGAAGGGGCTCAGCTTGGTCGACAAGGAGAACACGCCGCCGG
CCCTGAGCGGGACCCGCGTCTTGCCAGCAAGACCCGCGAGGAGGATCTTCCAGGAGCCCACGGAGCCGAAACTA
AAGCAGCTGCCCCCGCGTGGAGGATGAGCCGCTGCTGAGAGAAAACCCCGCCGCTTTGTCTATCTTCCCCATCG
AGTACCATGATATCTGGCAGATGTATAAGAAGGCAGAGGCTTCTTTTGGACCGCCGAGGAGGTTGACCTCTCCA
AGGACATTACGCACTGGGAATCCCTGAAACCCGAGGAGAGATATTTTATATCCCATGTTCTGGCTTTCTTTGCA
CAAGCGATGGCATAGTAAATGAAAACCTTGGTGGAGCGATTTAGCCAAGAAGTTCAGATTACAGAAGCCCGCTGTT
TCTATGGCTTCCAAATTGCCATGGAAAACATACATTCTGAAATGTATAGTCTTCTTATTGACACTTACATAAAAG
ATCCCAAAGAAAGGGAATTTCTCTTCAATGCCATTGAAACGATGCCTTGTGTCAAGAAGAAGGCAGACTGGGCCT
TGCGCTGGATTGGGGACAAAGAGGCTACCTATGGTGAACGTGTTGTAGCCTTTGCTGCAGTGAAGGCATTTTCT
TTTCCGGTTCTTTTGCCTCGATATTCTGGCTCAAGAAACGAGGACTGATGCCTGGCCTCACATTTTCTAATGAAC
TTATTAGCAGAGATGAGGGTTTACACTGTGATTTTGTCTGCCTGATGTTCAAACACCTGGTACACAAACCATCGG
AGGAGAGAGTAAGAGAAATAATTATCAATGCTGTTCCGGATAGAACAGGAGTTCCTCACTGAGGCCTTGCCTGTGA
AGCTCATTGGGATGAATTGCACTCTAATGAAGCAATACATTGAGTTTGTGGCAGACAGACTTATGCTGGAACGG
GTTTTAGCAAGGTTTTTCAAGTAGAGAACCCATTTGACTTTATGGAGAATATTTCACTGGAAGGAAAGACTAACT
TCTTTGAGAAGAGAGTAGGCGAGTATCAGAGGATGGGAGTGATGTCAAGTCCAACAGAGAATTCTTTTACCTTGG
ATGCTGACTTCTAAATGAAGTGAAGATGTGCCCTTACTTGGCTGATTTTTTTTTTCCATCTCATAAGAAAAATCA
GCTGAAGTGTTACCAACTAGCCACACCATGAATTGTCCGTAATGTTTATTAAACAGCATCTTTAAACTGTGTAGC
TACCTCACAACCAGTCTGTCTGTTTATAGTGCTGGTAGTATCACCTTTTGCCAGAAGGCCCTGGCTGGCTGTGAC
TTACCATAGCAGTGACAATGGCAGTCTTGGCTTTAAAGTGAGGGGTGACCCTTTAGTGAGCTTAGCACAGCGGA
TTAAACAGTCTTTTAAACCAGCACAGCCAGTTAAAGATGCAGCCTCACTGCTTCAACGCAGATTTTAAATGTTTAC
TTAAATATAAACCTGGCACTTTACAAACAAATAAACATTGTTTTGTACTACGGCGGCGATAATAGCTTGATTTA
TTTGGTTTCTACACCAAATACATTCTCCTGACCACTAATGGGAGCCAATTCACAATTCATAAGTGAATAAGTA
AGTTAAACTTGTGTAGACTAAGCATGTAATTTTTAAGTTTTATTTTAAATGAATTAAATATTTGTTAACCAACTT
TAAAGTCAGTCCTGTGTATACCTAGATATTAGTCAGTTGGTGCCAGATAGAAGACAGGTTGTGTTTTTATCCTGT
GGCTTGTGTAGTGTCTGGGATTCTCTGCCCCCTCTGAGTAGAGTGTGTGGGATAAAGGAATCTCTCAGGGCAA
GGAGCTTCTTAAAGTTAAATCACTAGAAATTTAGGGGTGATCTGGGCCTTCATATGTGTGAGAAGCCGTTTCATTT
TATTTCTCACTGTATTTTCTCAACGTCTGGTTGATGAGAAAAAATCTTGAAGAGTTTTTCATATGTGGGAGCTA
AGGTAGTATTGTAAATTTCAAGTCATCCTTAAACAAATGATCCACCTAAGATCTTGCCCCTGTTAAGTGGTGA
AATCAACTAGAGGTGGTTCTTACAAGTTGTTTCACTTGTGTTTGGTGTAAAGTAGGTTGTGTGAGTTAATTC
ATTTATATTTACTATGTCTGTTAAATCAGAAATTTTTTATTATCTATGTTCTTCTAGATTTTACCTGTAGTTCAT
AAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

699/6881
FIGURE 652

MLSLRVPLAPITDPQQLQLSPLKGLSLVDKENTPPALSGTRVLASKTARRIFQEPTTEPKTKAAAPGVEDEPLLRE
NPRRFVIFPIEYHDIWQMYKKAESFWTAEVDLSKDIQHWESLKPEERYFISHVLAFFAASDGIVNENLVERFS
QEVQITEARCFYGFQIAMENIHSEMYSLIDITYIKDPKEREFLFNAIETMPCVKKKADWALRWIGDKEATYGERV
VAFAAVEGIFFSGSFASIFWLKKRGLMPGLTFSNELISRDEGLHCDFACLMFKHLVHKPSEERVREIIINAVRIE
QEFLTEALPVKLIGMNCTLMKQYIEFVADRLMLELGF SKVFRVENPFDFMENISLEGKTNFFEKRVGEYQRMGVM
SSPTENSEFTLDAF

WO 2004/030615

PCT/US2003/028547

700/6881
FIGURE 653

GTCGCTGAGGCGCCCATGGCCTTCGCCCCGCCGGCTCCTGCGCGGGCCACTGTCGGGGCCGCTGCTCGGGCGGCGC
GGGGTCTGCGCTGGGGCCATGGCTCCGCCGCGCCGCTTCGTCTTGGAGCTTCCCGACTGCACCCTGGCTCACTTC
GCCCTAGGCGCCGACGCCCCCGGCGACGCAGACGCCCCCGACCCCGCCTGGCGGGCGCTGCTGGGGCCCCCGGAG
CGCAGCTACTCGCTGTGCGTGCCCGTGACCCCGGACGCCGGCTGCGGGGCCGGGTCCGGGGCGGCGCGGCTGCAC
CAGCGCCTGCTGCACCAGCTGCGCCGCGGCCCTTCCAGCGGTGCCAGCTGCTCAGGCTGCTCTGCTACTGCCCG
GGCGGCCAGGCCGGCGGCGCACAGCAAGGCTTCCTGCTGCGCGACCCCTGGATGACCCTGACACCCGGCAAGCG
CTGCTCGAGCTGCTGGGCGCTGTCAGGAGGCACCACGCCCCGCACTTGGGCGAGTTCGAGGCGGACCCGCGCGGC
CAGCTGTGGCAGCGCCTCTGGGAGGTGCAAGACGGCAGGCGGCTGCAGGTGGGCTGCGCACAGGTCTGTGCCCGTC
CCGGAGCCCCCGCTGCACCCGGTGGTGCCAGACTTGCCAGTTCCGTGGTCTTCCCGGACCGGGAAGCCGCCCGG
GCCGTTTTGGAGGAGTGACCTCCTTTATTCTGAAGCCCGGGCAGTGCTTGACCTGGTTCGACCACTGCCCCAAA
CAGATCCAGAAAGGAAAGTTCAGGTTGTTGCCATCGAAGGACTGGATGCCACGGGTAAAACCGGTGACCCAG
TCAGTGGCAGATTCACTTAAGGCTGTCTCTTAAAGTCACCACCTCTTGCAATTGGCCAGTGGAGGAAGATCTTT
GATGATGAACCAACTATCATTAGAAGAGCTTTTACTCTTTGGGCAATTATATTGTGGCCTCCGAAATAGCTAAA
GAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCACAGCACGGCCACCTATGCCATAGCCACTGAGGTG
AGTGGGGGTCTCCAGCACCTGCCCCAGCCCATCACCCTGTGTACCAGTGGCCAGAGGACCTGCTCAAACCTGAC
CTTATCCTGCTGCTCACTGTGAGTCTTGAGGAGAGGTTGCAGAGGCTGCAGGGCCGGGGCATGGAGAAGACCAGG
GAAGAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAAGGTAGAAATGTCTACCAGCGGATGGAGAATCCT
GGCTGCCATGTGGTTGATGCCAGCCCCCTCCAGAGAAAAGGTCTGCAGACGGTATTAAGCCTAATCCAGAATAGT
TTTAGTGAACCGTAGTACTCTGGCCAGGTGCCACGTCTAACTAGATTAGATGTTGTTTGAACATATGTTTCACTTAATCACT
CCATTTGTTATGCAGTGTTCCCAAATTTCTGTTCTACAAGCATGTTGTGTGGCAGAAAAGTGGAGACCAGGCATC
TTAATTTTACTTCAGCCATCGTACCCTCTTCTGACTGATGGACCCGTATCACAAAGGTCCCTCTCATCATGTTT
CAGTGAGAGGCCAGCGATTGCTTTCTTCTGGCATAGTAAACATTTCTTGAACATATGTTTCACTTAATCACT
ACCAAATATCTGGAAGACCTGTCTTACTCAGACAGCACAGGTGTACAGAAGCAGCAGACAAGATCTTCCAGATC
AGCAGGGAGACCCCGGAGCCTCTGCTTCTCCTACACTGGCATGCTGATGAGATCGTGACATGCCACATTGGCTT
CTTCCACATCTGGTTGCACTCGTCAATGATGGGCTCGCTGCATCTCCCTCAGTCCCAAATTTCTAGAGCCAAGTGTT
CCTGCAGAGGCTGTCTATGTGTCTGGCTGCCCAAGGACACTCCTGCAGAGCCATTTTGGGTAAGGAACACTTA
CAAAGAAGGCATTGATCTTGTGTCTGAGGCTCAGAGCCCTTTTGATAGGCTTCTGAGTCATATATAAAGACATTC
AAGCCAAGATGCTCCAAGTGAATATAACCAACCTTCTCTGAATTATATTTTGCTTATTTATATTTCTTTCTTT
TTTTCTAAAGTATGGCTCTGAATAGAATGCACATTTTCCATTGAAGTGGATGCATTTTCACTTAGCCAAATCCAGTA
ATTTATTTATATTAATCTATACATAATATGTTTCTCAGCATAGGAGCTATGATTCATTAATTAAGTGGAGTC
AAAACGCTAAATGCAATGTTTGTGTGATTTTCACTACACAACTTAATTTGTCTTGTAAATAAGTACAGTGG
ATCTTGGAGTGGGATTTCTTGGTAAATTTATCTTGCACTTGAATGTCTCATGATTACATATGAAATCGCTTTGACA
TATCTTTAGACAGAAAAAGTAGCTGAGTGAGGGGGAATTTATAGAGCTGTGTGACTTTAGGGAGTAGGTTGAAC
CAGGTGATTACCTAAATTCCTTCCAGTTCAAAGGCAGATAAATCTGTAAATATTTTATCCTATCTACCATTT
TTAAGAAGACATTACTCCAAAATAATTAATTTAAGGCTTTATCAGGTCTGCATATAGAATCTTAAATTTCTAATA
AAGTTTCATGTTAATGTCATAGGATTTTTAAAGAGCTATAGGTAATTTCTATATAATATGTGTATATTAAGT
TAATTGATTTAGTTGAAAGTATTTTAAAGCTGATAAATAGCATTAGGGTTCTTTGCAATGTGGTATCTAGCTGT
ATTATTGGTTTTATTTACTTTAAACATTTTGAAGCTTATACTGGCAGCCTAGAAAAACAAACAATTAATGTAT
CTTTATGTCCCTGGCACATGAATAAACTTTGCTGTGGTTTACT

WO 2004/030615

PCT/US2003/028547

701/6881
FIGURE 654

MAFARRLLRGPLSGPLLGRRGVCAGAMAPPRRFVLELEPDCTLAHFALGADAPGDADAPDPRLAALLGPPERSYSL
CVPVTPDAGCGARVRAARLHQRLHQLRRGPFQRCQLRLRLCYCPGGQAGGAQQGFLLRDPLDDPDTRQALLELL
GACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEE
CTSFIPPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT
IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHPVYQWPEDLLKPDILLLL
TVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSFSEP

WO 2004/030615

PCT/US2003/028547

702/6881
FIGURE 655

GTGGTGGGACTCGCGTCGCGGCCGCGGAGACGTGAAGCTCTCGAGGCTCCTCCCGCTGCGGGTCGGCGCTCGCCC
 TCGCTCTCCTCGCCCTCCGCCCCGGCCCCGGCCCCGCGCCGCCATGGAGAAGACTGAGCTGATCCAGAAGGCCA
 AGCTGGCCGAGCAGGCCGAGCGCTACGACGACATGGCCACCTGCATGAAGGCAGTGACCGAGCAGGGCGCCGAGC
 TGTCACACGAGGAGCGCAACCTGCTCTCCGTGGCCTACAAGAAGTGGTCGGGGGCCGAGGTCCGCCTGGAGGG
 TCATCTCTAGCATCGAGCAGAAGACCGACACCTCCGACAAGAAGTTGCAGCTGATTAAGGACTATCGGGAGAAAG
 TGGAGTCCGAGCTGAGATCCATCTGCACCACGGTGTGGAATTGTTGGATAAATATTTAATAGCCAATGCAACTA
 ATCCAGAGAGTAAGGTCTTCTATCTGAAAATGAAGGGTGATTACTTCCGGTACCTTGCTGAAGTTGCGTGTGGTG
 ATGATCGAAAACAAACGATAGATAATTCCCAAGGAGCTTACCAAGAGGCATTTGATATAAGCAAGAAAGAGATGC
 AACCCACACACCCAATCCGCCTGGGGCTTGCTCTTAACTTTTCTGTATTTTACTATGAGATTCTTAATAACCCAG
 AGCTTGCCTGCACGCTGGCTAAAACGGCTTTTGATGAGGCCATTGCTGAACCTTGATACACTGAATGAAGACTCAT
 ACAAGACAGCACCTCATCATGCAGTTGCTTAGAGACAACCTAACACTTTGGACATCAGACAGTGCAGGAGAAG
 AATGTGATGCGGCAGAAAGGGGTGAAAACATAATCCATACAGGGTGTATCCTTCTTTCTTCAAGAAACCTTTT
 TACACATCTCCATTCTTATTCACCTTGGATTTCCTATAGCAAAGAAACCCATTGATGTGTATGGAATCAACTGT
 TTATAGTCTTTTACACTGCAGCTTTGGGAAAACCTTATCCTTGATTTGTGTTTGTCTTGGCCTTCTTGGTGTG
 CAGTACTGCTGTAGAAAAGTATTAATAGCTTCATTTTATATAAACAATAAGTAACTCCCAAACACTTATGTAGAGG
 ACTAAAAATGTATCTGGTATTTAAGTAATCTGAACCAAGTCTGCAAGTGACTGTGTTTGTATTACTGTGAAAAT
 AAGAAAATGTAGTTAATTACAATTTAAAGAGTATTCACATAACTTCTTAATTTCTACATTCCTTCCCTTACTCT
 TCGGGGGTTTCTTTTTCAGTAAGCAACTTTTCCATGCTCTTAATGTATTCCTTTTGTAGGAATCCGGAAGTATT
 AGATTGAATGGAAGCACTTGCCATCTCTGTCTAGGGGTCACAAATTGAAATGGCTCCTGTATCACATACGGAG
 GTCTTGTGTATCTGTGGCAACAGGGAGTTTCTTATTCACCTTTTATTTGCTGCTGTTAAGTTGCCAACCTCCC
 CTCCCAATAAAAATTCACCTTACACCTCCTGCCTTTGTAGTTCTGGTATTCACTTTACTATGTGATAGAAGTAGCA
 TGTGCTGCCAGAATACAAGCATTGCTTTTGGCAAATTAAAGTGCATGTCATTCTTAATACACTAGAAAGGGGA
 AATAAATTAAAGTACACAAGTCCAAGTCTAAACTTTTAGTACTTTTCCATGCAGATTGTGTCACATGTGAGAGGG
 TGTCCAGTTTGTCTAGTGATTGTTATTTAGAGAGTTGGACCACTATTGTGTGTTGCTAATCATTGACTGTAGTCC
 CAAAAAGCCTTGTGAAAATGTTATGCCCTATGTAACAGCAGAGTAACATAAAATAAAAGTACATTTTATAAACC
 ATTTACTATGGCTTTTGTAAACATTCATACCCATATTTTAAAGGACAGGTGAATTTACTACTTTCTAAAGTTTAT
 TGATACTTCCCTTTTATGTAATAATGTAGTAGTGATACCTATATTTCCACATTGTGCATTGTGACACACTTGTCTA
 GGGATGCCTGGAAGTGTATAAAATTGGACTGCATTTCTTAGAGTGTTTTACTATAGATCAGTCTCATGGGCCATC
 TCTTCCCTCAGATGTAAATGATATCTGGTTAAGTGTTATATGGAATAAAGTGGACATTTTAAACTA

WO 2004/030615

PCT/US2003/028547

703/6881
FIGURE 656

MEKTELIQKAKLAEQAERYDDMATCMKAVTEQGAELSNEERNLLSVAYKNVVGRRSAWRVISSIEQKTDTSDDK
LQLIKDYREKVESELRSICTTVLELLDKYLIANATNPESKVFYLMKMGDYFRYLAEVACGDDRKQTIDNSQGAYQ
EAFDISKKEMQPTHPIRLGLALNFSVFYYEILNNPELACTLAKTAFDEAIAELDTLNEDSYKDSTLIMQLLRDNL
TLWTSDSAGEECDAAEGAEN

WO 2004/030615

PCT/US2003/028547

704/6881
FIGURE 657

GGCACGAGGCTCCGGTGTGTCTGTCTGGTTCAGTGTGGAGGTCGGCGCCGGCCCCCGCTTCCGCGCCCCCAC
GGGAAGGAAGCACCCCCGGTATTAAACGAACGGGGCGAAAGAAGCCCTCAGTCGCCGGCCGGGAGGCGAGCCG
ATGCCGAGCTGCTCCACGTCCACCATGCCGGGCATGATCTGCAAGAACCCAGACCTCGAGTTTACTCGCTACAG
CCCTGCTTCTACCCGGACGAAGATGACTTCTACTTCGGCGGCCCCGACTCGACCCCCCGGGGAGGACATCTGG
AAGAAGTTTGAGCTGCTGCCCACGCCCCCGTGTGCGCCAGCCGTGGCTTCGCGGAGCACAGCTCCGAGCCCCCG
AGCTGGGTACGGAGATGCTGCTTGAGAACGAGCTGTGGGGCAGCCCGGCCGAGGAGGACCGCTTCGGCCTGGGG
GGACTGGGTGGCTCACCCCCAACCCGGTCATCCTCCAGGACTGCATGTGGAGCGGCTTCTCCGCCCCGAGAAG
CTGGAGCGCGCCGTGAGCGAGAAGCTGCAGCACGGCCGCGGGCCGCCAACC GCCGGTTCACCGCCAGTCCCCG
GGAGCCGGCGCCGCCAGCCCTGCGGGTTCGCGGGCAGCGCGGGCTGCGGGAGCCGGCCGCGCGGGGCCGCCCTG
CCCCCGAGCTCGCCACCCGGCCGCCGAGTGCCTGGATCCCGCCGTGGTCTTCCCCTTTCCCGTGAACAAGCGC
GAGCCAGCGCCCGTGCCTCGCAGCCCCGCCAGTGCCTGGCGCGCGGGCCCTGCGGTCCGCTCGGGGGCGGGTATT
GCCGCCCCAGCCGGGGCCCCGGGGTGCCTCCGCGCCAGGCGGCCGCCAGACCAGCGGCGGCGACCAAG
GCCCTCAGTACCTCCGGAGAGGACACCCTGAGCGATTAGATGATGAAGATGATGAAGAGGAAGATGAAGAGGAA
GAAATCGACGTGGTCACTGTGGAGAAGCGGCGTTCTCTCCAACACCAAGGCTGTCACCACATTCACCATCACT
GTGCGTCCCAAGAACGCAGCCCTGGGTCCCGGGAGGGCTCAGTCCAGCGAGCTGATCCTCAAACGATGCCTTCCC
ATCCACCAGCAGCACAACTATGCCGCCCCCTCTCCCTACGTGGAGAGTGAGGATGCACCCCCACAGAAGAAGATA
AAGAGCGAGGCGTCCCCACGTCCGCTCAAGAGTGTATCCCCCAAAGGCTAAGAGCTTGAGCCCCGAAACTCT
GACTCGGAGGACAGTGAGCGTCGCAGAAACACAACATCCTGGAGCGCCAGCGCCGCAACGACCTTCGGTCCAGC
TTTCTCACGCTCAGGGACCACGTGCCGGAGTTGGTAAAGAATGAGAAGGCCGCCAAGGTGGTCATTTGAAAAAG
GCCACTGAGTATGTCCACTCCCTCCAGGCCGAGGAGCACCAGCTTTTGCTGGAAAAGGAAAAATTGCAGGCAAGA
CAGCAGCAGTTGCTAAAGAAAATTGAACACGCTCGGACTTGCT**TAG**ACGCTTCTCAAACTGGACAGTCACTGCCA
CTTTGCACATTTTGATTTTAAAAACAAACATTGTGTTGACATTAAGAATGTTGGTTTACTTTCAAATCGGT
CCCCTGTGAGTTCGGCTCTGGGTGGGCAGTAGGACCACAGTGTGGGGTCTGCTGGGACCTTGAGAGCCTGC
ATCCCAGGATGCTGGGTGGCCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGACGGTTG
GGAGCCTCTGGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTTCAAACAACAGAAAGTCATTCCTTTCTTTTA
AAATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATACCCCTGGGGAACATTTCTGTAAA
TACCATTGACACATCCGCTTTTGTATACATCCTGGGTAATGAGAGGTGGCTTTTGCGGCCAGTATTAGACTGGA
AGTTACATACCTAAGTACTGTAATAATACCTCAATGTTTGAGGAGCATGTTTGTATACAAATATATTGTTAATCT
CTGTTATGTACTGTACTAATTCTTACACTGCCTGTATACTTTAGTATGACGCTGATACATAACTAAATTTGATAC
TTATATTTTCGTATGAAAATGAGTTGTGAAAGTTTGTAGTAGATATTACTTTATCACTTTTTGAACCTAAGAACT
TTTGTAAGAAAATTTACTATATATATATGCCTTTTCTAGCCTGTTTCTTCTGTTAATGTATTTGTTCAITGT
TGGTGATAGAACTGGGTAAATGCAAAGTTCTGTGTTTAAATTTCTTCAAATGTATATATTTAGTGCTGCATCTT
ATAGCACTTTGAAATACCTCATGTTTATGAAAATAAATAGCTTAAATTAATAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

705/6881
FIGURE 658

MPSCSTSTMPGMICKNPDLEFDSLQPCFYDDEDDFYFGGPDSTPPGEDIWKKFELLPTPPLSPSRGFAEHSSEPP
SWVTEMLLENELWGSPAEEADFGLGGLGGLTPNPVILQDCMWSGFSAREKLERAVSEKLQHGRGPPTAGSTAQSP
GAGAASPAGRGHGGAAGAGRAGAALPAELAHPAECVDPVAVVFPFVVKREPAPVPAAPASAPAAGPAVASGAGI
AAPAGAPGVAPPRPGGRQTSGGDHKALSTSGEDTLSDSDDEDDEEEDDEEEDIDVVTVEKRRSSNTKAVTTFTIT
VRPKNAALGPGRASSELILKRCLPIHQHNYAAPSPYVESEDAPPQKKIKSEASPRPLKSVIPPKAKSLSPRNS
DSEDSERRRNHNI LERQRRNDLRSSF LTLRDHVP ELVKNEAKKV VILKKATEYVHSLQAEHQ LLLLEKEKLQAR
QQQLKKIEHARTC

WO 2004/030615

PCT/US2003/028547

706/6881
FIGURE 659

GTCAGTCCCTCCTGTAGCCGCCGCCGCCGCCGCCGCCGCCCTCTGCCAGCAGCTCCGGCGCCACCTCGGGCCG
GCGTCTCCGGCGGGCGGGAGCCAGGCGCTGACGGGCGCGGGGGGGCGGCCGAGCGCTCCTGCGGCTGCGACTCA
GGCTCCGGCGTCTGCGCTTCCCCATGGGGCTGGCCTGCGGCGCCTGGGCGCTCTGAGATTGTCAGTGTGTCCA
AGGGCACACGCAGAGGGATTGGAATTCCTGGAGAGTTGCCTTTGTGAGAAGCTGGAAATATTTCTTTCAATTCC
ATCTCTTAGTTTTCCATAGGAACATCAAGAAATCATGAACAACTTTGGTAATGAAGAGTTTGACTGCCACTTTCCT
CGATGAAGGTTTTACTGCCAAGGACATTCTGGACCAGAAAATTAATGAAGTTTCTTCTTCTGATGATAAGGATGC
CTTCTATGTGGCAGACCTGGGAGACATTCTAAAGAAACATCTGAGGTGGTTAAAAGCTCTCCCTCGTGTACCCCC
CTTTTATGCAGTCAAATGTAATGATAGCAAAGCCATCGTGAAGACCCTTGCTGCTACCGGGACAGGATTTGACTG
TGCTAGCAAGACTGAAATACAGTTGGTGCAGAGTCTGGGGGTGCCTCCAGAGAGGATTATCTATGCAAATCCTTG
TAAACAAGTATCTCAAATTAAGTATGCTGCTAATAATGGAGTCCAGATGATGACTTTTGATAGTGAAATTGAGTT
GATGAAAGTTGCCAGAGCACATCCCAAAGCAAAGTTGGTTTTGCGGATTGCCACTGATGATTCCAAAGCAGTCTG
TCGTCTCAGTGTGAAATTCGGTGCCACGCTCAGAACCAGCAGGCTCCTTTTGAACGGGCGAAAGAGCTAAATAT
CGATGTTGTTGGTGTGAGCTTCCATGTAGGAAGCGGCTGTACCGATCCTGAGACCTTCGTGCAGGCAATCTCTGA
TGCCCGCTGTGTTTTTGACATGGGGGCTGAGGTTGGTTTCAGCATGTATCTGCTTGATATTGGCGGTGGCTTTCC
TGGATCTGAGGATGTGAAACTTAAATTTGAAGAGATCACC GGCGTAATCAACCCAGCGTTGGACAAATACTTTCC
GTCAGACTCTGGAGTGAGAATCATAGCTGAGCCCGGCAGATACTATGTTGCATCAGCTTTCACGCTTGCAAGTAA
TATCATTGCCAAGAAAATTGTATTAAAGGAACAGACGGGCTCTGATGACGAAGATGAGTCGAGTGAGCAGACCTT
TATGTATTATGTGAATGATGGCGTCTATGGATCATTTAATTGCATACTCTATGACCACGCACATGTAAAGCCCCCT
TCTGCAAAAGAGACCTAAACCAGATGAGAAGTATTATTCATCCAGCATATGGGGACCAACATGTGATGGCCTCGA
TCGGATTGTTGAGCGCTGTGACCTGCCTGAAATGCATGTGGGTGATTGGATGCTCTTTGAAAACATGGGCGCTTA
CACTGTTGCTGCTGCCTCTACGTTCAATGGCTTCCAGAGGCCGACGATCTACTATGTGATGTCAGGGCCTGCGTG
GCAACTCATGCAGCAATTCCAGAACCCCGACTTCCCACCCGAAGTAGAGGAACAGGATGCCAGCACCTGCCTGT
GTCTTGTGCCTGGGAGAGTGGGATGAAACGCCACAGAGCAGCCTGTGCTTCGGCTAGTATTAATGTGTAGATAGC
ACTCTGGTAGCTGTAACTGCAAGTTTAGCTTGAATTAAGGGATTTGGGGGACCATGTAAGTTAATTACTGCTA
GTTTTGAAATGTCTTTGTAAGAGTAGGGTCGCCATGATGCAGCCATATGGAAGACTAGGATATGGGTCACACTTA
TCTGTGTTTCCTATGGAACTATTTGAATATTTGTTTTATATGGATTTTATTCACTCTTCAGACACGCTACTCAA
GAGTGCCCTCAGCTGCTGAACAAGCATTGTAGCTTGTACAATGGCAGAATGGGCCAAAAGCTTAGTGTTGTGA
CCTGTTTTTAAATAAAGTATCTTGAATAATTAGGC

WO 2004/030615

PCT/US2003/028547

707/6881
FIGURE 660

MNNFGNEEFDCHEFLDEGFTAKDILDQKINEVSSSDDKDAFYVADLGDILKKHLRWLKA
LPRVTPFYAVKCND
SKAIVKTLAATGTGFDCA
SKTEIQLVQSLGVPPERIIYANPCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAK
LVLRIATDDSKAVCRLSVKFGATLRTSRLLLERAKELNIDVVGVSFHVSGCTDPETFVQAISDARC
VDFDMGAEVGF
SMYLLDIGGGFPGSE
DVKLKFEEITGVINPALDKYFPSDSGVRIIAEPGRYYVASAFTLAVNIIAKKIVLKEQ
TGSDDEDESSEQTFMY
YVNDGVYGSFNCILYDHAHVKPLLQKRPKPDEKYYSSSIWGPTCDGLDRIVERCDLPEM
HVGDWMLFENMGAYTVAAASTFNGFQRP
TIYYVMSGPAWQLMQQFQNPDPPEVEEQDASTLPVSCAWESGMKRH
RAACASASINV

WO 2004/030615

PCT/US2003/028547

708/6881
FIGURE 661

ATGAGTCAGCAGCGGCCGGCGAGGAAGTTACCCAGTCTCCTCCTGGACCCGACGGAGGAGACGGTTTCGCCGTCGG
TGCCGAGACCCCATCAACGTGGAGGGCCTGCTGCCATCAAAAATAAGGATTAATTTAGAAGATAATGTACAATAT
GTGTCCATGAGAAAAGCTCTAAAAGTGAAGAGACCTCGTTTTGATGTATCGCTGGTTTTATTTAACTCGAAAAATT
ATGGATCTTGTCAGATCTGCTCCCGGGGTATTCTTGACTTAAACAAGGTTGCAACGAAACTGGGAGTCCGAAAG
CGGAGAGTGTATGACATCACCAATGTCTTAGATGGAATCGACCTCGTTGAAAAGAAATCCAAGAACCATATTAGA
TGGATAGGATCTGATCTTAGCAATTTTGGAGCAGTTCCCCAACAAAAGAAGCTACAGGAGGAACTTTCTGACTTA
TCAGCAATGGAAGATGCTTTGGATGAGTTAATTAAGGATTGTGCTCAGCAGCTGTTTGAGTTAACAGATGACAAA
GAAAATGAAAGACTAGCATATGTGACCTATCAAGACATTCATAGCATTCAAGGCCTTCCATGAACAGATCGTCATT
GCAGTTAAAGCTCCAGCAGAAACCAGATTGGATGTTCCAGCTCCCAGAGAAGACTCTATCACAGTGCACATAAGG
AGCACCAACGGACCTATCGATGTCTATTTGTGTGAAGTGGAGCAGGGTCAGACCAGTAACAAAAGGTCTGAAGGT
GTCGGGACCTCTTCATCTGAGAGCACTCATCCAGAAGGCCCTGAGGAAGAAGAAAATCCTCAGCAAAGTGAAGAA
TTGCTTGAAGTAAGCAACTGATGGCATTGAGAAATTTATGTATCACTGAGTTTTTTGGGAATATCTTCGTGGAGA
ATTACGCATCAAATTTGATTCTCAGAGCAATAAATTATCCATGAAGTGCTCTCGTTCTCAGTAGCGGCATCATGG
CCAGTAGTGTCTTTGAGGAGTTACCACTTAGATTACTGAGTAATTGTGGTTTTCCACATTTGAAAACAACTCCTT
TTATAATTATTCACTGCTTTTTGTGAGTGAAATAGACATCTTGCCCTCCTGAAGTAGCTTCATCACAGAGTGCAT
GAAGACAGACAGTCAGGCTGAAATGGACAGTTCTTTGTGGACTCTACCCTTCCCTTCAAGGAGTATGTCATATAT
CACAAAAGAAATTGCCTTACACTGGTTTCATGTTTGAGTTACTGTTGTACATTGCATAGATGTACACACGAATTT
AAATGTGATGTCTTTGTATATATCTGTATAATGTTGAGATTACTTACGAAATATGTCTGAGTGACACTTTTCACC
CTTGTACAGCCAAAATAATGTATATATGGAAAGTGACAGACAAATCTCTAATCTCTTTGGTACCTATAACTTAT
TAGAATCCTCTGGATGAGGGTTAGAAGAGACTTTTTCCAACTTCTACATGTAGAAGTATCATAAATGTGCTACA
CATTTATGTTTGTGGATTTAATTAAAGTATTTTAATATGGTTTTAGTGCTAAAATGGAGTCAGATACTTCTTG
GTTTTAAGCTGTCTACCTAATTGCTGTCTCCAGCAGACTGGTGGCATGCCAGTGGCTTTGGGGGCAAGGATAG
AAATGCCATCAGGAAATAGCTGAATTCATTGTGAAACATGAATTCAGTCATGGTGATAATTGGAAACTCCTTTCA
GGTTTTTGCAAGTAGATTTTGTAATGTTTGTGTATGCAGCCTTGCTGTTGAGTCAGTCCAAGGGGTTTTACTTAG
GACAAGTTGTACCTTGCCCTCTCTCCAGCTCTGCTCCACATTTTCACATACCTAGCTGTTTCTACCTCATTGGG
TAAGTCATTTACCACTCTGTGCCTCAGTTTACTCTGTAGTTTACCATTAGACTGTGAGCTCCTTGAGGGACTTTG
TCATAATCACTGTTACATCCCAGTGCCTCACACCATGCCTGGCCCTTAAGAAGTGCTCAATAAATGTCTGAACAA
ATAA

WO 2004/030615

PCT/US2003/028547

709/6881
FIGURE 662

CTCTGTAGCTGTGACCCTGATACCGCGTGGTGTGCTCCGAACACATGGTGCCAGAACGAAGCGGGCGTCCAGAA
GCCCTAGGTCCCAGAGGTCCGCTCAGCGGCAGGCGCATAAGGCGGGGCGGCGCGGGCCTTTCCTTCCATCGGAA
CCGTTCTCCCGGGGCTGAGTCCCTGCCCCGACTCCGAACGCCGAAGACCAGGGGCGGGAAGCGCGCGCCGCACT
GCCACGCCGTGTAGTCGGGAGGGAGGGAGCGAGCAGGCGAAGCCGCGGAGGACGGGGTGAAGATGGCGGCCTTC
TCCGAGATGGGTGTAATGCCTGAGATTGCACAAGCTGTGGAAGAGATGGATTGGCTCCTCCCAACTGATATCCAG
GCTGAATCTATCCATTGATCTTAGGAGGAGGTGATGTACTTATGGCTGCAGAAACAGGAAGTGGCAAAACTGGT
GCTTTTAGTATTCAGTTATCCAGATAGTTTATGAAACCTCTGAAAGACCAACAGGAAGGCAAAAAGGAAAAACA
ACAATTAAACTGGTGCTTCAGTGCTGAACAAATGGCAGATGAACCCATATGACAGAGGATCTGCTTTTGCAATT
GGGTCAGATGGTCTTTGTTGTCAAAGCAGAGAAGTAAAGGAATGGCATGGGTGTAGAGCTACTAAAGGATTAATG
AAAGGGAAACACTACTATGAAGTATCCTGTGCATGACCAAGGGTTATGCAGGGTCGGGTGGTCTACCATGCAGGCC
TCTTTGGACCTAGGTACTGACAAGTTTGGATTTGGCTTTGGTGGAACAGGAAAGAAATCCCATAAACAATTT
GATAATTATGGAGAGGAATTCATATGCATGATACCATTGGATGTTACCTGGATATAGATAAGGGACATGTCAAG
TTCTCCAAAATGGAAAAGATCTTGGTCTGGCATTGTAAATACCACCACATATGAAAACCAAGCCCTCTTTCCT
GCGTGTGTTTTGAAGAATGCTGAACTGAAATTTAACTTCGGTGAAGAGGAATTTAAGTTTCCACCAAAAGATGGC
TTTGTGTCTTTTCCAAGGCACCGGATGGTTACATTGTCAAATCACAGCACTCAGGTAATGCACAGGTGACACAA
ACAAAGTTTCTCCCAATGCTCCGAAAGCTCTCATTGTTGAACCTTCCCGGGAGTTAGCTGAACAACTTTGAAC
AACATCAAGCAGTTAAGAAATACATTGATAATCCTAAATTAAGGGAGCTTCTGATAATTGGAGGTGTTGCAGCC
CGGGATCAGCTCTCTGTTTTGGAAAATGGAGTAGATATAGTTGTAGGTACTCCGGGAAGACTAGATGACTTGGTG
TCAACTGGAAAGCTGAACTTATCTCAAGTTAGATTCTGGTCTGGATGAAGCTGATGGGCTTCTTTCTCAAGGT
TATTCTGATTTTATAAATAGGATGCACAATCAGATTCTCAGGTTACCTCTGATGGAAAAGACTTCAGGTGATT
GTTTGCTCTGCCACTTTGCATTCTTTTCGATGTAAAGAACTGTCCGAGAAGATAATGCATTTTCTACATGGGTT
GACTTAAAGGAGAAGACTCTGTTCCAGATACTGTACCATGTTGTTGTCCCAGTAAATCCCAAACTGACAGA
CTCTGGGAAAGGCTTGGAAAGAGCCACATTAGAACTGATGATGTACATGCAAAAGATAACACAAGACCTGGTGCT
AATAGTCCAGAGATGTGGTCTGAAGCTATTAATAATCCTGAAAGGGGAGTATGCTGTCCGGGCAATCAAGGAACAT
AAGATGGATCAAGCAATTATCTTCTGTAGAACCAAAATGACTGTGATAACTTGGAGCAGTACTTTATACAACAA
GGAGGAGGACCTGATAAAAAAGGACACCAGTTCTCATGTGTTTGTCTTCATGGTGACAGAAAGCCTCATGAGAGA
AAGCAAACTTGGAAAGATTTAAGAAAGGAGATGTAAGATTCTTGATTTGCACAGATGTAGCTGCTAGAGGAATT
GATATCCACGGTGTTCCTTATGTTATAAATGTCACTCTGCCCGATGAAAAGCAAACTACGTACATCGAATTGGC
AGAGTAGGAAGAGCTGAAAGGATGGGTCTGGCAATTTCCCTGGTGGCAACAGAAAAAGAAAAGGTTTGGTACCAT
GTATGTAGCAGCCGTGAAAAGGGTGTATAACACAAGACTCAAGGAAGATGGAGGCTGTACCATATGGTACAAC
GAGATGCAGTTACTATCTGAGATAGAAGAACACCTGAACCTGTACCATTTCTCAGGTTGAGCCGGATATAAAGGTA
CCAGTGGATGAATTTGATGGGAAAGTTACCTACGGTCAGAAAAGGGCTGCTGGTGGTGGAAAGCTATAAAGGCCAT
GTGGATATTTTGGCACCTACTGTTCAAGAGTTGGCTGCCCTTGAAAAGGAGGCGCAGACATCTTTCCTGCATCTT
GGCTACCTTCTAACCAGCTGTTCAAGACCTTCTGATTTTTTACATTTACTGAATAAGATTTGAGTAATGAAAGTC
TGTAGTCTTAAACTCTAAACAGTTGTACTGCTTCCAAGCAGCAGTATTTATAGTAACGTAAGCTATTAATGCT
AACTCTTGCATGTCAAGAAACATTAGTCTTAGGAATTCTTCAAAAATGGCATCCCAATGAAAATAAATTTGATG
ACTATA

WO 2004/030615

PCT/US2003/028547

710/6881
FIGURE 663

MAAFSEMGVMPETIAQAVEEMDWLLPTDIAESIPLILGGGDVLMMAETGSGKTGAFSIPVIQIVYETLKDQQEGK
KGKTTIKTGASVLNKWQMNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYEVSCHDQGLCRVGWS
TMQASLDLGTDKFGFGGGTGKKSHNKQFDNYGEEFTMHDTIGCYLDIDKGHVKF SKNGKDLGLAFEIPPHMKNQ
ALFPACVLKNAELKFNFGEFEFKFPPKDGVALSKAPDGYIVKSQHSQNAQVTQTKFLPNAPKALIVEPSRELAE
QTLNNIKQFKKYIDNPKLRELLI IGGVAARDQLSVLENGVDIVVGTPGRLDDLSTGKLNLSQVRFLVLDEADGL
LSQGYSDFINRMHNQIPQVTS DGKRLQVIVCSATLHSF DVKKLSEKIMHFPTWVDLKGEDSVPTVHHVVVPVNP
KTDRLWERLGKSHIRTD DVHAKDNTRPGANSPEMWSEAIKILKGEYAVRAIKEHKMDQAI IFCRTKIDCDNLEQY
FIQQGGGPDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFICTDVAARGIDIHGVPYVINVTLPDEKQNYV
HRIGRVGRAERMGLAISLVATEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEEHLNCTISQVEP
DIKVPVDEFDGKVTYGQKRAAGGGSYKGHV DILAPTVQELAALEKEAQTSFLHLGYLPNQLFRFT

WO 2004/030615

PCT/US2003/028547

711/6881
FIGURE 664A

GAACATGGCGGCCCCGAGTCAGGGCCGGCTTTGAGTCCAGGCACTGCAGAGGCCTAGAGGCAACCAAAAACATG
GTGCATCCTTTATCATCACGAAAGCAATTCGAGATCGTTTATTATTTTTACGCCAATACATCTGGTACAGCCCCG
CACCTTTTTTGCTCCCTGATGGACTGGTTCGCTTGGTTAATAAACAGATAAACTGGCATTGTTGTTACTTGCAAGCA
ATAGCACTAGAGTGCATCTATACCTGTGAACGAAATGATCAACTCTGTCTTTGCTATGACCTACTAGAATGTCTG
CCAGAAAGAGGATATGGTGATAAGACAGAGGCAACCACAAAGCTTCATGACATGGTAGACCAACTGGAACAAATT
CTCAGTGTGTGAGAGCTTTTGAAAAACATGGACTCGAGAAACCAATTTTCAATTTGTTAAAAACACTCAATCTAGC
TCAGAAGAGGCACGCAAGCTGATGGTTAGATTGACGAGGCACACTGGCCGGAAGCAGCCTCCTGTGAGTGAGTCT
CATTGGAGAACGTTGCTGCAAGACATGTTAACTATGCAGCAGAATGTATACACATGTCTAGATTCTGATGCCTGC
TATGAGATATTTACAGAAAGCCTTCTGTGCTCTAGTCGCCTTGAAACATCCACCTGGCTGGACAGATGATGCAC
TGCAGTGCTTGTTCAGAAAATCCTCCAGCTGGTATAGCCCATAAAGGGAAACCCCACTACAGGGTCAGCTACGAA
AAGAGTATTGACTTGGTTTTGCTGCCAGCAGAGAGTACTTCAATTTCTTCTACCAACCTCACTGATAGCTGCATG
GATCTAGCCAGGTGCTGCTTACAACGATAACAGACAGACCCCTGCCATTCAAGAGGAGCTAGATCTTATCCAA
GCCGTTGGATGTCTTGAAGAATTTGGGGTAAAGATCCTGCCTTTGCAAGTGCGATTGTGCCCTGATCGGATCAGT
CTCATCAAGGAGTGATTTTCCAGTCCCCACATGCTATAAACAATCCACCAAGCTTCTGGGCCTTGCTGAGCTG
CTGAGGGTTGCAGGTGAGAACCCAGAAAGAAAGGCGGGGACAGGTTCTAATCCTTTTAGTGGAGCAGGCACCTTCGC
TTCCATGACTACAAAGCAGCCAGTATGCATTGTGAGGAGCTGATGGCCACAGGTTATCCTAAAAGTTGGGATGTT
TGTAGCCAGTTAGGACAATCAGAAGGTTACCAGGACTTGGCCACTCGTCAAGAGCTCATGGCTTTTGCTTTGACA
CATTGCCCTCCTAGCAGCATTGAACTTCTTTTGGCAGCTAGCAGCTCTCTGCAGACAGAAATCTTTATCAAAGA
GTGAATTTCCAGATCCATCATGAAGGAGGGGAAAAATATCAGTGCTTCACCATTAACTAGTAAAGCAGTACAAGAG
GATGAAGTAGGTGTTCCAGGTAGCAATTCAGCTGACCTATTGCGCTGGACCACTGCTACCACCATGAAAGTCCTT
TCCAACACCACAACCACCACCAAAAGCGGTGCTGCAGGCCGTGAGTGATGGGCAGTGGTGGAAGAAGTCTTTAACT
TACCTTCGACCCCTTCAGGGGGCAAAAATGTGGTGGTGATATCAAATCGGAACCTACAGCCAATGAAGATCTAGAG
AAACAAGGGTGTCATCCTTTTTATGAATCTGTCATCTCAAATCCTTTTGTGCTGAGTCTGAAGGGACCTATGAC
ACCTATCAGCATGTTCCAGTGGAAGCTTTGCGAAGTATTGCTGAGAACTGGAAAATTGGCAGAGGCTAAAAAT
AAAGGAGAAGTATTTCCAACTGAAGTTCTCTTGAACCTAGCAAGTGAAGCCTTGCCAAATGACATGACCTTG
GCTCTTGCTTACCTTCTTGCTTACCACAAGTGTTAGATGCTAACCGGTGCTTTGAAAAGCAGTCCCCCTCTGCA
TTATCTCTCCAGCTGGCAGCGTATTACTATAGCCTCCAGATCTATGCCCGATTGGCCCCATGTTTCAGGGACAAG
TGCCATCCTCTTTACAGGGCTGATCCCAAAGAACTAATCAAGATGGTCACCAGGCATGTGACTCGACATGAGCAC
GAAGCCTGGCCTGAAGACCTTATTTCACTGACCAAGCAGTTACACTGCTACAATGAACGTCTCCTGGATTTCACT
CAGGCGCAGATCCTTCAGGGCCTTCGGAAGGGTGTGGACGTGCAGCGGTTTACTGCAGATGACCAGTATAAAAGG
GAACTATCCTTGGTCTGGCAGAACTCTAGAGGAAAGCGTCTACAGCATTGCTATTTCTCTGGCACAACGTTAC
AGTGTCTCCCGCTGGGAAGTTTTATGACCCATTGAGGTTCTCTTACGGACAGTGTTTTGTCCCACTAGAA
ATTGAAAATAGAGCCCAAGACCTTCATCTCTTTGAGACTTTGAAGACTGATCCAGAAGCCTTTTACCAGCACATG
GTCAAGTATATTTACCCTACTATTGGTGGCTTTGATCAGGAAAGGCTGCAGTATTATTTCACTCTTCTGAAAAAC
TGTGGCTGTGAGATTGTTGGGAACTGTGCCATTAAACCAGAAACCATTCGACTGCTGAAGAAGTTTTAAGGTT
GTTGCATCAGGTCTTAATTACAAAAAGCTGACAGATGAAAACATGAGTCCCTTGAAGCATTGGAGCCAGTTCTT
TCAAGTCAAAATATCTTGTCTATTTCCAACTTGTTCCCAAATCCCTGAAAAGGATGGACAGATGCTTTCCCCA
AGCTCTCTGTACCATCTGGTTACAGAAGTTGTTCTGGACTGGAGACCCTCATCTCATTAAACAAGTCCCAGGC
TCTTACCCGGAGTGGCTTCATGCCTATGATGCTGTCATGAAGTACTTTGATCGTCTCCACCCAGGTGACCTCATC
ACTGTGGTAGATGCAGTTACATTTTCTCCAAAGCTGTGACCAAGCTGTCTGTGGAAGCCCGTAAAGAGATGACT
AGAAAGGCTATTAAAGACAGTCAAACATTTTATTGAGAAGCCAAGGAAAAGAACTCAGAAGACGAAGCTCAAGAA
GCTAAGGATTCTAAAGTTACCTATGCAGATACTTTGAATCATCTGGAGAAATCACTTGCCCACCTGGAACCCCTG
AGCCACAGCTTCATCCTTTCTCTGAAGAATAGTGAGCAGGAAACACTGCAAAAATACAGTCACCTCTATGATCTG
TCCCGATCAGAAAAAGAGAAACTTCATGATGAAGCTGTGGCTATTTGTTTAGATGGTCAGCCTCTAGCAATGATT
CAGCAGCTGCTAGAGGTGGCAGTTGGCCCTCTTGACATCTCACCAAGGATATAGTGAGAGTGCAATCATGAAA
ATAATTTCTGCATTGAGTGGTGGCAGTGCTGACCTTGGTGGGCCAAGGGACCCACTGAAGGTCCTGGAAGGTGTT
GTTGCAGCAGTCCACGCCAGTGTGGACAAGGGTGAAGAGCTGGTTTACCTGAGGACCTGCTGGAGTGGCTGCGG
CCTTTCTGTGCTGATGACGCTGGCCGGTGGCGCCCGCATTACGTGCTGCAGATTTTGGGGCAATCATTTCAC

WO 2004/030615

PCT/US2003/028547

712/6881
FIGURE 664B

CTGACTGAGGAGGACAGCAAGCTCCTCGTGTTCCTTTAGAACTGAAGCCATTCTCAAAGCCTCCTGGCCCCAGAGA
CAGGTAGACATAGCTGACATTGAGAATGAAGAGAACCGCTACTGTCTATTCATGGAACCTCCTGGAATCTAGTCAC
CACGAGGCTGAATTTGAGCACTTGGTTTTACTTTTGCAAGCTTGGCCACCTATGAAAAGTGAATATGTCATAACC
AATAATCCATGGGTGAGACTAGCTACAGTGATGCTAACCAGATGTACGATGGAGAACAAGGAAGGATTGGGGAAT
GAAGTTTTGAAAATGTGTCGCTCTTTGTATAACACCAAGCAGATGCTGCCTGCAGAGGGTGTGAAGGAGCTGTGT
CTGCTGCTGCTTAACCAGTCCCTCCTGCTTCCATCTCTGAAACTTCTCCTCGAGAGCCGAGATGAGCATCTGCAC
GAGATGGCACTGGAGCAAATCACGGCAGTCACTACGGTGAATGATTCCAATTGTGACCAAGAACTTCTTTCCCTG
CTCCTGGATGCCAAGCTGCTGGTGAAGTGTGTCTCCACTCCCTTCTATCCACGTATTGTTGACCACCTCTTGGCT
AGCCTCCAGCAAGGGCGCTGGGATGCAGAGGAGCTGGGCAGACACCTGCGGGAGGCCGCCATGAAGCCGAAGCC
GGGTCTCTCCTTCTGGCCGTGAGGGGGACTCACCAGGCCTTCAGAACCTTCAGTACAGCCCTCCGCGCAGCACAG
CACTGGGTGTGAGGGCCACCTGTGGCCCTGCTCCTTAGCAGAAAAAGCATCTGGAGTTGAATGCTGTTCCAGAA
GCAACATGTGTATCTGCCGATTGTTCTCCATGGTTCCAACAAATTGCAAAATAAACTGTATGGAACG

WO 2004/030615

PCT/US2003/028547

713/6881
FIGURE 665

ATGGAGATCTCGGCTGCGAAGTGTGTGTCATCAGCATCTGGCTTTCTGGGTTATGATGTGGTCAGGGATGTGTCTTCT
GGCCCATTTTGGAGGCGCAAAAATGGTGATCCATGTTTGGATTTATGTGGAAGGGACAGTTCCACAGTATGGAAA
AGGGGAGACAGTCCCAGGAAGCGTGAAGAGGAAAGGTCATTGGGAATCTCTCAGTACCTCTGCCCTAATCTCTTC
TCTCCTACGGAGGCAGTTAAGTCTAAAGCCATTTGTCTGGTTTTCCATATCTGAACTTCAAGCAGCATCTTCTGGA
CTTAGTTCTTGGTGGCTGGAGCAGGGAAAGTGTGGCCTCATTGAAATGGGATCAGGTTTCAGGATGTTTCATGTG
TCTGTGTCTTTCTCACACATTGTGAGGAACAGGACAGTCCCTCTGATGCGCTGGTACCTGGCCGCCATGCAGATC
ATGAGGGGAGAGAAGCAGGCTGCTTCGGGGGAATCCTGCCATAGAGGCTGGAGCTTCATGTGCATCTCAGCCAGCC
CTGCAGCAGCCCTCAGCAGCCCTTCTGTGGGGCTGGGGTATCTGTTGCCCAGGAAATCACTGGGCTGAGGAAGTA
GGAGATGAATGGCTCTGTGCTATCACACCATCTTCTGCATTGAGTCTTCTTCGCTTTCTTATCATCGTCATCATG
ATTATCATCAATAAATTTGTAAGGAAGGAAACAGGACTGCTTATTGATTTTCATTTCTATGCTACTGAGAGCCAA
GGCTACGGATTTCTTTCCCCAGGAATGGAGAGAGGAAAGAGATGTGAGATTGGCTACCCAATGTTGCATCAGTA
CCCCATTCTATCATCAACGGGTACAAACGAGTCCTGGCCTTGTCTGTGGAGACGGATTACACCTTCCCACTCGCT
GAAAAGGTCAAGGCCTTCTTGGCTGATCCATCTGCCTTTGAGATGGAGGAGTGGAGGGGTGATGATAAAATGGAA
GCTCCCGTGTCAAGAGATCAGGCAAATGGGGAGACTCCGTGGGATCCTCTGAAGAATCTACATGCACGTACTTAC
GAGAATCAGATTAGGGATGCCTACCACACAGGAGTACCAATGTTTAGTATTAGCCCGTAA

WO 2004/030615

PCT/US2003/028547

714/6881
FIGURE 666

MRSRLRSVSSASGFLGYDVVRDVSSGPFWRRKNGDPCLDLCGRDSSTVWKRGDSPRKREEERSLGISQYLCPNLF
SPTEAVKSKAICLVSISELQAASSGLSSWWLEQGKCGLIEMSGSFRMFHVSVSF SHIVRNRTVPLMRWYLAAMQI
MRGEKQAASGNPAIEAGWERTGAQM

WO 2004/030615

PCT/US2003/028547

715/6881
FIGURE 667

CGCGAAGAAGCTGGCAGGGGCACGAGCCGGGGGCGGGTTTGAAGACGCGTCGTTGGGTTTTGGAGGCCGTGAAAC
AGCCGTTTGAGTTTGGCTGCGGGTGGAGAACGTTTGTTCAGGGGGCCGGCCAAGAAGGAGGCCCGCCTGTTACGAT
GGTGTCCATGAGTTTCAAGCGGAACCGCAGTGACCGGTTCTACAGCACCCGGTGCTGCGGCTGTTGCCATGTCCG
CACCGGGACGATCATCCTGGGGACCTGGTACATGGTAGTAAACCTATTGATGGCAATTTTGCTGACTGTGGAAGT
GACTCATCCAAACTCCATGCCAGCTGTCAACATTTCAGTATGAAGTCATCGGTAATTACTATTTCGTCTGAGAGAAT
GGCTGATAATGCCTGTGTTCTTTTTGCCGTCTCTGTTCTTATGTTTATAATCAGTTCAATGCTGGTTTTATGGAGC
AATTTCTTATCAAGTGGGTTGGCTGATTCCATTCTTCTGTTACCGACTTTTTGACTTCGTCCTCAGTTGCCTGGT
TGCTATTAGTTCTCTCACCTATTTGCCAAGAATCAAAGAATATCTGGATCAACTACCTGATTTTCCCTACAAAGA
TGACCTCCTGGCCTTGGACTCCAGCTGCCTCCTGTTTCATTGTTCTTGTGTTCTTTGCTTATTTCATCATTTTTAA
GGCTTATCTAATTAACGTGTTTTGGAAGTGTCTATAAATACATCAACAACCGAAACGTGCCGGAGATTGCTGTGTA
CCCTGCCTTTGAAGCACCTCCTCAGTACGTTTTGCCAACCTATGAAATGGCCGTGAAAATGCCTGAAAAAGAACC
ACCACCTCCTTACTTACCTGCCTGAGAAATTCTGCCTTTGACAATAAATCCTATACCAGCTTTTTGTTTGTTTA
TGTTACAGAATGCTGCAATTCAGGGCTCTTCAAACCTGTTTGATATAAAATATGTTGCTTTTGTTTAAGCATT
ATTTTCAAACACTAAGGAGCTTTTTGACATCTGTTAAACGTCTTTTTGTTTTTTTGTAAAGTCTTTTACATTTA
ATAGTTTTTGAAGACAATCTAGGTTAAGCAAGAGCAAAGTGCCATTGTTTGCCTTTAATTGGGGGGTGGGAAGGG
AAAGAGGGTACTTGCCACATAGTTTCTTTTTAACTGCACCTTCTTTATATAATCGTTTGCATTTTGTACTTGC
TACCCTGAGTACTTTCAGGAAGACTGACTTAAATATTCGGGGTGAGTAAGTAGTTGGGTATAAGATCTGAACCTT
TCATCTGCAGAGGCAAGAAAAATATTTGACATTGTGACTTGACTGTGGAAGATGATGGTTGCATGTTTCTAGTTT
GTATATGTTTCCATCTTTGTGATAAGATGATTTAATAAATCTCTTTAAATACTT

WO 2004/030615

PCT/US2003/028547

716/6881
FIGURE 668

MVSMSFKRNRSDRFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQYEVIGNYYSSER
MADNACVLFAVSVLMFIISSMLVYGAI SYQVGWLIPFFCYRLDFVL SCLVAISSLT YLPRIKEYLDQLPDFPYK
DDLLALDSSCLLFIVLVFFALFIIFKAYLINCWNCYKYINN RNVPEIAVYPAFEAPPQYVLPTYEMAVKMPEKE
PPPPYLPA

WO 2004/030615

PCT/US2003/028547

717/6881
FIGURE 669

GCGGCTTGCGGGGACACAGCTCCCGAAAGCGACGTTTCGGCCACCGGAGGAGCGGGAGCCAAGCAGGCGGAGCTC
GGCGGGAGAGGTGCGGGCCGAATCCGAGCCGAGCGGAGAGGAATCCGGCAGTAGAGAGCGGACTCCAGCCGGCGG
ACCCTGCAGCCCTCGCCTGGGACAGCGGCGCGCTGGGCAGGCGCCCAAGAGAGCATCGAGCAGCGGAACCCGCGA
AGCCGGCCCCGAGCCGCGACCCGCGCAGCCTGCCGCTCTCCCGCCGCGGTCCGGGCAGCATGAGGCGCGCGGCG
CTCTGGCTCTGGCTGTGCGCGCTGGCGCTGAGCCTGCAGCCGGCCCTGCCGCAAATTGTGGCTACTAATTTGCC
CCTGAAGATCAAGATGGCTCTGGGGATGACTCTGACAACCTTCTCCGGCTCAGGTGCAGGTGCTTTGCAAGATATC
ACCTTGTCACAGCAGACCCCTCCACTTGGAAGGACACGCAGCTCCTGACGGCTATTCCCACGTCTCCAGAACCC
ACCGGCCTGGAGGCTACAGCTGCCTCCACCTCCACCTGCCGGCTGGAGAGGGGGCCCAAGGAGGGAGAGGCTGTA
GTCTGCCAGAAGTGGAGCCTGGCCTCACCGCCCCGGGAGCAGGAGGCCACCCCCGACCCAGGGAGACAGCATCA
GGGTAAAGAAGACTTTTTTTTTTTTTTTTAAACTAGGAGAACCAAATCTGGAAGCCAAAATGTAGGCTTAGTTT
GTGTGTTGTCTCTTGAGTTTGTGCTCATGTGTGCAACAGGGTATGGACTATCTGTCTGGTGGCCCCGTTTCTGG
TGGTCTGTTGGCAGGCTGGCCAGTCCAGGCTGCCGTGGGGCCGCCGCTCTTTCAAGCAAGGCCAGAGGCCCCCA
GCCCAGGGCTCCTGCACCTACTTGCTTATTTGACAACGTTTCAGCGACTCCGTTGGCCACTCCGAGAGGTGGGCC
AGTCTGTGGATCAGAGATGCACCACCAAGCCAAGGGAACCTGTGTCCGGTATTGATACTGCGACTTTCTGCCTG
GAGTGTATGACTGCACATGACTCGGGGGTGGGGAAAGGGGTGGGCTGACCATGCTCATCTGCTGGTCCGTGGGAC
GGTGCCCAAGCCAGAGGCTGGGTTTATTGTGTAACGACAATAAACGGTACTTGTCATTTGGGC

WO 2004/030615

PCT/US2003/028547

718/6881
FIGURE 670

ACTGCGCGCCCCGCGCGGAGTCCCCGCGCGCGTCATGCAGTCCCCGCGGGTGCTCGTCACCTCCAGGCGACTTCA
GAATGCCCACACTGGCCTCGACCTGACTGTGCCCCAGCACCAGGAGGTACGGGGCAAGATGATGTCTGGACACGT
GGAGTACCAGATCCTGGTGGTGACCCGTCTGGCTGCGTTCAAGTCGGCCAAGCACAGGCCCCGAGGATGTCTGTCCA
GTTCTTGGTCTCCAAAAAGTACAGCGAGATTGAGGAGTTTACCAGAACTGAGCAGTCGTTATGCAGCAGCCAG
CCTCCCCCACTACCCAGGAAGGTCCCTGTTTGTGGGGAGTCTGACATCCGGGAGAGGAGAGCCGTGTTCAATGA
GATCCTGCGCTGTGTCTCCAAGGATGCCGAGTTGGCAGGCAGCCCAGAGCTGCTAGAGTTCCTTAGGTACCAGATC
CCCAGGGGCTGCAGGGCTCACCAGCAGAGATTCTCTGTCTGGATGGCACAGACAGTCAGACAGGGAATGATGA
AGAGGCTTTTCGACTTTTTTGTAGGAGCAAGACCAAGTGGCAGAAGAGGGTCCGCCCCGTCCAGAGCCTGAAGGGCGA
GGATGCTGAGGAATCCTTGGAGGAGGAGGAGGCGCTGGACCCCTCTGGGCATTATGCGCTCCAAGAAGCCCCAAGAA
ACATCGGTGTGAAGGGAAGGGACTGGGCCCTGCAGGGTCAGAACCCTCCCCACCCCCAGGGGAGGCCAGGCAGAAG
CCTGGGTACAGCACCCAGAACTGCATGGTTCCATTTCTCCGGGGCTGTGGGGCCAAAGTAGAAGCCTGCGGGC
TGCGGGAGCGGCTCTCACCCCTAGGAGCCAGAGCCCCAATGTGTCTTATCCCCGTGGACATGAAGGGGAGGGAGGG
TGTGGGGATGCCTTGCCAACCAGAAGCCCAGCCCCAAGGATGAAGCAAGACATGTGGGGCCGTAGCGAGGTGTCA
CATGGGGCAGGGAAGCTTCATGCCCACGGGTTCTGCCAGCCCCAGCACAGACCCAACTGGGGCTGGGCCTCTAT
CCCTCCTCTGCCTCTGTTTCGCATAGTAAGAAGGAGTGACCGGTATCCTCCCTTCCCTTACCCTAAGCTGTAGCC
TGGGTGACTGACTGGCCTGGGCCTGGGGTGGGGACGTCCCCAAGCCAAATTACTCCAGGGCCTCTGCTCCTCGTG
GCTGCCAGGGGCTGCAGGGTCTGGGTGGGTCTCCCAGGAGAGGAATACTGAGTGGGAGATCGGCTGTCTGGAGT
GTTCTGATGCAAGTCTCTCTCTCCTGAGCCTCCTCTTGATGCAAGCTCTAAAGGGAGAAGTCAGGCCCTGCCTCT
CCAGGGTATAGACGGCCCTGCTAGGCCCCAGTTCTTCTCCTTCCCCCTTCCCAGGAAAGGCCAGCCCAGTCCA
TGGCCTTCTTGGGCCTCTGGGCACAGAGCCAATGTTTGTGTCATTGCAGCTCTCAGCAAACCTGGGTCTAGCTTTCC
CCACAGCTCAGCCTGGGGCCTGGGCAGGGCTCCCAGCCTGCACCGCCTCCCACTGCCAGTGGGGCATGATTCTCT
CAGGCTTCTGCCCCGAGGCCTTTCGTGCTCCTCAGGGTCTGGACTTGGTCAGTGGCCTTTACCAGTGGAGCTGCC
TTCCCAGGGAGAAGGAGCCGTGCGCCAGGGCAGGGCCCGTGCTTAGACTTCTCCCGACCCCCAGAGCGCTGGTA
CACAGGTCTAGGCACCACACAGTGCTTTGGAAATTCTCAGTGAATGATGTTTAATAAAGCAAAAAATGTC

WO 2004/030615

PCT/US2003/028547

719/6881
FIGURE 671

MQSPAVLVTSRRLQNAHTGLDLTVPQHQEVRGKMMSGHVEYQILVVTRLAAFKSAKHPEDVVQFLVSKKYSEIE
EFYQKLSSRYAAASLPPLPRKVLVFGESDIRERRAVFNEILRCVSKDAELAGSPELLEFLGTRSPGAAGLTSRDS
SVLDGTDSQTGNDEEAFDFFEEQDQVAEEGPPVQSLKGEDAEESELEEEAALDPLGIMRSKKPKKHRCEGKGLGPA
GSEPPHPQGRPGRSLGHSTQNCMPFSPGLWGQSRSLRAAGAALTGARAQCVLFPVDMKGREGVGMPCQPEAQP
QG

WO 2004/030615

PCT/US2003/028547

720/6881
FIGURE 672

ATGGGTCAAAGTCAGAGTGGTGGTCATGGTCCTGGAAGTGGCAAGAAGGATGACAAGGACAAAAAAGAAATAT
GAACCTTCTGTACCAACTAGAGTGAGGAAAAAGAAGAAAAACAAAGGGACCAGATGCAGTCAGCAAACTGCCA
CTGGTGACACCTCACACTCAGTGCCGGTTAAAAATTACTGACATTAGAGAGAATTAAAGACTATCTTCTCATGGAG
GAAGAATTCATTAGAAATCAGGAACAGATGAAACCATTAGAAGAAAAAGCAAAAGGAGGAAAGATCAAAAGTGGAT
GATCTGAGGGGGACCCCGATACAAGGATCTTCTGGAAACTGGCTGCTCGGTCTGCTCAACCACAAGGTGCATGC
CGTGATGGGGTGCTGATGGATGACACGGATCCCTGGTCACAGTGATGAAGATGGAAAAGACCCCCAGGAGACC
TATGCCAATATTGGGGGGCTGGACAACCAAAATTCAGGAAATAAAGGAAGCTGTGGAGTTTCTCTCACCCATCCT
GAATATTATGAAGAGATGGGTAAAAAGCCTCCTAAGGGGGTCATTCTCTATGGTCCACCTGGCACAGGCAAAACC
TTGTTATCCAAAGCAGTAGCAAACCAAAACCTCAGCCACTTTCTTGAGAGTGGTTGGCTCTGAACTTATTGAGAAG
TACCTAGTTGCTGAAGAGCATGAACTATCCATCATGTTTACTGATGAAATTGGAGCCATTGGGACAAAAAGATAT
GACTCAAATTCTGGTGGCCGCATTGACAGGAAGATCAAGTTCTCCCTGCCTGATGAAAGGACTAAGAAGCGTATC
TTTCAGAATCACACAAGCAGGATGACACTGGCCGATGAAGTAACCCCTGGACGACTTGATCATGGTTAAAGATGAC
CTCTCTGGTGCTGACATCAAGGCAATCTGTACAGAAGCTGGTCTGATGGCCTCAAGAGAACGTAGAATGAAAGTA
ACGAATGAATTCTTCAAAAAATATAAAGAAATGTTCTTTATAAGAAACAGGAAGGCACCCCTGAGGGGGCTCTATC
TCTAGTGAACCACAGCTGCCATCAGGAAAATGGTTGGGCGATTCTCGACCCCTGAAAAGGATGAGCAACTTGT
CCCAAAGCTGGAGAAGACACTCCTGAGGGCTATTTAGGACAACCTTATGACTCAGCTCTTTGAGCAGAAAGAGGCC
AAAAAGTTTCAAGCAGAAAAAGCCCTGAACTCTTGGAAGAGCTGGCTTCAAGCCTGGCTTAG

WO 2004/030615

PCT/US2003/028547

721/6881
FIGURE 673

MGQSQSGGHGPGSGKKDDDKKKKKYEPSVPTVRKKKKKTKGPDAVSKLPLVTPHTQCRLKLLTLERIKDYLLME
EEFIRNQEOMKPLEEKQKEERSKVDDLRGTPIQGSSGNWLLGPAQPQGACRDGVLMDDDTDLVTVMKMEKTPQET
YANIGGLDNQIQEIKEAVEFFPLTHPEYYEEMGKKPPKGVILYGPPGTGKTLLSKAVANQTSATFLRVVGSELIQK
YLVAEEHEL SIMFTDEIGAIGTKRYDSNSGGRIDRKIKFSLPDERTKKRIFQNHTSRMTLADEVTLDDLIMVKDD
LSGADIKAICTEAGLMASRERRMKVTNEFFKKYKEMFFIRNRKAPLRGSISSEPQLPSGKWLGDSSTPEKDEQLV
PKAGEDTPEGYLGQLMTQLFEQKEAKKFSRKSPELLEELASSLA

WO 2004/030615

PCT/US2003/028547

722/6881
FIGURE 674

GACGGCGCCTTCGCGAAACACTATGCTAATGGCATGGTGCCGCGGTCTGTCTTGCTGTGCCTGCGGCAGGGGCT
CGGAACCAATTCATTCTGCACGGCTGGGGCAGGAGCCCTTCGAGGGAGCTCGGTCACTGTGTTGCAGGTCCTC
GCCTAGAGACCTGCGAGATGGAGAAAGAGACGACGAGGCGGCACAAAGGAAAGCCCCAGGAGCAGAGTCTTGCCC
ATCTCTCCCTCTGAGCATCTCGGACATTGGGACTGGATGTCCTTCGTCACTGGAAAACCTCAGACTGCCGACGCT
GCGGGAAGAGTCATCACCTCGAGAGCTCGAGGACTCGAGCGGAGACCAGGGCCGGTGCGGTCCCACACACCAGGG
ATCCGAGGATCCTTCGATGCTCTCGCAGGCCAGTCCGCTATCGAGGTCTGAAGAGCGTCACGTCTCCCCTTCTTG
TTCAACTTCCAGAGAGAGACCCTTTCAGGCTGGGGAGCTGATTTTAGCTGAGACTGGGGAGGGAGAAAACAAAATT
TAAGAAATTATTTAGGTTGAACAACCTTCGGACTCTTAAATAGTAACTGGGGGGCAGTCCCCTTCGGCAAGATCGT
GGGGAAGTTCCCCGGCCAGATACTGAGGAGTTCCTTCGGTAAGCAGTACATGCTGAGGAGGCCAGCCTTGGAAGA
CTATGTAGTATTGATGAAAAGAGGGACTGCCATAACATTCCTCAAAGGATATTAATATGATTCTCTCAATGATGGA
TATCAACCCAGGTGATACTGTTTTGGAAGCTGGCTCAGGCTCTGGTGGAATGAGCTTATTTTTATCCAAAGCAGT
TGGATCACAAGGACGAGTCATAAGTTTTGAGGTACGAAAAGACCACCATGATCTGGCTAAGAAGAATTACAAACA
CTGGCGTGATTGATGAAATTAAGTCATGTAGAAGAGTGGCCAGACAATGTGGATTTTATTCATAAGGACATTC
AGGAGCAACCGAAGACATAAAATCTTTAACATTTGACGCAGTAGCTTTGGATATGTTAAATCCTCATGTTACTTT
GCCTGTTTTTTACCCACATCTTAAGCATGGTGGTGTATGTGCTGTATATGTAGTAAACATCACACAGGTTATTGA
ACTTTTAGATGGAATTCGCACCTGTGAACCTTGCTCTTTCATGTGAAAAGATAAGCGAGGTCATTGTCAGAGATTG
GTTGGTTTGCCTTGCAAAACAGAAAATGGAATTTTAGCTCAAAAAGTAGAATCTAAAATCAACACAGATGTACA
ACTAGATTCTCAAGAGAAAATTTGGAGTTAAAGGTGAGCTGTTTCAAGAGGATGACCATGAAGAATCGCATTCGA
TTTTCCATATGGATCATTTCCTATGTTGCTAGACCAGTACACTGGCAACCTGGTCATACAGCTTTTCTTGTCAA
GTTGAGGAAGGTCAAACCACAACCTTAACCTGAGTACTCCAGATGACAGTAACTGACTTGAAGATGGAAAAATATCA
AAATAGAACCTTTATATTGAAAATCACTGCTTCCATAGATTGGCATTTTTAGCTATTACTATGACTTATATAACTT
ATACATATAATTTTGAAAATAACAATAAAGATGTATAACATAGCAAACTGCTTAAACATCCCATTTTGACAC
TTGTCTTGACAGTTAGTTTGACATTTTGTAGTTAATGATTCCAAATTGGTTTAGTTGGGCCATCTCATTCTTCACT
TCCTGTAAACCACTCCATAGATTTGTCTTTCTTCAAGAAATTAGTTTTCTTTCTTTATTTGATTGATGGTCATT
GACTACTGAAATAAAATATGCATTTTAAGATAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

723/6881
FIGURE 675

MLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSLCCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSIS
DIGTGCLSSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSSEDPMSLSQAQSAIEVEERHVSPSCSTSRERP
FQAGELILAETGEGETKFKKLFRLNNFGLLSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRPALEDYVVLMKR
GTAITFPKDINMILSMMDINPGDTVLEAGSGSGGMSLFSLKAVGSQGRVISFEVRKDHDLAKKNYKHWRDSWKL
SHVEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVFYPHLKHGGVCAVYVVNITQVIELLDGIRT
CELALSCEKISEVIVRDWLVLAKQKNGILAQKVESKINTDVQLDSQEKIGVKGELFQEDDHEESHSDFPYGSFP
YVARPVHWQPGHTAFLVKLRKVKPQLN

WO 2004/030615

PCT/US2003/028547

724/6881
FIGURE 676

ATGCAACAAGCTTCCTACCCCCAACCCGGCCAGACAAAGCCCCGGCAGCAGGGCCGGCACTTCCGAGCCTCCGGA
CTCGGGACGCCGCGCTCTTACCCTGGCCTCATCCAGAGTGACGCCGGCGCCACCGCTTCCCCCGGCTTTGGCGGC
GGGGCAGCTGGCGGCGCGGGTCTTGGAGGAGCGGGTCCGAGAGGAGATGAAATGGCTGCTGCCTCCGGTCGCCCC
AGGCTCTGCTCCGGCCCCCAGGCCCCAGGCCCCGGGACCAGGAGACTTGGACCCGAGAAGGCGGAGAGAGCTCTTCCG
GGTGTTCACCATGGTCCAGCCAGGGGGACGGAGTCCACGCCGCGCCCCGGGAGAGCCGAGCAAGGCCGGCCCCGCCG
GCCGCTGCCCCGCCCCCGGCGCGGCGTCAGCGCTCGGCGGCCGGGGAGCGACGCTCTAGGCTGTGAGCTCGGTGG
TTTCCAGCTCTCCCCGACCGCAGGGCTGGGGCGACCAGAAAAGCCAGACTAATCAGGACGAGTTCGGGCGTGGAA
TTGGGCCTGAAGCCCTCATGCCCAGCCAGGCCTGAATGCCCCAGACCCCAACCGTCACCCCGTGGCCTGGATGGA
GCAGGGGACGGCCGGCGAAGGCGCGGGGTGGAAGGGGAGCGGCGACGAAGGCGCGAGGAGCTGACTGGGAATCCC
CAAGCTACCCGAGGCAAGACACTGAACTTGAGTCGCACTTTTCATGCCTGTAGAAATGAGAATGACAGCTGTGAT
AAAAAAAAAATTTCATCTGGGCGGTATCTGGAAGTTGGGCGTTCCGAACTTACAGTTATGCGCAACACAATGTTT
CTATTTTCAAAGGCGAACGCTGCACGATCGCAGTCCAGTGATACAAATAATAAAGAGTTTATTACTTGTGAGCA
ATGATGAATGTTTCGTGTGGCATCCAGCGTTGAGTTCCTATTCTTACTTGGAATCATTGGTCCCTGTGTCTGGGG
CCAGCACTGATGGACACAATAAGTTTGAAGTTCGTCTTCCCTCTCATGTATCATACTGGAATGGGATCCAACAC
TTGATGTGGGACCTAGGAAAAGGCCTGAAGATTCCCCAGCTATACCAGTCTGGAGTGGTTGTCCTGGTTCTTACT
GTGTTATTTGTAGGGCTGGCAGCTGTGTGA

WO 2004/030615

PCT/US2003/028547

725/6881
FIGURE 677

MQQASYPQPGQTKPRQQGRHFRASGLGTPRSYPGLIQSDAGATASPGFGGGAAGGAGLGGAGPRGDEMAAASGRP
RLCSGPRPRPGTRRLGPEKAERALPGVHHGPARGTESTPRPGEPKAGPPAAAPPPARRQSAAGERRSRLSARW
FPALPDRRAGATRKARLIRTSSGVELGLKPSCPARPECPRPHRHPRGLDGAGDGRRRRRGVEGERRRRREELTGNP
QATRGKTLNLSRTFHACRNENDSCDKKKIHLGGIWNLGVPKLTVMRNTMFLFSKANAARSQSSDTNNKRVYYLSA
MMNVRVASSVEFLFLGTHWSLCLGPALMDTTKFALVFPLMYHTWNGIQHLMWDLGKGLKIPQLYQSGVVVLVLT
VLFVGLAAV

WO 2004/030615

PCT/US2003/028547

726/6881
FIGURE 678A

ACAGAGAGATTGGTGTIIITTTGTGAGGCAGTGAGACCTAAGGTAACCTTTATCAAAAGGATGGAGTTGGGAAAAGG
AAAAC TACTCAGGACTGGACTGAATGCGTTGCATCAAGCAGTGCCATCCATGGCCTTGCCCTGGACCGATGG
GAATCAAGTTGTCCTAACTGATTGCGGCTTCACAGTGGAGAGGTCAAGTTTGGGGACTCCAAAGTCATTGGACA
GTTTGAATGTGTCGTGGGTGTCTCGGGCCCCACCTGTTGCAGATGATACACCTGTTCTACTCGCTGTCCAGCA
TGAGAAGCATGTCACTGTGTGGCAGCTGTGTCCCAGCCCTATGGAGTCAAGCAAATGGCTGACGTCTCAGACTTG
TGAGATTAGAGGATCACTACCTATCCTTCCCCAGGGCTGTGTGTGGCACCCAAAATGTGCTATTCTGACTGTGTT
GACTGCTCAGGATGTCTCCATTTTCCCTAATGTTCACTCTGATGATTCCCAGGTAAAGGCAGACATCAACACCCA
GGGCCGCAATCACTGTGCATGTTGGACCCAGGATGGCCTGAGGCTGGTGGTGGCAGTAGGCAGCAGCCTGCATT
TTATATTTGGGACAGCGCTCAGAAAGACTCTTCACAGGTGCTCCTCCTGCCTGGTGTGTTGATGTGGACAGCCACGT
CTGCTCCATCAGCAACTGTGGACTCACAGGTTGCTATAGCTACTGAGCTTCCATTGGATAAGATCTGTGGCTT
AAATGCATCTGAAACCTTTAATATCCCACCTAACAGTAAAGACATGACTCCGTATGCTTTACCAGTTATTGGTGA
AGTACGCTCTATGGATAAAGAGGCAACTGATTCTGAAACAAATTCTGAAGTATCAGTTTCTTCTTCTCTATTAGA
ACCTCTGGATCTAACTCACATACATTTCAATCAACATAAGTCTGAGGGTAATTCTCTTATTTGTCTAAGAAAAA
GGACTACTTGACAGGAACCTGGCCAAGATTCTTCACATTTGGTCTTGTGACCTTTAAGAAGGCAGTTACCATGAC
GAGAAAAAGTCACTATTCCAGGCATTCTGGTTCCTGATCTGATAGCATTTAATCTTAAAGCCACGTAGTGGCAGT
GGCTTCCAACACTTGTAATATAATTTTGATCTACTCTGTCTATTCCATCTTCAGTCCCAAACATCCAGCAAATTCG
ATTAGAGAACACTGAAAGACCAAAAGGGATATGTTTCTTGACAGACCAACTATTACTAATTTTGGTAGGAAAACA
AAAAC TACTGATACAACATTTCTTCTTCTTCAAAGTCTGATCAGTATGCCATTAGCTTGATTGTTAGAGAAAT
AATGTTGGAAGAAGAACCTTCAATAACATCAGGTGAAAGCCAGACTACCTACTCTACTTTTCACTGCTCCGTTAA
TAAAGCAAATAGAAAAAAGTTAATTGAAAGTCTTTCCTCAGATTTTGTACCAAACAAAGGGCTGTGCTGAC
AGTTAATACCAGTAGTCAGAATGGAAGGCCTGGAAGAACCTTATTAAAGAAATCCAGAGTCTCTGTCTAGTAT
CTGTGATGGCTCCATAGCTCTAGATGCTGAGCCTGTTACCCAGCCAGCATCGCTGCCAGACACAGCAGCACACC
AGACCACACCAGCACACTGGAGCCTCCTCGTTTGCTTCAAAGAAAGAACTTACAAAGTGAAGGAAACTTATCA
GCTGTCTAAGGAGGTGGAAATTTTATCTAGGAACCTGGTTGAAATGCAACGGTGTCTTTCTGAACCTTACAAACCG
TCTGCATAATGGGAAGAAATCCTCTTCAGTGTATCCACTCTCTCAAGATCTTCTTATGTTACATCATTACCA
GAAACCTTATTATCTAGGTCCTGTTGTTGAAAAAGAGCGGTGCTTCTCTGTGATGGTAACTAAGGCTCAGTAC
AGTTCAGCAGACTTTTGGCCTTTCTCTCATTGAAATGCTACATGATTCCCACTGGATTCTTCTCTCTGCTGACAG
TGAGGGCTTTATCCCGTTAACCTTCACAGCCACACAGGAAATAATCATAAGAGATGGCAGCCTGTCCAGGTCAGA
TGCTTTCAGAGACTCTTTTTCTCACAGTCCAGGTGCTGTTTCTTCTTAAAGTCTTTACAGGCCTTGCTGCCCC
CAGTTTAGATACCCTGGCTGTTGTAACCATGTAGATGGCATGGCTTGATATCTGCAGTGTCTTGTGTGTAGC
TCTTCAGATGAGACCATTACAAACAAGGCCTGCTTGACACTGGACACTGCCAATGAGACTCCCACTGCACCTCAG
GCGAAGCGCTTGCCATGGTGGCTCTCCTGGTTTCCCCCTGTTTCCCCCTGAGCTGAGGCTCGCTGCTGTGTAGCA
GAGCTCAGTCTTTATTAGATGGCTCCGAAAGTGGTGTATTGATTCATGACTGTGTGGTTTTGACTAAGGGCAG
AATTCTCAGAACAAACAATATTATGGTGCCATATGGATGGTGTGTTTTATGGTTTTCTCTGAGGCTTTGTGTCCCTT
GTCCAAGCTGCATTGAAGCTGTCTTAGGAGCACTTAAAGATACCTTGGCATTGTTATAGGCTTTTTCTTGGC
TTCAAGAGGAGGTTGAGGAGTCTGCTGGGGGGCATGTGCTCTAGCATATTAACCTCAAACCAGCAAGAATTAGCA
GAGCTCCAAGGAGGACCAGAGACCCACTGGCTTCTGCTCTCAGGAACAGGAAGTGGCTCTGATGTTGCCTGGACC
TCCCAGAATTTAAACCAACCCCTCTTGCTTCTTAAACAAATTCTGGCTGACGAAGTCCAGGTACTCTTAAAAAC
TGGCCCTGGGAAAATTTTGAATGAAATTTCAAGGGAATTTGTCCCTCTGGGTTCCACTTGAGGTTGTGCCGATG
CTGCTACCACACTGTGAGCCAGGTAAGTCTTACTGCAGGATTTTGTGCTGTGGCCACTCATGAGTGTCCCTGA
AATAACTTTTTTTTTTTTTTAAATCCAGTTTGGGATCACGCAACTTTCCTATTTTTCTCCAGTAGTCAGCTCCC
TTAGTTAACTTGTCACTTTAATTTGATATTTTTATTTTCTCTCCTTTTAAAGTCTTAGAGACCAGCAGAGAATCTG
TGAGAGAAAGTATTTAGGAAGTTAGAAATCAACCGAATCTGAGGTAGTCCATAAAAGTGCCATTTTGTTCAC
TTATGGGCTAAAGTACCAGCTTAGTCAGGTAAGAGCCCTGACCACCTCAGATGGTAACACCACTTCTCACTGCC
TTCAGATGGAATCACAGATTTCACTCAGGCGCATAACAAATGATCAGTGAAGTGGCTAGGCATCTGCAGATAAA
TTGTTTTCAGCCATAGAAGCTCCATTAGCACATATGCTTCTTTTCCCCCTTCTTTAAATCATCTGGAAAGAA
ACTATTTTGTGCCCTTGGGGACTCCTGTCTGTCTGTTACAGTTTACCAAGATGGAGCTGGGTTAGGAAAGAAGTG
AGGGCCCATTTTGTGGTTCAAGTGCCTAGACAGCTGCTGGGGTAGGAAGCACAGGCAATGTCTGCAATCAGCTG

WO 2004/030615

PCT/US2003/028547

727/6881
FIGURE 678B

TGGGAGAGCGGTGACTGAGAACAGTCTGAGGCCTGGCTCCACTTGGAAGTATCTGGGGTGCGATGAAATCACAAT
TATCTTGAAGCCTAAAGAGGGAAC TACAAGACTGT TAACTAAGATCAATGTGGGCACCTAAAAGGGTATGTTAAA
ATCACCATTTCTCAGGTCAAATACTGTGAAATAAAAAATGGAAACGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

WO 2004/030615

PCT/US2003/028547

728/6881
FIGURE 679

MELGKGKLLRTGLNALHQAVHP IHGLAWTDGNQVVLTDLRLHSGEVKFGDSKVIQFECVCGLSWAPPVADDTPV
LLAVQHEKHVTVWQLCPSPMESSKWLTSTQCEIRGSLPILPQGCVWHPKCAILTVLTAQDVSI FPNVHSDDSQVK
ADINTQGRIHCACWTQDGLRLVVAVGSSLHSYIWD SAQKTLHRCSSCLVFDVD SHVCSITATVDSQVAIATELPL
DKICGLNASETFNIPPNSKDMTPYALPVIGEVRSM DKEATDSETNSEVSVSSSYLEPLDLTHIHFNQHKSEGNSL
ICLRKKDYLTGTGQDSSHLVLVTFKKAVTMRKVTIPGILVPDLIAFNLKAHVAVASNTCNI ILIYSVIPSSVP
NIQQIRLENTERPKGICFLTDQLLLILVGKQKLTDTTFLPSSKSDQY AISLIVREIMLEEEPSITSGESQTTYST
FSAPLNKANRKKLIESLSPDFCHQNKGLLLTVNTSSQNGRPGR TLIKEIQSPLSSICDGSIALDAEPVTQPASLP
RHSSTPDHTSTLEPPRLPQRKNLQSEKETYQLSKEVEILSRNLVEMQRCLSEL TNRLHNGKKSSSVYPLSQDLPY
VHIYYQKPYYLGPVVEKRAVLLCDGKLR LSTVQQTFGLSLIEMLHDSHWILL SADSEGFIPLTFTATQEIIIRDG
SLSRSDVFRDSFSHSPGAVSSLKVFTGLAAPSLDTTGCCNHVDGMA

WO 2004/030615

PCT/US2003/028547

729/6881
FIGURE 680

TTCTCTTAGCAGCACCCAGCTTGCCACCCATGCTCAAGATGGGCGGGATGCCAGCCTGTTACATAAAATGTGCCA
AAAGCCTGGCCATGCCTGGAAAATGGACCAATCCGCCCGCCAAGAGGTGGGTCTCGTTCCCTAGAGAGAAGGAA
GTTTCCTCTCCTTGAAGTGAGAGCTAGAATCGCACTTTCTGTCAAGCTGAGAGAAAGACTCTTTTCCAGAGGCTA
AAAGGACAAGAAAATCTGATTTGCTTGCTTCTAACTTTGCGTTTTAAAGGGGGAAGGAGGAAAGGAAAGAGGGG
AGGGTGCTTCTGCTTAGCCCCACCCCTCCGGCTACCCAGGTCCAGCCGTCCATTCCGGTGAGGCAGAGGCAGT
CCTGGGGCTCTGGGGCTCGGGCTTTGTACCGGGACCCGAGGAGCCAGAACCCTCGGCGCCGCCTGGTGCATG
GGAGGGGAGCCGGGCCAGGAACAATATGTTAGCCGTGCACTTTGACAAGCCGGGAGGACCGGAAAACCTCTACGT
GAAGGAGGTGGCCAAGCCGAGCCCGGGGGAGGGTGAAGTCCTCCTGAAGGTGGCGGCCAGCGCCCTGAACCGGGC
GGACTTAATGCAGAGACAAGGCCAGTATGACCCACCTCCAGGAGCCAGCAACATTTTGGGACTTGAGGCATCTGG
ACATGTGGCAGAGCTGGGGCCTGGCTGCCAGGGACACTGGAAGATCGGGGACACAGCCATGGCTCTGCTCCCCGG
TGGGGGCCAGGCTCAGTACGTCACTGTCCCCGAAGGGCTCCTCATGCCTATCCCAGAGGGATTGACCCTGACCCA
GGCTGCAGCCATCCCAGAGGCCCTGGCTCACCGCCTTCCAGCTGTTACATCTTGTGGGAAATGTTTACGGCTGGAGA
CTATGTGCTAATCCATGCAGGACTGAGTGGTGTGGGCACAGCTGCTATCCAATCACC CGGATGGCTGGAGCTAT
TCCTCTGGTCACAGCTGGCTCCCAGAAGAAGCTTCAAATGGCAGAAAAGCTTGGAGCAGCTGCTGGATTCAATTA
CAAAAAAGAGGATTTCTCTGAAGCAACGCTGAAATTCACCAAAGGTGCTGGAGTTAATCTTATTCTAGACTGCAT
AGGCGGATCCTACTGGGAGAAGAACGTCAACTGCCTGGCTCTTGATGGTTCGATGGGTTCTCTATGGTCTGATGGG
AGGAGGTGACATCAATGGGCCCCGTGTTTTCAAAGCTACTTTTTAAGCGAGGAAGTCTGATCACCAGTTTGCTGAG
GTCTAGGGACAATAAGTACAAGCAAATGCTGGTGAATGCTTTACGGAGCAAATCTGCCTCACTTCTCCACGGA
GGGCCCCAACGTCTGCTGCCGTTCTGGACAGAATCTACCCAGTGACCGAAATCCAGGAGGCCATAAGTACAT
GGAGGCCAACAAAGACATAGGCAAGATCGTCCTGGAATGCCCCAGTGAAGGAGGATGGGGCAGGACAGGACGCG
GCCACCCAGGCCTTCCAGAGCAAACCTGGAGAAGATTACAATAGACAGGCCAAGAAACCCGGTGCTTCTCTCC
AGAGCCGTTTAAAGCTGATATGAGGAAATAAAGAGTGAAGTGG

WO 2004/030615

PCT/US2003/028547

730/6881
FIGURE 681

GGCACGAGGGTCCCGTTACCGCCTCCTGCTCCTGCCGCGCGCACCCCCGGGGCTTCGGCTCCGGCACGGGTGCGG
CCCAGCTTTCTTGACCTGAGGCCGCCGGCCAGCCGCCGCCATGGGTGCCTACCTCTCCCAGCCCAACACGGTGA
AGTGCTCCGGGGACGGGGTCCGGCGCCCCGCGCCTGCCGCTGCCCTACGGCTTCTCCGCCATGCAAGGCTGGCGCG
TCTCCATGGAGGATGCTCACAACGTGATTCTGAGCTGGACAGTGAGACAGCCATGTTTTCTGTCTACGATGGAC
ATGGAGGGGAGGAAGTTGCCTTGTACTGTGCCAAATATCTTCTGATATCATCAAAGATCAGAAGGCCTACAAGG
AAGGCAAGCTACAGAAGGCTTTAGAAGATGCCTTCTTGGCTATTGACGCCAAATTGACCACTGAAGAAGTCATTA
AAGAGCTGGCACAGATTGCAGGGCGACCCACTGAGGATGAAGATGAAAAAGAAAAAGTAGCTGATGAAGATGATG
TGGACAATGAGGAGGCTGCACTGCTGCATGAAGAGGCTACCATGACTATTGAAGAGCTGCTGACACGCTACGGGC
AGAAGTGTCAAAAGGGCCCTCCCCACAGCAAATCTGGAGGTGGGACAGGCGAGGAACCAAGGGTCCCAGGGCCTCA
ATGGGGAGGCGAGGACCTGAGGACTCAACTAGGGAACTCCTTCACAAGAAAATGGCCCCACAGCCAAGGCCTACA
CAGGCTTTTCTCCAACCTCGGAACGTGGGACTGAGGCGAGGCCAAGTTGGTGAGCCTGGCATTCCCCTGGTGAGG
CTGGGCCCTTCTGCTCTTCAGCCTCTGACAAGCTGCCTCGAGTTGCTAAGTCCAAGTTCTTTGAGGACAGTGAGG
ATGAGTCAGATGAGGCGGAGGAAGAAGAGGAAGACAGTGAGGAATGCAGCGAGGAAGAGGATGGCTACAGCAGTG
AGGAGGCAGAGAATGAGGAAGATGAGGATGACACCGAGGAGGCTGAAGAGGACGATGAAGAAGAAGAAGAAGAGA
TGATGGTGCCAGGGATGGAAGGCAAAGAGGAGCCTGGCTCTGACAGTGGTACAACAGCGGTGGTGCCCTGATAC
GAGGGAAGCAGTTGATTGTAGCCAACGCAGGAGACTCTCGCTGTGTGGTATCTGAGGCTGGCAAAGCTTTAGACA
TGTCTATGATCACAAACCAGAGGATGAAGTAGAACTAGCACGCATCAAGAATGCTGGTGGCAAGGTCACCATGG
ATGGGCGAGTCAACGGGGGCTCAACCTCTCCAGAGCCATTGGGGACCACTTCTATAAGAGAAACAAGAACCCTGC
CACCTGAGGAACAGATGATTTAGCCCTTCTGACATCAAGGTGCTGACTCTCACTGACGACCATGAATTCATGG
TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCAATCAATCAAAGATCAGCC
AGCGTGATGAAAATGGGGAGCTTCGGTTATTGTTCATCCATTGTGGAAGAGCTGCTGGATCAGTGCTGGCACCAG
ACACTTCTGGGGATGGTACAGGGTGTGACAACATGACCTGCATCATCATTGCTTCAAGCCCCGAAACACAGCAG
AGCTCCAGCCAGAGAGTGGCAAGCGAAAAGTAGAGGAGGTGCTCTCTACTGAGGGGGCTGAAGAAAATGGCAACA
GCGACAAGAAGAAGAAGGCCAAGCGAGACTAGCAGTCACTCAGACCCCTGCCACCTAGACTGTTTTCTGAGCCC
TCCGGACCTGAGACTGAGTTTTGTCTTTTTCCTTTAGCCTTAGCAGTGGGTATGAGGTGTGCAGGGGGAGCTGGG
TGGCTTCACTCCGCCCATTCCAAAGAGGGCTCTCCCTCCACACTGCAGCCGGGAGCCTCTGCTGTCCTTCCCAGC
CGCCTCTGCTCCTCGGGCTCATCACCGGTTCTGTGCCTGTGCTCTGTTGTGTTGGAGGGAAGGACTGGCGGTTCT
GGTTTTTACTCTGTGAACCTTTATTTAAGGACATTCTTTTTTATTGGCGGCTCCATGGCCCTCGGCCGCTTGCAAC
CGCTCTCTGTTGTACACTTTCAATCAACACTTTTTTCAGACTAAAGGCCAAAACCTAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

731/6881

FIGURE 682

MGAYLSQPNTVKCSGDGVGAPRLPLPYGFSAMQGWRVSMEDAHNCIPELDSETAMFSVYDGHGGEEVALYCAKYL
PDIIKDQKAYKEGKLQKALEDAFLAIDAKLTTEEVikelAQIAGRPTEDeDEKEKVADEDDVDNEEAALLHEEAT
MTIEELLTRYGQNCHKGPPHSKSGGGTGEEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFSSNSERGTEAG
QVGEPGIPTGEAGPSCSSASDKLPRVAKSKFFEDSEDESDEAEEDSEECSEEDDGYSSSEAEENEDEDDEE
AEEDDEEEEEEMVPGMEGKEEPGSDSGTTAVVALIRGKQLIVANAGDSRCVVSEAGKALDMSYDHKPEDEVELA
RIKNAGGKVTMDGRVNGGLNLSRAIGDHFYKRKNLPPPEQMISALPDIKVLTLTDDHEFMVIACDGIWNVMSSQ
EVVDFIQSKISQRDENGELRLLSSIVEELLQCLAPDTSGDGTGCDNMTCIICFKPRNTAELQPESGKRKLEEV
LSTEGAEENGNSDKKKKAKRD

WO 2004/030615

PCT/US2003/028547

732/6881
FIGURE 683

CCACTGCCGCTGCCGCCGCTCTCCTTAGTCGCCGGCATGACGACCGCTCTACCTCGCAGGTGCGCCAGAACTT
GCTGAGAAATTGATGAAGCTGTAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGT
GCGGGGAGAATGCGATGGGAGAGCGGGCTGAATGCGATGGATTACATTTGGAAAAAATTGTGCATTTTGCATTAC
ATTTGGAAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCCCCATTTGT
GTGACTTCATTGAGACACATTACCTGAATGAACAAGTGAAGGCCATCAAAGAATTGGGTGACCACGTGACCAACA
TGCACGAGATGGGAGCGCCCGAATCTGGCGTGGCAGAATACCTCTTTGACAAGCACACCCTGGGAGACAGTGATA
ATGAAAAGCTAAGCCTCAGGCTAATTTCCCATAGCCATAGGGTGAAGTACCTTGTCACCAAGGCAGCGCATGTAT
GTTGGGGTTTCTTTACCTTTTCTATAAGTTGTTCCAAGACACCCACTTAAGTTCTTTGATTTGTACCATTCTT
CAAATAAAATAAATTTGGTACCC

WO 2004/030615

PCT/US2003/028547

733/6881
FIGURE 684

CCCTATCCGGACAGGTGGCTCTTGCCCTTTAGACTACAGTTCCCAGCATGCCAGGCGATTGCGTCCCAGAACCG
ACGTCCCACCGCCTTCCCACATCGGATCGCAGGGCTCCCAAAATGGCGAGTGAGGCTGCGGGGACTCGCTGAGCA
GCGGAGGGGGAGCGTGAGAGCCGCTGCGGCCCTCACAGTCCGGAGCCCGGCCGTGCCGTAGGGAACATG

CACTTTTCCATTCCCGAAACCGAGTCCCGCAGCGGGGACAGCGGCGGCTCCGCCTACGTGGCCTATAACATTAC
GTGAATGGAGTCTGCACTGTGCGGTGCGCTACAGCCAGCTCCTGGGGCTGCACGAGCAGCTTCGGAAGGAGTAT
GGGGCCAATGTGCTTCCCTGCATTCCCCCAAAGAGCTTTTCTCTCTGACTCCTGCTGAGGTAGAACAGAGGAGA
GAGCAGTTAGAGAAGTACATGCAAGCTGTTTCGGCAAGACCCATTGCTTGGGAGCAGCGAGACTTTCAACAGTTTC
CTGCGTCGGGCACAACAGGAGACACAGCAGGTCCCCACAGAGGAAGTGCTCTTGAAGTGCTGCTCAGCAACGGG
CAGAAAGTTCTGGTCAACGTGCTAACTTCAGATCAGACTGAGGATGTCTTGGAGGCTGTAGCTGCAAAGCTGGAT
CTCCAGATGACTTGATTGGATACTTTAGTCTATTCTTAGTTCGAGAAAAAGAGGATGGAGCCTTTTCTTTTGTA
CGGAAGTTGCAAGAGTTTGAGCTGCCTTATGTGTCTGTACACAGCCTTCGGAGTCAAGAGTATAAGATTGTGCTA
AGGAAGAGTTATTGGGACTCTGCCTATGATGACGATGTATGGAGAACCAGGTTGGCCTGAACCTGCTTTATGCT
CAGACGGTATCAGATATTGAGCGTGGGTGGATCTTGGTCACCAAGGAACAGCACCGGCAACTCAAATCTCTGCAA
GAGAAAGTCTCCAAGAAGGAGTTCTTGAGACTGGCCCAGACGCTGCGGCACTATGGCTACTTGCGCTTTGATGCC
TGTGTGGCTGACTTCCCAGAAAAGGACTGTCTGTGGTGGTGAGCGCGGGCAACAGTGAGCTCAGCCTGCAGCTC
CGCCTGCCTGGCCAGCAACTCCGAGAAGGCTCCTTCCGGGTACCCGCGATGCGATGCTGGCGGGTCACCTCCTCT
GTACCATTGCCAGTGGAAGCACGAGCAGCCAGGCCGGGGCGGGGTGAGGTGCGCCTGGAACCTGGCTTTTGAA
TACCTCATGAGCAAGGACCGGCTACAGTGGGTACCATCACTAGCCCCCAGGCTATCATGATGAGCATCTGCTTG
CAGTCCATGGTTGATGAACTGATGGTGAAGAAATCTGGCGGCAGTATCAGGAAGATGCTGCGCCGGCGGGTGGG
GGTACTCTGAGACGCTCAGACAGCCAGCAAGCAGTGAAGTCCCCACCACTGCTTGAGTCACCTGATGCCACCCGG
GAGTCTATGGTCAAACCTCTCAAGTAAGCTGAGTGCCGTGAGCTTGCGGGGAATTGGCAGTCCCAGCACAGATGCC
AGTGCCAGTGATGTCCACGGCAATTTGCGCTTCGAGGGCATTGGAGATGAGGATCTGTAATCTCCACTGCTTGGA
TGTCTGCCCTCTACCCAGAGGAATTTACAGAACTTGCCCTGTGCTGTGTCCCCATGCTAGGGGCGGAGGGG
TCTTTTCTTCTTCTTCTACCTACCCCTTTTCTCTTGGCCAGGGGCTCGTATCCTACCTTTCTTGTCCCCT
GGGCTGGCTGCACAGAGGATTGCCCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTT
GCACAAAGTCTAAGGGACCATGGCTGCCTGCCTTGGGGAGGAACCATAGCTCCCTCTGGGCCGCTTCTGGCCTCT
TGGAGCCATGGGCCAAAGGCCAAGGGGATGGGCAGAGTCTGTGTTTGGTCTGGCCAGTTCGCCATCATTAAAC
TCAGCCTGACTGCTGCCT

WO 2004/030615

PCT/US2003/028547

734/6881
FIGURE 685

MHFSIPETESRSGDSGGSAYVAYNIHVNGVLHCRVRYSQLLGLHEQLRKEYGANVLPAPPPKKLFSLTPAEVEQR
REQLEKYMQAVRQDPLLGSSETFNSFLRRAQQETQQVPTTEVSLEVLLSNGQKVLVNVLTSDQTEDVLEAVAAKL
DLPDDLIGYFSLFLVREKEDGAFSFRKLQEFELPYVSVTSLRSQYKIVLRKSYWDSAYDDDV MENRVGLNLLY
AQTVSDIERGWILVTKEQHRQLKSLQEKVSKKEFLRLAQTLRHYGYLRFDACVADFPEKDCPVVVSAGNSELSLQ
LRLPGQQLREGSFRVTRMRCWRVTSSVPLPSGSTSSPGRGRGEVRLELAFEYLMKDRLOWVTITSPQAIMMSIC
LQSMVDELMVKKSGGSIRKMLRRRVGGTLRRSDSQAVKSPPLLESPDATRESMVKLSSKLSAVSLRGIGSPSTD
ASASDVHGNFAFEGIGDEDL

WO 2004/030615

PCT/US2003/028547

735/6881
FIGURE 686

GATGGCTGCTGTGGCCGTGGCTGTTTCGCGAGGACTCGGGATCCGGGATGAAGGCGGAGCTTCCCCCTGGGCCTGG
GGCAGTGGGGAGGGAAATGACCAAAGAAGAAAAGCTGCAGCTTCGGAAGGAAAAGAAAACAGCAGAAGAAGAAACG
GAAGGAAGAAAAGGGGGCAGAACCAGAGACTGGCTCTGCTGTATCTGCAGCCCAATGTCAAGTAGGCCCAACCAG
AGAACTGCCAGAATCGGGCATTTCAGTTGGGCACTCCTCGGGAGAAAAGTTCCAGCTGGTTCGGAGTAAGGCCGAAC
TCGGGCTGAGCGTCGAGCCAAGCAGGAGGCCGAGCGGGCCCTGAAACAGGCAAGAAAAGGGGAACAAGGAGGACC
ACCTCCTAAGGCCAGCCCCAGCACAGCTGGAGAAACCCCTCAGGAGTGAAGCGTCTCCCTGAGTACCCTCAGGT
TGATGACCTACTTCTGAGAAGGCTTGTTAAAAAACAGAGCGTCAACAGGTTCTTACACGAAAGGATTATGGATC
CAAAGTCAGTCTCTTCTCTCACCTACCCAGTACAGCAGACAAAACCTCTCTGACCCAGTTTATGAGCATCCCATC
CTCTGTGATCCACCCAGCCATGGTGCGACTCGGCCTGCAGTACTCCCAGGGCCTGGTCAGTGGCTCCAATGCCCC
GTGTATTGCCCTGCTTCGTGCCCTTGACAGAGGTGATTCAGGATTACACAACACCGCCTAATGAAGAACTCTCCAG
GGATCTAGTGAATAAACTAAAACCCCTACATGAGCTTCCTGACTCAGTGCCGTCCCCTGTCAGCGAGCATGCACAA
CGCCATCAAGTTTCCTTAACAAGGAAATCACCAGTGTGGGCAGTTCCAAGCGGGAAGAGGAGGCCAAGTCAGAACT
TCGAGCAGCCATTGATCGGTATGTGCAAGAGAAGATTGTGCTAGCAGCTCAGGCAATTTACGCTTTGCTTACCA
GAAGATCAGTAATGGAGATGTGATCCTGGTATATGGATGCTCATCTCTGGTATCACGAATTTTCAGGAGGCTTG
GACAGAGGGCCGGCGGTTTCGGGTGGTAGTGGTGGACAGCCGGCCATGGCTGGAAGGAAGGCACACACTACGTTT
TCTAGTCCATGCTGGTGTCCCAGCCTCCTACCTGCTGATTCTGTCAGCCTCCTATGTGCTCCCAGAGGTTTCCAA
GGTGCTATTGGGAGCTCATGCACTCTTGGCCAACGGGTCTGTGATGTCACGGGTAGGGACAGCACAGTTAGCCCT
GGTGGCTCGAGCCATAATGTACCAGTGTGGTTTGTGCTGTGAAACATAACAAGTTCTGTGAGCGTGTGCAGACTGA
TGCCTTTGTCTCTAATGAGCTAGATGACCCTGATGATCTGCAATGTAAGCGGGGAGAACATGTTGCGCTGGCTAA
CTGGCAGAACCACGCATCCCTACGGTTGTTGAATCTAGTCTATGATGTGACTCCCCAGAGCTTGTGGATCTGGT
GATCACGGAGCTGGGGATGATCCCTTGCACTTCTGTACCTGTTGTTCTACGAGTCAAGAGCAGTGACCAGTGACG
GGGGAAACACAGGGTTAATAAATGCCATACTCCCTACCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAC

WO 2004/030615

PCT/US2003/028547

736/6881
FIGURE 687

MAAVAVAVREDSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQKKKKRKEEKGAEPETGSASVAAQCQVGPTR
ELPESGIQLGTPREKVPAGRSKAELRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKRLPEYPQV
DDLLLRRLVKKPERQQVPTRKDYGSKVSLFSLPQYSRQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVSGSNAR
CIALLRALQQVIQDYTTTPNEELSRDLVNKLKPYMSFLTQCRPLSASMHNAIKFLNKEITSVGSSKREEEAKSEL
RAAIDRYVQEKIVLAAQAISRFAVYQKISNGDVILVYGCSLVSRLQEAWTEGRRFRVVDVSRPWLEGRHTLRS
LVHAGVPASYLLIPAASYVLPVSKVLLGAHALLANGSVMSRVGTAQLALVARAHNPVVLVCCETYKFCERVQTD
AFVSNELDDPDDLQCKRGEHVALANWQNHASLRLLNLVYDVTPPELVDLVITELGMIPCSSVPVVLVRVKSSDQ

WO 2004/030615

PCT/US2003/028547

737/6881
FIGURE 688

AGGACTTTGGCGAGGGGGCAGCCATTTTGGGGGGTGCTGATGGATACCTGCGGGGTGCGCTATGTTGCCCTGGGG
GAGGCCGGCCCCGTGGGGAACATGACTGTGGTAGACTCTCCTGGACAAGAGGTGCTAAATCAGCTTGATGTCAAG
ACCTCTTCAGAAATGACCAGTGCAGAGGCTTCCGTAGAGATGTCAATTACCTACCCCTTTGCCTGGATTTGAGGAT
TCTCCTGATCAGAGGAGGCTCCCTCCAGAGCAGGAAAGCCTCTCCAGACTGGAACAGCCAGATCTTTCTTCAGAG
ATGTCAAAGGTCTCAAAGCCTAGGGCCTCAAAGCCTGGCCGGAAGAGAGGTGGTAGGACACGAAAAGGCCCCAAA
AGGCCCAACAGCCTAATCCTCCATCAGCCCCACTGGTTTCTGGTCTCTTAGATCAATCCAACCCTCTGTCCACC
CCCATGCTTAAGAAACGAGGTGCGAAAGTCCAAGGCAGAGCTGCTGCTGCTGAAGTTGTCAAAGACCTAGATCGG
CCAGAATCTCAATCTCCAAAGAGGGCCCCCTGAGGACTTTGAGACCCCTTCTGGGGAACGACCCCGCCGAAGGGCT
GCCCAAGTGGCACTTCTGTATCTTCAGGAAGTGGCTGAAGAGCTCTCAACAGCCCTGCCTGCCCCCTGTGTCTCTGT
CCTGAGGGCCCCAAGGTGAGCAGCCCCACCAACCGAAGAAGATCCGGCAGCCAGCAGCCTGTCCAGGTGGAGAA
GAGGTGGATGGTGCTCCACGGGATGAAGACTTTTTTCTCCAGGTTGAGGCTGAAGATGTGGAAGAAAGTGAGGGC
CCAAGTGAGAGCTCATCTGAACCTGAGCCTGTAGTGCCCCGAAGCACCACGAGGATCTACTTCAGGGAAACAG
AAACCACACTGCCGAGGAATGGCTCCCAATGGCTTACCAATCATATCATGGCTCCTGTTTGAAGTGCCTCCAT
CTCACCAGGACTTCCGAGAGCAGAAACATTCTACTGGGAGTTTGCTGAGTGGATTCTTTAGCCTGGAAGTGG
CACTTGTTATCTGAGCTTGAGGCCGCTCCCTACCTGCCCCAGGAGGAGAAGTCTCCATTGTTTCTGTACAACGT
GAAGGGCTACCTGAAGATGGCACCCTCTACCGAATAAACAGATTAGCTCGATCACAGCACATCCAGAGCGCTGG
GATGTGTCTTTCTTACGGGGGGACCGCTCTGGGCTCTGGACTGGTGCCAGTGGCCAGAGGGGGCAGGAGCCTCG
CAATATGTGGCTCTTTTTCTCCAGCCCTGACATGAATGAGACACACCCTAGCCAGCTTCATTGCGGTCTCTGGG
CTGCTCCAGCTCTGGGGCCTTGGGACCTTGCAGCAAGAAAGCTGTCTGGCAACAGGGGCCACTTTGTCTATGGG
ATTGCTTGTGACAACGGCTGCATCTGGGACCTCAAGTTCTGCCCCAGTGGAGCATGGGAAGTTCAGGCAACCCCT
CGGAAGGCTCCTCTCCTGCCCCGGTTGGGTCTCTTGGCTCTGGCCTGCTCAGACGGGAAAGTACTGCTATTCACT
CTACCCCATCCGGAGGCCCTGCTGGCTCAGCAACCCCCAGATGCAGTGAAGCCTGCCATATATAAGGTACAATGT
GTGGCAACTCTGCAGGTGGGGTCTATGCAAGCTACAGACCCCTCTGAGTGTGGTCACTGCTTACCTGGCCTGG
ATGCCTACCAGGCCCCACCAACACCTAGCTGCTGGATATTATAATGGCATGGTGGTTTTCTGGAACCTTCCCACT
AACTACCCCTGCAGCGGATACGGCTCTCTGATGGCTCCTTAAAGCTCTACCCCTTCCAGTGTTCCTAGCCCAT
GACCAGGCTGTGCGTACCCTTCAATGGTGCAAAGCTAACAGCCATTTCTTGTCTCTGCGGGGAGTGACCGGAAA
ATCAAATTCTGGGACCTTCGACGTCCTTACGAACCCATAAACTCTATCAAGCGCTTCTTGAGTACAGAACTGGCC
TGGCTGCTTCCCTACAATGGTGTCACTGTGGCTCAGGACAAGTCTATGCCTCTTATGGACTCTGTGGGATTCTAT
TATATTGACGCTGGTTACCTTGGTTTCAAGGCCTACTTCACTGCTCCTCGAAAAGGCACCGTTTGGAGTCTTTCA
GGATCCGACTGGCTTGGGACAATAGCTGCAGGAGATATATCCGGGGAGCTCATTGCTGCTATATTACCAGATATG
GCACTGAATCCAATAAATGTCAAGCGACCTGTAGAGCGAAGATTTCCTATATATAAAGCAGATCTGATACCGTAT
CAGGACAGTCTGAAGGTCCAGACCATTTCTGCTTCTATCTGGGGTCCCCAACCCCTCCCAAGGCTCGAACTTAC
ACTGAAACTGTCAACCATCACTACTTGTCTTTCAAGACACAGATTGGGTTTCACTTCCATGATCTGCTCCGTAGA
GAACCAATGCTGCGCATGCAGGAGGGAGAGGGGCATTCTCAACTCTGCCTGGACAGGCTGCAGCTGGAGGCTATT
CATAAGGTACGTTTACGCCAAACCTGGACTCCTATGGATGGCTGGTATCTGGGGGGCAGTCAGGGCTGGTTTGA
ATCCATTTTGTCCGTGGACTCGCCTCCCCACTGGGCCACCGTATGCAGCTTGAAAGCCGAGCCCACTTCAATGCT
ATGTTCCAACCATCCTCCCCCACTAGACGGCCTGGCTTCTCTCCAACAGCCATCGCCTTCTGCCCCACTCCCTAG

CCTTGGCCCCACACAGATCCTTGGAGTGAAGTCGGTCAAGAACAAATGGCCCTATGCACAGAGCCATAGGAAC
GGGGGCCCTTCCCTGGACAGTGATCATGCCAGGCCTGGACCTTTAGGCCTGCCTCCCCAGGACTCCTTAGATCCCA
CTCTTTCTACAGACTTCTGTGATCACAGCCCCCTGCGGGCAGGGGGGCTCTCCCTCCACCAACTCTCAAGGCTCC
TCAGCCTAAGACTATGGCTCATGAGAAACACTCAGGCCTGACCTAGGCTTGGGAGTCAAACCTGCTCATATTGAGC
ATATTGTAAAGTGGGTAAAGCCAAAGTAAAGGTACTGGGTGTTTTTGTGACCACTTGTGAATGGGTGTATGGAGAA
CTGAAAAGGGTATCTGCATGAAGGCTCCTGTCTGACTATTCCAGGATCCAATATTACTGCCTTCTGAAACTTCCT
CTTtagggtaaccatcatgtatgccccagaggggtatagtaattcgtgagactgaagttgcttagagtacttctt
tgaccaaggaataaccacagacaccctaccgatagaacagtggctcagatcttacttgctcctgcttacgaagtat
tcccaatcaactggctcatctgaccctacttgaacactcctgaacagtcagtttttttaaaatcttcttttatatca
agtcagagagtatacttctataaaatttcaactcatggatgttaggaaatctagtcatttccctgtgattgcccctg
ttaagtatttaaccatagctatcatggtttcccaaatcttctctagattaaatatcttcagttacttc

WO 2004/030615

PCT/US2003/028547

738/6881

FIGURE 689

MDTCGVGYVALGEAGPVGNMTVVDSPGQEVNLQLDVKTSSSEMTSAEASVEMSLPTPLPGFEDSPDQRRLLPPEQES
LSRLEQPDLSSEMSKVS KPRASKPGRKRGGTRKGPKRPPQPNPPSAPLVPGLLDQSNPLSTPMPPKKRGRKSKAE
LLLLKLSKDLD RPESQSPKRPPEDFETPSGERPRRRAAQVALLYLQELAEELSTALPAPVSCPEGPKVSSPTKPK
KIRQPAACPGGEEVDGAPRDEDFFLQVEAEDVEESEGPSESSSEPEPVVPRSTPRGSTSGKQKPHCRGMAPNGLP
NHIMAPVWKCLHLTKDFREQKHSYWEFAEWIPLAWKWHLLSELEAAPYL PQEEKSPLFSVQREGLPEDGTLYRIN
RFSSITAHPERWDVSFFTGGPLWALDWCPVPEGAGASQYVALFSSPDMNETHPLSQLHSGPGLLQLWGLGTLQQE
SCPGNRAHFVYGIACDNGCIWDLKFCPSGAWELPGTPRKAPLLPRLGLLALACSDGKVLLFSLPHPEALLAQPP
DAVKPAIYKVQCVATLQVGSMAQATDPSECGQCLSLAWMPTRPHQHLAAGYYNGMVVFWNLPTNSPLQRI RLS DGS
LKLYPFQCF LAHDQAVRTLQWCKANSHFLVSAGSDRKIKFWDLRPHYEPINSIKRFLSTELAWLLPYNGVTVAQD
NCYASYGLCGIHYIDAGYLGFKAYFTAPRKGTVWSLSGSDWLGTIAAGDISGELIAAILPDMA LNP INVKRPVER
RFPIYKADLIPYQDSPEGPDHSSASSGVNPPKARTYTETVNHHYLLFQD TD LGSFHDLLRREPMLRMQEGEGHS
QLCLDRLQLEA IHKVRFS PNLD SYGWLVS GGQSGLVRIHFVRGLASPLGHRMQLESRAHFNAMFQPSSPTRPGF
SPTSHRLLPTP

WO 2004/030615

PCT/US2003/028547

739/6881
FIGURE 690

GAGGGACGGTGGGGGTGACCCCTCTCCTCTTGGCTTGACAGGAAGCATGGCACTCTGGCGGGCATAACCAGCGGG
CCCTGGCCGCTCACCCGTGGAAAGTACAGGTCTTGACAGCTGGGTCCCTGATGGGCCTGGGTGACATTATCTCAC
AGCAGCTGGTGGAGAGGCGGGGTCTGCAGGAACACCAGAGAGGCCGGACTCTGACCATGGTGTCCCTGGGCTGTG
GCTTTGTGGGCCCCTGTGGTAGGAGGCTGGTACAAGTTTTTGGATCGGTTTCATCCCTGGCACCACCAAAGTGGATG
CACTGAAGAAGATGTTGTTGGATCAGGGGGGCTTTGCCCCGTGTTTTCTAGGCTGCTTTCTCCCACTGGTAGGGG
CACTTAATGGACTGTCAGCCCAGGACAACCTGGGCCAAACTACAGCGGGATTATCCTGATGCCCTTATCACCAACT
ACTATCTATGGCCTGCTGTGCAGTTAGCCAACTTCTACCTGGTCCCCCTTCATTACAGGTTGGCCGTTGTCCAAT
GTGTTGCTGTTATCTGGAACTCCTACCTGTCCTGGAAGGCACATCGGCTCTAAGCCTGCCTCACTCCATCGTTTC
CACCTTGCAGTGATGCAGCTTGACCCTGGAACGGTCAGACAACCTCCTCAAAGTGGGCATAACCAGTTTCCACGGG
GTTGGGTTGCCGGTCAGAGCTTAAGAGGACTAGCACCCCTGCAATGCCCTCTTCACTCTAAAATGTACACTGACT
GCTTTAGAGCCCTTGATAATAGTCTTATTTCCACACATACTAGGCACTCCATAAATATCTGTTGAACCTTCATG
ACCTTATCAACTTTACACCCATATCCCAGCAAATGCCACTCATCCCCACTCTTCATAGACACATTTGTTACTCTA
ACCCTGCCTAGGCTTCTTGTAGCTCCAGCTCTTTAGAGACTCCCGGAACCCTTTATATGGTGCCTCAGTAAATAT
GTTATTAAATATGTAATCCGG

WO 2004/030615

PCT/US2003/028547

740/6881
FIGURE 691

MALWRAYQRALAAHPWKVQVLTAGSLMGLGDIISQQLVERRGLQEHQRGRTLTMVSLGCGFVGPVVGWYKVLDR
FIPGTTKVDALKKMLLDQGGFAPCFLGCFPLPLVGALNGLSAQDNWAKLQRDYPDALITNYYLWPAVQLANFYLP
LHYRLAVVQCVAVIWNSYLSWKAHRL

WO 2004/030615

PCT/US2003/028547

741/6881
FIGURE 692A

CGCCCCCGCCTCTGAGCTCCCTTCCC**ATG**CGGGCCCTAGTGTGGAGGACGGGTGGTCTGCGGGGCCAGCCCT
TTGGGGCCGCGTGTGCGACTGCCGGGAAGTGGTGTTCAAACCGGCATGGTCGGCTACCCCGAGGCCCTCACTG
ATCCCTCCTACAAGGCACAGATCTTAGTGCTCACCTATCCTCTGATCGGCAACTATGGCATCCCCCAGATGAAA
TGGATGAGTTGGTCTCTGCAAGTGGTTTGAATCCTCGGGCATCCACGTAGCAGCACTGGTAGTGGGAGAGTGCT
GTCCTACTCCCAGCCACTGGAGTGCCACCCGCACCCTGCATGAGTGGCTGCAGCAGCATGGCATCCCTGGCTTGC
AAGGAGTAGACACTCGGGAGCTGACCAAGAAGTTGCGGGAACAGGGGTCTCTGCTGGGGAAGCTGGTCCAGAATG
GAACAGAACCCTTCATCCCTGCCATTCTTGGACCCCAATGCCCGCCCCCTGGTACCAGAGGTCTCCATTAAGACTC
CACGGGTATTCAATACAGGGGGTGCCCTCGGATCCTTGCTTTGGACTGTGGCCTCAAGTATAATCAGATCCGAT
GCCTCTGCCAGCGTGGGGCTGAGGTCACTGTGGTACCCTGGGACCATGCACCTAGACAGCCAAGAGTATGAGGGTC
TCTTCTTAAGTAATGGGCTGGTGACCCTGCCTCCTATCCAGTGTGCTATCCACACTGAGCCGTGTTTTATCTG
AGCCTAATCCCCGACCTGTCTTTGGGATCTGCCTGGGACACCAGCTATTGGCCTTAGCCATTGGGGCCAAGACTT
ACAAGATGAGATATGGGAACCGAGGCCATAACCAGCCCTGCTTGTGGTGGGCTCTGGGCGCTGCTTTCTGACAT
CCCAGAACCATGGGTTTGTCTGTGGAGACAGACTCACTGCCAGCAGACTGGGCTCCTCTCTTCACCAACGCCAATG
ATGGTTCCAATGAAGGCATTGTGCACAACAGCTTGCCCTTTCTTCAGTGTCCAGTTTCACCCAGAGCACCAGCTG
GCCCTTCAGATATGGAAGTGTCTTTTCGATATCTTTCTGGAAGTGTGAAAGAGGGCCACAGCTGGGAACCTGGGG
GCCAGACAGTTAGAGAGCGGCTGACTGAGCGCCTCTGTCCCCCTGGGATTCCCACTCCCGGCTCTGGACTTCCAC
CACCACGAAAGTTCTGATCCTGGGCTCAGGGGGCCTCTCCATTGGCCAAGCTGGAGAATTGACTACTCGGGCT
CTCAGGCAATTAAGGCCCTGAAGGAGGAAAACATCCAGACGTTGCTGATCAACCCCAATATTGCCACAGTGCAGA
CCTCCCAGGGGCTGGCCGACAAGGTCTATTTTCTTCCCATACACCTCATTATGTAACCCAGGTGATACGTAATG
AACGCCCCGATGGTGTGTTACTGACTTTTGGGGGCCAGACTGCTCTGAAGTGTGGTGTGGAGCTGACCAAGGCCG
GGGTGCTGGCTCGGTATGGGGTCCGGGTCTGGGCACACCAGTGGAGACCATTGAGCTGACCGAGGATCGACGGG
CCTTTGCTGCCAGAATGGCAGAGATCGGAGAGCATGTGGCCCCGAGCGAGGCAGCAATTCTCTTGAACAGGCC
AGGCAGCCGCTGAACGGCTGGGGTACCCTGTGCTAGTGCCTGCAGCCTTTGCCCTGGGTGGCTGGGCTCTGGCT
TTGCCCTCTAACAGGGAGGAGCTCTCTGCTCTCGTGGCCCCAGCTTTTGCCCATACCAGCCAAGTGTAGTAGACA
AGTCTCTGAAGGGATGGAAGGAGATTGAGTACGAGGTGGTGAGAGACGCCTATGGCAACTGTGTACGGTGTGTA
ACATGGGAACTTGGACCCACTGGGCATCCACACTGGTGAGTCCATAGTGGTGGCCCTAGCCAGACACTGAATG
ACAGGGAGTATCAGCTCCTGAGGCAGACAGCTATCAAGGTGACCCAGCACCTGGGAATTGTTGGGGAGTGCAATG
TGCAGTATGCCCTGAACCTGAGTCTGAGCAGTATTACATCATTGAAGTGAATGCCAGGCTCTCTCGCAGCTCTG
CCCTGGCCAGTAAGGCCACAGGTTATCCACTGGCTTATGTGGCAGCCAAGCTAGCATTGGGCATCCCTTTGCCTG
AGCTCAGGAACTCTGTGACAGGGGTACAGCAGCCTTTGAACCCAGCGTGGATTATTGTGTGGTGAAGATTCTC
GATGGGACCTTAGCAAGTTCTGCGAGTCAGCACAAAGATTGGGAGCTGCATGAAGAGCGTTGGTGAAGTCAATG
GCATTGGGCGTTTCAATTGAGGAGGCCTTCCAGAAGGCCCTGCGCATGGTGGATGAGAAGTGTGGGCTTTGATC
ACACAGTGAAACAGTCAAGCATATGGAGTTGGAGACTCCAACAGATAAGCGGATTTTTGTGGTGGCAGCTGCTT
TGTGGGCTGGTTATTAGTGGACCGCTGTATGAGCTCACACGCATCGACCGCTGGTTCCCTGCACCGAATGAAGC
GTATCATCGCACATGCCAGCTGCTAGAACAAACACCGTGGACAGCCTTTGCCGCCAGACCTGCTGCAACAGGCCA
AGTGTCTTGGCTTCTCAGACAAACAGATTGCCCTTGCAGTCTTGAGCACAGAGCTGGCTGTTTCGCAAGCTGCGTC
AGGAACTGGGGATCTGTCCAGCAGTGAAACAGATTGACACAGTTGCAGCTGAGTGGCCAGCCCAGACAAATTACC
TATACCTAACGTATTGGGGCACCACCCATGACCTCACCTTTGGAACACCTCATGTCTTAGTCTTGGCTCTGGCG
TCTACCGTATTGGCTCTAGCGTTGAATTTGACTGGTGTGCTGTAGGCTGCATCCAGCAGCTCCGAAAGATGGGAT
ATGAGATCTCTTTGAGGTGGTGATGGACATCTATGAGCTCGAGAACCCTGAAGGTGTGATCCTATCCATGGGTG
GACAGCTGCCAAACAACATGGCCATGGCGTTGCATCGGCAGCAGTGCCGGGTGCTGGGCACCTCCCCTGAAGCCA
TTGACTCGGCTGAGAACCCTTTCAAGTTTTCCGGCTCCTTGACACCATTGGTATCAGCCAGCCTCAGTGGAGGG
AGCTCAGTACGCTCGACTGCTCGCCAATTCTGCCAGACCGTGGGGTACCCCTGTGTGGTGCGCCCTCCTATG
TGCTGAGCGGTGCTGCTATGAATGTGGCTACACGGATGGAGACCTGGAGCGCTTCTGAGCAGCGCAGCAGCCG
TCTCCAAAGAGCATCCCGTGGTTCATCTCCAAGTTTCATCCAGGAGGCTAAGGAGATTGACGTGGATGCCGTGGCCT
CTGATGGTGTGGTGGCAGCCATCGCCATCTCTGAGCATGTGGAGAATGCAGGTGTGCATTACGGTGTGCGACGC
TGGTGACCCCCCACAAGATATCACTGCCAAAACCTGGAGCGGATCAAAGCCATTGTGCATGCTGTGGGCCAGG

WO 2004/030615

PCT/US2003/028547

742/6881
FIGURE 692B

AGCTACAGGTCACAGGACCCCTTCAATCTGCAGCTCATTGCCAAGGATGACCAGCTGAAAGTTATTGAATGCAACG
TACGTGTCTCTCGCTCCTTCCCCCTTCGTTTCCAAGACACTGGGTGTGGACCTAGTAGCCTTGGCCACGCGGGTCA
TCATGGGGGAAGAAGTGGAACCTGTGGGGCTAATGACTGGTTCTGGAGTCGTGGGAGTAAAGGTGCCTCAGTTCT
CCTTCTCCCGCTTGGCGGGTGCTGACGTGGTGTGGGTGTGGAAATGACCAGTACTGGGGAGGTGGCCGGCTTTG
GGGAGAGCCGCTGTGAGGCATACCTCAAGGCCATGCTAAGCACTGGCTTTAAGATCCCCAAGAAGAATATCCTGC
TGACCATTGGCAGCTATAAGAACAAAAGCGAGCTGCTCCCAACTGTGCGGCTACTGGAGAGCCTGGGCTACAGCC
TCTATGCCAGTCTCGGCACAGCTGACTTCTACACTGAGCATGGCGTCAAGGTAACAGCTGTGGACTGGCACTTTG
AGGAGGCTGTGGATGGTGTGAGTGCCACACAGCGGAGCATCCTGGAGCAGCTAGCTGAGAAAACTTTGAGCTGG
TGATTAACCTGTCAATGCGTGGAGCTGGGGGCCGCGCTCTCTCTTCTTGTACCAAGGGCTACCGCACCCGAC
GCTTGGCCGCTGACTTCTCCGTGCCCCCTAATCATCGATATCAAGTGACCAAACTCTTTGTGGAGGCCCTAGGCC
AGATCGGGCCAGCCCTCCTTTGAAGGTGCATGTTGACTGTATGACCTCCCAAAGCTTGTGCGACTGCCGGGAT
TGATTGATGTCCATGTGCACCTGCGGGAACAGGTGGGACACATAAGGAGGACTTTGCTTCAGGCACAGCCGCTG
CCCTGGCTGGGGGTATCACCATGGTGTGTGCCATGCCATAACCCGGCCCCCATCATTGACGCCCTGCTCTGG
CCCTGGCCCCAGAAGCTGGCAGAGGCTGGCGCCCGGTGCGACTTTGCGCTATTCTTGGGGCCTCGTCTGAAAATG
CAGGAACCTTGGGCACCGTGGCCGGGTCTGCAGCCGGGTGAAGCTTTACCTCAATGAGACCTTCTCTGAGCTGC
GGCTGGACAGCGTGGTCCAGTGGATGGAGCATTCGAGACATGGCCCTCCACCTCCCCATTGTGGCTCACGCAG
AGCAGCAAACCGTGGCTGCTGTCTCATGGTGGCTCAGCTCACTCAGCGCTCAGTGACATATGTCACGTGGCAC
GGAAGGAGGAGATCCTGCTAATTAAAGCTGCAAAGGCACGGGGCTTGCCAGTGACCTGCGAGGTGGCTCCCCACC
ACCTGTTCTTAAGCCATGATGACCTGGAGCGCTGGGGCTGGGAAGGGGAGGTCCGGCCTGAGCTTGGCTCCC
GCCAGGATGTGGAAGCCCTGTGGGAGAACATGGCTGTCTCATCGACTGCTTTGCCTCAGACCATGCTCCCCATACCT
TGGAGGAGAAGTGTGGGTCCAGGCCCCACCTGGGTTCACAGGGTTAGAGACCATGCTGCCACTACTCCTGACGG
CTGTAAGCGAGGGCCGGCTCAGCCTGGACGACCTGCTGCAGCGATTGCACCACAATCCTCGGCGCATCTTTTACC
TGCCCCCGCAGGAGGACACCTATGTGGAGGTGGATCTGGAGCATGAGTGGACAATTCACGACCATGCCCTTCT
CCAAGGCCCACTGGACACCTTTTGAAGGGCAGAAAGTGAAGGGCACCGTCCGCCGTGTGGTCTGCGAGGGGAGG
TTGCCTATATCGATGGGCAGGTTCTGGTACCCCGGGCTATGGACAGGATGTACGGAAGTGGCCACAGGGGGCTG
TTCTCAGCTCCCACCTCAGCCCTGCCACTAGTGAGATGACCACGACACCTGAAAGACCCCGCGTGGCATCC
CAGGGCTTCTGATGGCCGCTTCCATCTGCCGCCCGAATCCATCGAGCCTCCGACCCAGGTTTGCCAGCTGAGG
AGCCAAAGGAGAAGTCTCTCGGAAGGTAGCCGAGCCAGAGCTGATGGGAACCCCTGATGGCACCTGTACCCCTC
CACCACAGTACCGAGACAGGCATCTCCCCAGAACCCTGGGGACCCCTGGCTTGCTGCACCCCAAGCCTCACCCT
TGCTGCACTCATTAGTGGGCCAACATATCCTGTCCGTCCAGCAGTTTACCAAGGATCAGATGTCTCACCTGTTCA
ATGTGGCACACACACTGCGTATGATGGTGCAGAAGGAGCGGAGCCTCGACATCCTGAAGGGGAAGGTGATGGCCT
CCATGTTCTATGAAGTGAGCACACGACAGCAGCTCCTTTGCAGCAGCCATGGCCCGGCTGGGAGGTGCTGTGC
TCAGCTTCTCGGAAGCCACATCGTCCGTCCAGAAGGGCGAATCCCTGGCTGACTCCGTGCAGACCATGAGCTGCT
ATGCCGACGTGCTCGTGTCCGGCACCCCAAGCCTGGAGCAGTGGAGCTGGCCGCAAGCACTGCCGGAGGCCAG
TGATCAATGCTGGGGATGGGGTCGGAGAGCACCCCAAGCCTGGAGCAGTGGAGCTGGCCGCAAGCACTGCCGGAGGCCAG
TGGGAAGTGTCAATGGCATGACGATCAGATGGTGGGTGACCTGAAGCACGGACGCACAGTACATTCCCTGGCCT
GCCTGCTCACCCAGTATCGTGTGAGCTGCGCTACGTGGCACCTCCAGCCTGCGCATGCCACCCACTGTGCGGG
CCTTCTGCTGGCCTCCCGCGGCACCAAGCAGGAGGAATTCGAGAGCATTGAGGAGGCGCTGCCTGACACTGATGTGC
TCTACATGACTCGAATCCAGAAGGAACGATTTGGCTCTACCCAGGAGTACGAAGCTTGCTTTGGTCAGTTTATCC
TCACTCCCCACATCATGACCCGGGCCAAGAAGAAGATGGTGGTGTGACCCGATGCCCCGTGTCAACGAGATAA
GCGTGGAAGTGGACTCGGATCCCCGCGCAGCCTACTTCCGCCAGGCTGAGAACGGCATGTACATCCGCATGGCTC
TGTTAGCCACCGTGCTGGGCCGTTTCTAGGGCCTGGCTTCTCAGCCTCTTCTCTTTAGGCCCAGCTGCTGGGC
AAGGAATTCCAGTGCCTCCTACGGGGGCAGCACACTTAGATATTCCTGGACATCCAGATTGCTCACATGTGCTGA
CCACACTTCAGGCTCTGGACTGGAGCTCTTGGCATGGGGGTGGGGCCTCAGATGCTGGGGCCAGTCTGCCCCA
TCTTCATTCTGCACCTTAAACCTGTACAGTCATTTTTCTACTGACTTAATAAACAGCCGAGCTGTCCCTTG

WO 2004/030615

PCT/US2003/028547

743/6881
FIGURE 693

MAALVLEDGSVLRGQPFGA AVSTAGEVVFQ TGMVGYPEAL TDPSYKAQ IILVLTYP LIGNYGIP PDEMDEFGLCKW
FESSGIHVAALVVGECCTP SHWSATRTLHEWLQQHGIPGLQGVD TRELTKKLREQGS LLGKLVQNGTEPSSLPF
LDPNARPLVPEVSIKTPRVFNTGGAPRILALDCGLKYNQIRCLCQRGA ETVVPWDHALDSQEYEGFLSNGPGD
PASYP SVVSTLSRVLSEPNRPVFGICLGHQ LLLALAIGAKTYKMRYGNRGNQPC LLVGSGRCF LITSQNHGFAVE
TDSL PADWAPLFTNANDGSNEGIVHNSLPFFSVQFHPEHQAGP SDMELLFDIFLETVKEATAGNPGGQTVRERLT
ERLCPPGIPTPGSGLPPPRKVLILGSGGLSIGQAGEFDYSGSQA IKALKEENIQ TLLINPNIA TVQTSQGLADKV
YFLPITPHYVTQVIRNERPDGVLLTFGGQTALNCGVELTKAGVLARYGVRVLGTPVETIELTEDRRFAARMAEI
GEHVAPSEAANSLEQAQAAAERLGYPVLVRAAFALGGLGSGFASNREELSALVAPAF AHTSQVLVDKSLKGWKEI
EYEVVRDAYGNCVTVCNMENLDPLGIHTGESIVVAPSQT LNDREYQLLRQTAIKVTQHLGIVGECNVQYALNPES
EQYYII EVNARLSRSSALASKATGYPLAYVA AKLALGIPLPELRNSVTGGTAAFEPSVDYCVVKIPRWDLSKFLR
VSTKIGSCMKSVGEVMGIGRSFEEAFQKALRMVDENCVGFDHTVKPVSDMELETPTDKRIFVVAALWAGYSVDR
LYELTRIDRWFLHRMKRIIAHAQLLEQHRGQPLPPDLLQQA KCLGFS DKQIALAVLSTELAVRKLRLQELGICPAV
KQIDTVA AEWPAQTNYLYLTWGTTHDLTFRTPHVLVLGSGVYRIGSSVEFDWCAVGCIQQLRKMGYKTIMVNYN
PETVSTDYDMCDRLYFDEISFEVMDIYELENPEGVILSMGGQLPNMAMALHRQQCRVLGTSPEAIDSAENRFK
FSRLLD TIGISQPQWRELS DLESARQFCQTVGYPCVVRPSYVLSGAAMNVAYTDGDLERFLSSAAVSKEHPVVI
SKF IQEAKEIDVDAVASDGVVAIAIASEHVENAGVHSGDATLVTPPDITAKTLERIKAIHVAVGQELQVTGPFN
LQLIAKDDQLKVIECNVRVRSRFPFVSKTLGVLDLVALATRVIMGEEVEPVGLMTGSGVVGKVPQFSFSLAGAD
VVLGVEMTSTGEVAGFGESRCEAYLKAMLSTGFKIPKKNILLTIGSYKNKSELLPTVRLLESGLYSLYASLGTA
FYTEHGVKVTAVDWHFEEAVDGECPQRSILEQLAEKNFELVINLSMRGAGGRRLSSFVTKGYRTRRLAADFSVP
LIIDIKCTKLFVEALGQIGPAPPLKVHVDCMTSQKLVRLPGLIDVHVHLREPGGTHKEDFASGTAAALAGGITMV
CAMPNTRPPIIDAPALALAQKLAEAGARCDFALFLGASSENAGTLGTVAGSAAGLKLYLNETFSELRLDSVVQWM
EHFETWPSHLP IVAHAEQQTVA AVLMAQLTQRSVHICHVARKEEILLIKA AKARGLPVTCEVAPHHFLSHDDL
ERLGP GKGEVRPELGS RQDVEALWENMAVIDCFASDHAPHTLEEKCGSRPPPGFPGLETMLPLLLTAVSEGRLSL
DDLLQRLHHPRRIFHLPPQEDTYVEVDLEHEWTIPSHMPFSKAHWTPFEGQKVKGTVRRVLRGEVAYIDGQVL
VPPGYQGDVRKWPQGA VPQLPPSAPATSEMTTTPERPRRGIPGLPDGRFHLPPRIHRASDPGLPAEEPKEKSSRK
VAEPELMGTPDGTCTYPPPPVPRQASPNLGTPLLLHPSLVGQHILSVQQFTKDQMSHLFNVAHTLRMM
VQKERSLDILKGKVMASMFYEVSTRTSSSF AAAMARLGGAVLSFSEATSSVQKGESLADSVQTMSCYADVVL RH
PQP GAVELAAKHCRRPVINAGDGVGEHPTQALLDIFTIREELGTVNGMTITMVGDLKHGRTVHSLACLLTQYRVS
LRYVAPPSLRMPPTVRA FVASRGTKQEEFESIEEALPD TDVLYMTRI QKERFGSTQEYEACFGQFILT PHIMTRA
KKKMVMHMPMRVNEISVEVSDPRAAYFRQAENGMYIR MALLATVLRG

WO 2004/030615

PCT/US2003/028547

744/6881
FIGURE 694

GGAGCACCAAGGGAACGGAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCC
CTGCTCCTCGCTCTGGGCGTGGAAAGGGCTCTGGCGCTACCCGAGGTACAGAAGCAAGTTTGAGGTGGGCTGAA
GCAGGGTCACTGGCCAGCCGTGCGTCGCGCTCGCCAGCGGCTCCCCCTTCTCCTCGGCGGGCCTGCGGTTCTGAT
TTCGTCCCTGACGCTTCCCGACCCTGCCCAGCCAGATATGCACCAATGTCCAGGGAGCGTGCAAAATTTGTCAA
AAGTGGCCTTTTATTGTAAACGACACGAGAGCTAATGCTGCATGCCCCTTGCTGCCTGAATCAGAAGGGCACCA
TCTTGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAAACTTTCATCAGGCACATACCACTGTCA
TCATAGACCTGCAAGCAAACCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTA⁷CTCAGCTCCAGACTC
TGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTATATAGACAACC
AAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAATGGATCTTGTG
TACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATGCGCCAGGGCT
CGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTTGGGCGACCC
AGCGCCGAAAAGCCAAGACTTCA⁸TGA⁹ACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAACTATCTTAGC
CCAGTCAGGGAGCTCTGCTTCCCTAGAAAGGCATCTTTCGCCAGTGGATTGCGCTCAAGGTTGAGGCCGCCATTGG
AAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTC¹⁰CCATTGGTGTGTTGCCTATAATAAACACTT
TTTCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

745/6881
FIGURE 695

MLHARCCLNQKGTILGLDLQNCSEDPGPNFHQAHTTVIIDLQANPLKGDLANTFRGFTQLQTLILPQHVNCPGG
INAWNTITSYIDNQICQGQKNLCNNTGDPMECPENGSCVPDGPGLLQCVCADGFHGYKCMRQGSFSLMFFGILG
ATTLSVSILLWATQRRKAKTS

WO 2004/030615

PCT/US2003/028547

746/6881
FIGURE 696

GGAGCACCAAGGGAACGGAATAATGGCGCCTCACGGCCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCC
CTGCTCCTCGCTCTGGGCGTGGAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCCAGGGAGCGTGCAA
AATTGTCAAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAATGCTGCATGCCCGTTGCTGCCTGAATCAG
AAGGGCACCATCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAACTTTTCATCAGGCACAT
ACCACTGTCATCATAGACCTGCAAGCAAACCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAG
CTCCAGACTCTGATACTGCCACAACATGTCAACTGTCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTAT
ATAGACAACCAAATCTGTCAAGGGCAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAAT
GGATCTTGTGTACCTGATGGTCCAGGTCTTTTGCAAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATG
CGCCAGGGCTCGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTT
TGGGCGACCCAGCGCCGAAAAGCCAAGACTTCATGAACACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAA
CTATCTTAGCCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTTCGCCAGTGGATTTCGCCTCAAGGTTGAGG
CCGCCATTGGAAGATGAAAAATTGCACTCCCTTGGTGTAACAAATACCAGTTCCCATTGGTGTGTTGCCTATA
ATAAACACTTTTTCTTTTAAAAA

WO 2004/030615

PCT/US2003/028547

747/6881
FIGURE 697

MLHARCCLNQKGTILGLDLQNCSEDPGPNFHAHTTVIIDLQANPLKGD LANTFRGFTQLQTLILPQHVNCPGG
INAWNTITSYIDNQICQGQKNLCNNTGDPEMCPENGSCVPDGPGLLQCV CADGFHGYKCMRQGSFSLLMFFGILG
ATTLSVSILLWATQRRKAKTS

WO 2004/030615

PCT/US2003/028547

748/6881
FIGURE 698

GC GCCCTAGCCCTCTTTTCGGGGATACTGGCCGACCCCTCTTCCTTTTCCCCTTTAGTGAAGGCCTCCCCCGTCG
CCGCGCGGCTTCCCGGAGCCGACTGCAGACTCCCTCAGCCCGGTGTTCCCGCGTCCGGACGCCGAGGTGCGCGC
TTCGCAGAACTCGGGCCCCCTCCATCCGCCCTCAGAAAAGGGAGCGATGTTGATCTCAGGAAGCACAAAGGGACC
TTCTAGCTCTGACTGAACCACGGAGCTCACCTGGACAGTATCACTCCGTGGAGGAAGACTGTGAGACTGTGGC
TGGAAGCCAGATTGTAGCCACACATCCGCCCTGCCCTACCCAGAGCCCTGGAGCAGCAACTGGCTGCAGATCA
CAGACACAGTGAGGATATGAGTGTAGGGGTGAGCACCTCAGCCCTCTTTCCCAACCTCGGGCACAAAGCGTGGG
CATGTCTACCTTCTCCATCATGGAATATGTGGTGTTCGTCCTGCTGCTGGTTCCTCTCTCTTGCCATTGGGCTCTA
CCATGCTTGTGCTGGCTGGGGCCGGCATACTGTTGGTGAGCTGCTGATGGCGGACCGCAAAATGGGCTGCCCTCC
GGTGGCACTGTCCCTGCTGGCCACCTTCCAGTCAGCCGTGGCCATCCTGGGTGTGCCGTGAGAGATCTACCGATT
TGGGACCCAAATATTGGTTCCTGGGCTGCTGCTACTTTCTGGGGCTGCTGATACCTGCACACATCTTCATCCCCGT
TTTCTACCGCTGCATCTCACCAGTGCCATGAGTACCTGGAGCTTCGATTCAATAAAACTGTGCGAGTGTGTGG
AACTGTGACCTTCATCTTTTCTGATGGTGATCTACATGGGAGTTGTGCTCTATGCTCCGTGATTGGCTCTCAATGC
AGTGACTGGCTTTGATCTGTGGCTGTCCGTGCTGGCCCTGGGCATTGTCTGTACCGTCTATACAGCTCTGGGTGG
GCTGAAGGCCGTCACTGAGACAGATGTGTTCCAGACACTGGTCATGTTCCCTCGGGCAGCTGGCAGTTATCATCGT
GGGGTCAGCCAAAGTGGGCGGCTTGGGGCGTGTGTGGGCCGTGGCTTCCAGCACGGCCGCAATCTCTGGGTTTGA
GCTGGATCCAGACCCCTTTGTGCGGCACACCTTCTGGACCTTGGCCCTTCGGGGGTGTCTTCATGATGCTCTCCTT
ATACGGGGTGAACCAGGCTCAGGTGCAGCGGTACCTCAGTTCCCGCACGGAGAAGGCTGCTGTGCTCTCCTGTTA
TGCAGTGTTCCTTCCAGCAGGTGTCCCTCTGCGTGGGCTGCCTCATTGGCCTGGTCACTTTGTGATGGATCTCCT
GGAGTATCCCATGAGCATTCAGCAGGCTCAGGCAGCCCCAGACAGTTTCGTCTGTACTTTGTGATGGATCTCCT
GAAGGGCTGCCAGGCTGCCAGGCTCTTCATTGCCTGCCTCTTCAGCGGCTCTCTCAGCACTATATCCTCTGC
TTTAAATTCAATTGGCAACTGTTACGATGGAAGACCTGATTCGACCTTGGTTCCCTGAGTTCTCTGAAGCCCGGGC
CATCATGCTTTCCAGAGGCTTGCCTTTGGCTATGGGCTGCTTTGTCTAGGAATGGCCTATATTTCCCTCCAGAT
GGGACCTGTGCTGCAGGCAGCAATCAGCATCTTTGGCATGGTTGGGGGACCGCTGCTGGGACTCTTCTGCCTTGG
AATGTTCTTTCCATGTGCTAACCCTCCTGGTGCTGTGTGGGCGCTGTGGCTGGGCTCGTCATGGCCTTCTGGAT
TGGCATCGGGAGCATCGTGACCAGCATGGGCTTCAGCATGCCACCTCTCCCTCTAATGGGTCCAGCTTCTCCCT
GCCCACCAATCTAACCCTTGCCACTGTGACCACACTGATGCCCTTGACTACCTTCTCCAAGCCACAGGGCTGCA
GCGGTTCTATTCTTGTCTTACTTATGGTACAGTGTCTCACAACCTCCACCACAGTGATTGTGGTGGGCTGATTGT
CAGTCTACTCACTGGGAGAAATGCGAGGCGGTCCCTGAACCTGCAACCATTACCCAGTGTTGCCAAAGCTCCT
GTCCCTCCTTCCGTTGTCTGTGAGAAGCGGCTCCACTGCAGGAGCTACGGCCAGGACCACCTCGACACTGGCCT
GTTTCCTGAGAAGCCGAGGAATGGTGTGCTGGGGGACAGCAGAGACAAGGAGGCCATGGCCCTGGATGGCACAGC
CTATCAGGGGAGCAGCTCCACCTGCATCCTCCAGGAGACCTCCCTGTGATGTTGACTCAGGACCCCGCCTCTGTC
CTCACTGTGCCAGGCCATAGCCAGAGGCCACCCTGTAGTACAGGGATGAGTCTTGGTGTGTTCTGCAGGGACAGG
CCTGGATGATCTAGCTCATACCAAGGACCTTGTCTGAGAGGTTCTTGCTGCAGGAGAAGCTGTACATCTCA
AGCATGTGAGGCACCGTTTTTCTCGTCGCTTGCCAATCTGTTTTTAAAGGATCAGGCTCGTAGGGAGCAGGATC
ATGCCAGAAATAGGGATGGAAGTGCATCCTCTGGGAAAAAGATAATGGCTTCTGATTCAACATAGCCATAGTCCT
TTGAAGTAAGTGGCTAGAAACAGCACTCTGGTTATAATGGCCCCAGGGCCTGATTGAGGACTGACTCTCCACCAT
AAAACCTGGAAGCTGCTTCCCTGTAGTCCCCATTTCAGTACCAGTTCTGCCAGCCACAGTGAGCCCTATTATTA
CTTTTCAAGATTGTCTGTGACACTCAAGCCCTCTCATTTTTATCTGTCTACCTCCATTCTGAAGAGGGAGGTTTTG
GTGTCCCTGGTCTCTGGGAATAGAAGATCCATTGTCTTTGTGTAGAGCAAGCACGTTTTCCACCTCACTGTCT
CCATCCTCCACCTCTGAGATGGACACTTAAGAGACGGGGCAATGTGGATCCAAGAAACCAGGGCCATGACCAGG
TCCACTGTGGAGCAGCCATCTATCTACCTGACTCCTGAGCCAGGCTGCCGTGGTGTCACTTTCTGTCTATCCGTGCT
CTGTTTTCTTTTGGAGTTTCTTCTCCACATTATCTTTGTTCCTGGGGAATAAAACTACCATTGGACCTAAAAAA
AAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

749/6881
FIGURE 699

MSVGVSTSAPLSPTSGTSMSTFSIMDYVVFVLLLVLSLAIGLYHACRGWGRHTVGELLMADRKMGCPLVALSL
LATFQSAVAILGVPSEIYRFGTQYWFLGCCYFLGLLIPAHIFIPVFYRLHLTSAYEYLELRFNKTVRVCGTVTFI
FQMVIYMGVVLVYAPSLALNAVTFGFDLWLSVLALGIVCTVYTALGGLKAVIWTDFQTLVMFLGQLAVIIVGS AKV
GGLGRVWAVASQHGRI SGFELDPDPFVRHTFWTLAFGGVFMMLSLYGVNQAQVQRYLSSRTEKAAVLSCYAVFPF
QQVSLCVGCLIGLVMFAYYQEYPMSIQQAQAAPDQFVLYFVMDLLKGLPGLPGLFIACLFSGSLSTISSAFNSLA
TVT MEDLIRPWFPEFSEARAIMLSRGLAFGYGLLCLGMAYISSQMGPVLQAAISIFGMVGGPLLGLFCLGMFFPC
ANPPGAVVGLLAGLVMAFWIGIGSIVTSMGFSMPSPSNGSSFSLPTNLT VATVTTL MPLTTFSKPTGLQRFYSL
SYLWYSAHNSTTVIVVGLIVSLLTGRMRGRSLNPAT IYPVLPKLLSLLPLSCQKRLHCRSYGQDHLDTGLFPEKP
RNGVLGDSRDKEAMALDGTAYQGSSTCILQETSL

PCT/US2003/028547

GCCTGCGCGGAGGGAGCCGCGAGACAGGTGCGCATGCGCAGTGC CGCGTCTGCGAGACCGGAGCCGA
GCTGAGGCTCGGCTTCCTGCTGATGGTCAGGGTTTTGGCAACTCCCCGGTGTGAGAGGGGTAGGGAGTGCTCCCCG
GCGGCGACGGGGCCGAGTTACACAGCCGCCGGGGCAGTAGTCAAGGCCCGGCGCGGCATGTCTCTGGGTGCCGCG
GTGCGGGCAGTGAACGCGCGCCGGGCGGGATGGGCCGGCGCCGGGCGCCAGAGCTGTACCGGGCTCCGTTCCTCGT
TGTACGCGCTTCAGGTTCGACCCAGCACTGGGCTGCTCATCGCTGCGGGCGGAGGAGGCGCCGCAAGACAGGCA
TAAAGAATGGCGTGCACTTTCTGCAGCTAGAGCTGATTAATGGGCGCTTGAGTGCCCTCTTGCTGCACTCCCATG
ACACAGAGACACGGGCCACCATGAAC TTGGCACTGGCTGGTGACATCCTTGCTGCAGGGCAGGATGCCC ACTGTG
AGCTCCTGCGCTTCCAGGCACATCAACAGCAGGGCAACAAGGCAGAGAAGGCCGGTTCCAAGGAGCAGGGGGCCTC
GACAAAGGAAGGGAGCAGCCCCAGCAGAGAAGAAATGTGAGCGGAAACCCAGCACGAGGGGGCTAGAACTCAGGG
TAGAGAATTTGCAGGCGGTGCAGACAGACTTTAGCTCCGATCCACTGCAGAAAGTTGTGTGCTTCAACCACGATA
ATACCCTGCTTGCCACTGGAGGAACAGATGGCTACGTCCGTGTCTGGAAGGTGCCAGCCTGGAGAAGGTCTTG
AGTTCAAAGCCCACGAAGGGGAGATTGAAGACCTGGCTTTAGGGCCTGATGGCAAGTTGGTAACCGTGGGCCGGG
ACCTTAAGGCCTCTGTGTGGCAGAAGGATCAGCTGGTGACACAGCTGCAC TTGGCAAGAAATGGACCCACCTTTT
CCAGCACACCTTACCGCTACACGGCTGCAGGTTTGGGCAGGTTCCAGACCAGCCTGCTGGCCTGCGACTCTTCA
CAGTGCAAAT TCCCCACAAGCGCCTGCGCCAGCCCCCTCCCTGCTACCTCACAGCCTGGGATGGCTCCA ACTTCT
TGCCCCCTTCGGACCAAGTCCTGTGGCCATGAAGTCGTCTCCTGCTCGATGTGAGTGAATCCGGCACCTTCCTAG
GCCTGGGCACAGTCACTGGCTCTGTTGCCATCTACATAGCTTTCTCTCTCCAGTGCCTCTACTACGTGAGGGAGG
CCCATGGCATTGTGGTGACGGATGTGGCCTTTCTACCTGAGAAGGGTCGTGGTCCAGAGCTCCTTGGGTCCCATG
AAACTGCCCTGTTCTCTGTGGCTGTGGACAGTCTGTTGCCAGCTGCATCTGTTGCCCTCACGGCGGAGTGTTCCCTG
TGTGGCTCCTGCTCCTGCTGTGTGTGCGGGCTTATTATTGTGACCATCCTGCTGCTCCAGAGTGCCTTTCCAGGTT
TCCCTTTAGCTTCCCTGCTTCTCTGGGAATCAGGAGCCTGGACACTGCCATCTCTAGAGCAGAGTGGAGGCCTGGAC
TCCCTTTTGCTCACTCCATTGCGGTCCACAGCTGAGGTTGCCGCTGACAAGATGAATGGGC ACTGCCTGCCCTTCT
AGTGAAAAGGCTTGCGCTATGGCCCTGTGTGACTCCAGGTCCAGGAACCTTGCCCTTCGTCTGTGATCCATC
CAGAACAGCGGTATCTGAAGCCCAGGCCATACTCCCTGCCTCCTTTCTTCTGCCTACCAGAGGCTCCAGAGTTGA
GCTTGTCTCTTATCTAGAAACATGTGAAGATGCCCAAGAGCCTGGAGGC ACTGCTGTCTTCTTGCAGAAACAGTT
TCTCCTCCTCCCTCAGCCTTGTGGCCAGTTCCTCTTACATGAAGCCCCTGGCATT TTGCTGGGGAAGGGACTGG
CCTGGTACTTTGCTGTTAGGGCAGGAAGGGGCAAAAGGAAGACTTGGGTAGTAATCTGGGGGTTT CAGATGGGTAGC
ACTAAGCCAGCTGGCCTAAAGATGCAATAAGTTCTAGGTAGTCTACCCTTACCTTGAGGAATGGGAAAATGAAC
CTCAGCCCATTAGGCAGGAAAAGTTGATATTTAATAAACAAGGAAAGAGTGA ACTGAGACCC

WO 2004/030615

PCT/US2003/028547

751/6881
FIGURE 701

GTAGCCTCATGGAAGAGAAGCAGATCCTGTGCGTGGGGCTAGTGGTGCTGGACGTCATCAGCCTGGTGGACAAGT
ACCCTAAGGAGGACTCGGAGATAAGGTGTTTGTCCAGAGATGGCAGCGCGGAGGCAACGCGTCCAACTCCTGCA
CCGTTCTCTCCCTGCTCGGAGCCCCCTGTGCCTTCATGGGCTCAATGGCTCCTGGCCATGTTGCTGATTTTGTCC
TGGATGACCTCCGCCGCTATTCTGTGGACCTACGCTACACAGTCTTTAGACCACAGGCTCCGTCCCCATCGCCA
CGGTCAATCATCAACGAGGCCAGTGGTAGCCGCACCATCCTATACTATGACAGGAGCCTGCCAGATGTGTCTGCTA
CAGACTTTGAGAAGGTTGATCTGACCCAGTTCAAGTGGATCCACATTGAGGGCCGGAACGCATCGGAGCAGGTGA
AGATGCTGCAGCGGATAGACGCACACAACACCAGGCAGCCTCCAGAGCAGAAGATCCGGGTGTCCGTGGAGGTGG
AGAAGCCACGAGAGGAGCTCTTCCAGCTGTTTGGCTACGGAGACGTGGTGTGTTGTGTCAGCAAAGATGTGGCCAAGC
ACTTGGGGTTCCAGTCAGCAGAGGAAGCCTTGAGGGGCTTGATGGTTCGTGTGAGGAAAGGGGCTGTGCTTGTCT
GTGCCTGGGCTGAGGAGGGCGCCGACGCCCTGGGCCCTGATGGCAAATTGCTCCACTCGGATGCTTTCCCGCCAC
CCCGCGTGGTGGATACACTGGGAGCTGGAGACACCTTCAATGCCTCCGTTCATCTTCAGCCTCTCCAGGGGAGGA
GCGTGCAGGAAGCACTGAGATTCCGGGTGCCAGGTGGCCGGCAAGAAGTGTGGCCTGCAGGGCTTTGATGGCATCG
TGTGAGAGCAGGTGCCGGCTCCTCACACACCATGGAGACTACCATTGCGGCTGCATCGCCTTCTCCCCCTCCATCC
AGCCTGGCGTCCAGGTGGCCCTGTTTCAGGGGACAGATGCAAGCTGTGGGGAGGACTCTGCCTGTGTCTGTGTTT
CCCACAGGGAGAGGCTCTGGGGGGATGGCTGGGGGATGCAGAGCCTCAGAGCAAATAAATCTTCTCAGAGCCAG
CTTCTCCTCTCAATGTCTGAACTGCTCTGGCTGGGCATTCTGAGGCTCTGACTCTTCGATCCTCCCTCTTTGTG
TCCATTCCCCAAATTAACCTCTCCGCCAGGCCAGAGGAGGGGCTGCCTGGGCTAGAGCAGCGAGAAGTGCCCT
GGGCTTGCCACCAGCTCTGCCCTGGCTGGGGAGGACACTCGGTGCCCCACACCCAGTGAACCTGCCAAAGAAACC
GTGAGAGCTCTTCGGGGCCCTGCGTTGTGCAGACTCTATTCCCACAGCTCAGAAGCTGGGAGTCCACACCGCTGA
GCTGAAGTACAGGCCAGTGGGGGGCAGGGGTGCGCTCCTCTGCCCTGCCACCAGCCTGTGATTTGATGGGGT
CTTCATTGTCCAGAAATACCTCCTCCCGCTGACTGCCCCAGAGCCTGAAAGTCTCACCCTTGAGGCCACCTGG
AATTAAGGGCGTGCTCAGCCACAAATGTGACCCAGGATACAGAGTGTGCTGTCTCAGGGAGGTCCGATCTGG
AACACATATTGGAATTGGGGCCAACTCCAATATAGGGTGGGTAAGGCCTTATAATGTAAAGAGCATATAATGTAA
AGGGCTTTAGAGTGAGACAGACCTGGATTCAAATCTGCCATTTAATTAGCTGCATATCACCTTAGGGTACAGCAC
TTAACGCAATCTGCCTCAATTTCTTCATCTGTCAAATGGAACCAATTCTGCTTGGCTACAGAATTATTGTGAGGA
TAAAAATCATATATAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

752/6881
FIGURE 702

MEEKQILCVGLVVLDVISLVDKYPKEDSEIRCLSQRWQRGGNASNSCTVLSLLGAPCAFMGSMAPGHVADFVLDD
LRRYSVDLRYTVFQTTSVP IATVIINEASGSRTILYYDRSLPDVSATDFEKVDLTQFKWIIHIEGRNASEQVKML
QRIDAHNTRQPPEQKIRVSVEVEKPREELFQLFGYGDVVFVSKDVAKHLGFQSAEEALRGLYGRVRKGAVLVCAW
AEEGADALGPDGKLLHSDAFPPPRVVDTLGAGDTFNASVIFSLSQGRSVQEALRFGCQVAGKKCGLQGF DGIV

WO 2004/030615

PCT/US2003/028547

753/6881
FIGURE 703

GTAGCCTCATGGAAAGAGAAGCAGATCCTGTGCGTGGGGCTAGTGGTGCTGGACGTCATCAGCCTGGTGGACAAGT
ACCCTAAGGAGGACTCGGAGATAAGGTGTTTGTCCAGAGATGGCAGCGCGGAGGCAACGCGTCCAACCTCCTGCA
CCGTTCTCTCCCTGCTCGGAGCCCCCTGTGCCTTCATGGGCTCAATGGCTCCTGGCCATGTTGCTGACTTCCTGG
TGGCCGACTTCAGGCGGCGGGGCGTGGACGTGTCTCAGGTGGCCTGGCAGAGCAAGGGGGACACCCCCAGCTCCT
GCTGCATCATCAACAACTCCAATGGCAACCGTACCATTGTGCTCCATGACACGAGCCTGCCAGATGTGTCTGCTA
CAGACTTTGAGAAGGTTGATCTGACCCAGTTCAAGTGGATCCACATTGAGGGCCGGAACGCATCGGAGCAGGTGA
AGATGCTGCAGCGGATAGACGCACACAACACCAGGCAGCCTCCAGAGCAGAAGATCCGGGTGTCCGTGGAGGTGG
AGAAGCCACGAGAGGAGCTCTTCCAGCTGTTTGCTACGGAGACGTGGTGTTTGTTCAGCAAAGATGTGGCCAAGC
ACTTGGGGTTCCAGTCAGCAGAGGAAGCCTTGAGGGGCTTGATGGTTCGTGTGAGGAAAGGGGCTGTGCTTGTCT
GTGCCTGGGCTGAGGAGGGCGCCGACGCCCTGGGCCCTGATGGCAAATTGCTCCACTCGGATGCTTTCCCGCCAC
CCCGCGTGGTGGATACACTGGGAGCTGGGAGACCTTCAATGCCTCCGTCATCTTCAGCCTCTCCCAGGGGAGGA
GCGTGCAGGAAGCACTGAGATTGCGGTGCCAGGTGGCCGGCAAGAAGTGTGGCCTGCAGGGCTTTGATGGCATCG
TGTGAGAGCAGGTGCCGGCTCCTCACACACCATGGAGACTACCATTGCGGCTGCATCGCCTTCTCCCCTCCATCC
AGCCTGGCGTCCAGGTTGCCCTGTTTCAGGGGACAGATGCAAGCTGTGGGGAGGACTCTGCCTGTGTCTGTGTTT
CCCACAGGGAGAGGCTCTGGGGGGATGGCTGGGGGATGCAGAGCCTCAGAGCAAATAAATCTTCTCAGAGCCAG
CTTCTCCTCTCAATGTCTGAAGTGTCTGGCTGGGCATTCTGAGGCTCTGACTCTTCGATCCTCCCTCTTTGTG
TCCATTCCCCAAATTAACCTCTCCGCCAGGCCAGAGGAGGGGCTGCCTGGGCTAGAGCAGCGAGAAGTGCCCT
GGGCTTGCCACCAGCTCTGCCCTGGCTGGGGAGGACACTCGGTGCCCCACACCCAGTGAACCTGCCAAAGAAACC
GTGAGAGCTCTTCGGGGCCCTGCGTTGTGCAGACTCTATTCCCACAGCTCAGAAGCTGGGAGTCCACACCGCTGA
GCTGAAGTACAGGCCAGTGGGGGGCAGGGGTGCGCCTCCTCTGCCCTGCCACCAGCCTGTGATTGATGGGGT
CTTCATTGTCCAGAAATACCTCCTCCCGCTGACTGCCCCAGAGCCTGAAAGTCTCACCTTGGAGCCCACCTTGG
AATTAAGGGCGTGCCCTCAGCCACAAATGTGACCCAGGATACAGAGTGTGCTGTCTCAGGGAGGTCCGATCTGG
AACACATATTGGAATTGGGGCCAACTCCAATATAGGGTGGGTAAAGGCCTTATAATGTAAAGAGCATATAATGTAA
AGGGCTTTAGAGTGAGACAGACCTGGATTCAAATCTGCCATTTAATTAGCTGCATATCACCTTAGGGTACAGCAC
TTAACGCAATCTGCCTCAATTTCTTCATCTGTCAAATGGAACCAATTCTGCTTGGCTACAGAATTATTGTGAGGA
TAAAAATCATATATAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

754/6881
FIGURE 704

MEEKQILCVGLVVLDVISLVDKYPKEDSEIRCLSQRWQRGGNASNSCTVLSLLGAPCAFMGSMAPGHVADFLVAD
FRRRGVDVSQVAWQSKGDT PSSCCIINNSNGNRTIVLHDTSLPDVSATDFEKVDLTQFKWIIHIEGRNASEQVKML
QRIDAHNTRQPPEQKIRVSVEVEKPREELFQLFGYGDVVFVSKDVAKHLGFQSAAEEALRGLYGRVRKGAVLVCAW
AEEGADALGPDGKLLHSDAFPPPRVVDTLGAGDTFNASVIFSLSQGRSVQEALRFGCQVAGKKCGLQGF DGIV

WO 2004/030615

PCT/US2003/028547

755/6881
FIGURE 705

ATGCCCCCGCACCCCTCTGGAGCTGCTACCTCTGCTGCCTGCTGACGGCAGCTGCAGGGGCGCCAGCTACCCCT
CCTCGAGGTTTCAGCCTCTACACAGGTTCCAGTGGGGCCCTCAGCCCCGGGGGGCCCCAGGCCAGATTGCCCCC
CGGCCAGCCAGCCGCCACAGGAAGTGGTGTGCCTACGTGGTGACCCGGACAGTGAGCTGTGTCTTGAGGATGGA
GTGGAGACATATGTCAAGTACCAGCCTTGTGCCTGGGGCCAGCCCCAGTGTCCCCAAAGCATCATGTACCGCCGC
TTCTCCGCCCTCGCTACCGTGTGGCCTACAAGACAGTGACCGACATGGAGTGGAGGTGCTGTGAGGGTTATGGG
GGCGATGACTGTGCTGAGAGTCCCGCTCCAGCGCTGGGGCCTGCGTCTTCCACACCACGGCCCCCTGGCCCGGCCT
GCCCCCCCCAACCTCTCTGGCTCCAGTGCAGGCAGCCCCCTCAGTGGACTGGGGGGAGAAGGTCTGGGGAGTCA
GAGAAGGTGCAGCAGCTGGAGGAACAGGTGCAGAGCCTGACCAAGGAGCTGCAAGGCCTGCGGGGCGTCTGCAA
GGACTGAGCGGGGCGCCTGGCAGAGGATGTGCAGAGGGCTGTGGAGACGGCCTTCAACGGGAGGCAGCAGCCAGCT
GACGCGGCTGCCCCGCCCTGGGGTGCATGAAACCCCTCAATGAGATCCAGCACCAGCTGCAGCTCCTGGACACCCGC
GTCTCCACCCACGACCAGGAGCTGGGTCACTCAACAACCATCATGGCGGCAGCAGCAGCAGTGGGGGCAGCAGG
GCCCCAGCCCCAGCCTCAGCCCCCTCCGGGCCCCAGTGAGGAGCTGCTGCGGCAGCTGGAGCAGCGGTTGCAGGAG
TCCTGCTCCGTGTGCCTGGCCGGGCTAGATGGCTTCCGCCGGCAGCAGCAGGAGGACAGGGAGCGGCTGCGAGCG
ATGGAGAAGCTGCTGGCCTCGGTGGAGGAGCGGCAACGGCACCTCGCAGGGCTGGCGGTGGGCGCAGGCCCCCT
CAGGAATGCTGCTCTCCAGAGCTGGGCCGGCGACTGGCAGAGCTGGAGCGCAGGCTGGATGTCTGGCCGGCTCA
GTGACAGTGCTGAGTGGGCGGGCAGGCACAGAGCTGGGAGGAGCCGCGGGGCAGGGAGGCCACCCCCAGGCTAC
ACCAGCTTGGCCTCCCGCCTGTCTCGCCTGGAGGACCGCTTCAACTCCACCCTGGGCCCTTCGGAGGAGCAGGAG
GAGAGCTGGCCTGGGGCTCCTGGGGGGCTGAGCCACTGGCTGCCTGCTGCCCGGGGCGACTAGAGCAGTTGGGG
GGGCTGCTGGCCAATGTGAGCGGGGAGCTGGGGGGGCGGTTGGATCTGTTGGAGGAGCAGGTGGCAGGGGCCATG
CAGGCATGCGGGCAGCTCTGCTCTGGGGCCCCCTGGGGAGCAGGACTCTCAAGTCAGCGAGATCCTCAGTGCCTTG
GAGCGCAGGGTGCTGGACAGTGAGGGGCAGCTGCGGCTGGTGGGCTCCGGCCTGCACACGGTGGAAGCAGCGGG
GAGGCCCGGCAGGCCACGCTGGAGGGATTACAAGAGGTTGTGGGCCGGCTCCAGGATCGTGTGGATGCCCAGGAT
GAGACAGCTGCAGAGTTCACTACGGCTGAATCTCACTGCGGCCCGGCTAGGCCAACTGGAGGGGCTGCTGCAG
GCCCATGGGGATGAGGGCTGTGGGGCCTGTGGCGGAGTCCAAGAGGAAGTGGCCGCCTTCGGGATGGTGTGGAG
CGCTGCTCCTGCCCCCTGTTGCCTCCTCGGGGTCTGGGGCTGGTCCAGGTGTTGGGGGCCCAAGCCGTGGGCC
CTGGACGGCTTCAGCGTGTTTGGGGGCAGCTCAGGCTCAGCCCTGCAGGCCCTGCAAGGAGAGCTCTCTGAGGTT
ATTCTCAGCTTCAGCTCCCTCAATGACTCACTGAATGAGCTCCAGACCACTGTGGAGGGCCAGGGCAGCTGATCTG
GCTGACCTGGGGGCAACCAAGGACCGTATCATTTCTGAGATTAAACAGGCTGCAGCAGGAGGCCACAGCAGTGCT
ACAGAGAGTGAAGAGCGCTTCCGAGGCCTAGAGGAGGGACAAGCAGGCCGGCCAGTGCCCCAGCTTAGAGGGG
CGATTGGGCGCTCTTGAGGGTGCTGTGAACGGTTGGACACTGTGGCTGGGGGACTGCAGGGCCTGCGCGAGGGC
CTTTCCAGACACGTGGCTGGGCTCTGGGCTGGGCTCCGGGAAACCAACCACCAGCCAGATGCAGGCAGCCCTG
CTGGAGAAGCTGGTGGGGGACAGGCCGGCCCTGGGCAGGCGGCTGGGTGCCCTTAACAGCTCCCTGCAGCTCCTG
GAGGACCGTCTGCACCAGCTCAGCCTGAAGGACCTCACTGGGCCTGCAGGAGAGGCTGGGCCCCAGGGCCCTCCT
GGGCTGCAGGGACCCCCAGGCCCTGCTGGACCTCCAGGATCACCAGGCAAGGACGGGCAAGAGGGCCCCATCGGG
CCACCAGGTCTCAAGGGGAACAGGGAGTGGAGGGGGCACCAGCAGCCCTGTGCCCCAAGTGGCATTTCAGCT
GCTCTGAGTTTGCCCCGGTCTGAACAGGCACGGTCCCTTCGACAGAGTCCTGCTCAATGATGGAGGCTATTAT
GATCCAGAGACAGGCGTGTTACAGCGCCACTGGCTGGACGCTACTTGCTGAGCGCGGTGCTGACTGGGCACCGG
CACGAGAAAGTGGAGGCCGTGCTGTCCCGCTCCAACCAGGGCGTGGCCCGCTAGACTCCGGTGGCTACGAGCCT
GAGGCCCTGGAGAATAAGCCGGTGGCCGAGAGCCAGCCAGCCGGGCACCCTGGGCGTCTTCAGCCTCATCCTG
CCGCTGCAGGCCGGGGACACGGTCTGCGTGCACCTGGTTCATGGGGCAGCTGGCGCACTCGGAGGAGCCGCTCACC
ATCTTCAGCGGGGCCCTGCTCTATGGGGACCCAGAGCTTGAACACGCGT**TAG**ACTGGGGTCCCGCCGACGTGTCT
ACGTGCGCTGAAGAGACAGCGGGGGCGCGGGCTCCTGGGGTCTGCGCTGAGACGGGGCACCTAGCCCTGGGCGA
GCGCCGACCCGGGCGCCGACGCGCCAGAGCGGCCTCTCCCCACGCCCGGGGCGCGCCGGCTCAGGG
AGGCTCGGGGCGGCCATGCAGACTTTTGGCCTGGCGGATCCCCAAGAACCCTCCAGGGCCGGCTGCGGAG
GAGCCGATCCTCGCACCCCTCCGCTCCCTCCACTGGCCCTCAGGTCGATTCCCTGGGCTCCAGGCTCCCCCGCG
GGGCGCGCCACCGCCATACTAAACGATCGAGGAATAAAGACACTTGGTTTTTCT

WO 2004/030615

PCT/US2003/028547

756/6881
FIGURE 706

MAPRTLWSCYLCCLLTAAAGAASYPPRGFSLYTGSSGALSFGGPQAQIAPRPASRHRNWCAYVVTRTVSCVLEDG
VETYVKYQPCAWGQPQCPSIMYRRFLRPRYRVAYKTVTDMEWRCQGYGGDDCAESPAPALGPASSTPRPLARP
ARPNLSGSSAGSPLSGLGGEGPGESEKVQQLLEEQVQSLTKELQGLRGVLQGLSGRLAEDVQRAVETAFNGRQQPA
DAAARPGVHETLNEIQHQLQLLDTRVSTHDQELGHLNNHHGGSSSSSGGSRAPAPASAPPGPSEELLRQLEQRLQE
SCSVCLAGLDGFRQQQEDRERLRAMEKLLASVEERQRHLAGLAVGRRPPQECCSPELGRRRLAELERRLDVVAGS
VTVLSGRRGTELGAAGQGGHPPGYTSLASRLSRLED RFNSTLGPSEEQEE SWPGAPGGLSHWLPAARGRLEQLG
GLLANVSGELGGRLDLLEEQVAGAMQACGQLCSGAPGEQDSQVSEILSALERRVLDSEGQLRLVGSGLHTVEAAG
EARQATLEGLQEVVGRQLQDRVDAQDETA AEFTLRLNLTAARLGQLEGLLQAHGDEGCGACGGVQEELGRLRDGVE
RCSCPLLPPRPGAGPGVGGPSRGPLDGF SVFGSSGSALQALQGESEVILSFSSLNDSLNELQTTVEGQGADL
ADLGATKDRI ISEINRLQQEATEHATESEERFRGLEEGQAQAGQCPSLEGR LGRLEGVCERLDTVAGGLQGLREG
LSRHVAGLWAGLRETNNTTSQMQAALLEKLVGGQAGLGRR LGALNSSLQ LLEDRLHQLSLKDLTG PAGEAGPPGPP
GLQGPPGPAGPPGSPGKDGQEGPIGPPGPQGEQGVGAPAAPVPQVAFSAALSLPRSEPGTVPFDRVLLNDGGYY
DPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNQGVARVDSGGYEPEGLENKPVAESQSPGTLGVFSLIL
PLQAGDTVCVDLVMGQLAHSEEPLTIFSGALLYGDPELEHA

WO 2004/030615

PCT/US2003/028547

757/6881
FIGURE 707

GGCACGAGGGGCACCGCGGCGCTCGGGTGTTTTGGGGGCCCCGGGTGGAGGGCCCCGGGTGCCGGGGCCCAAGGTG
CGGCCTCGCTAGCGGGAGAGGGAGCGGGATCACCGGCCCGGAGAGAGCTCTCAGGGCCAGAGCGGGGCAGGAGGA
TGCTTTCCAGCCCCACCATGGAGCTGCGCTGTGGGGGATTGCTGTTTCAGTTCTCGCTTTGATTCAGGGAATCTA
GCCCCAGTGGAGAAGGTGGAATCTTTGTCCAGTGATGGGGAAGGGGTAGGAGGTGGGGCGTCAGCCCTGACCAGT
GGCATTGCCTCTTCCCTGACTATGAATTCAACGTGTGGACCCGACCAGACTGTGCTGAAACGGAATTTGAGAAT
GGGAACAGGTTCATGGTTCTACTTCAGCGTCCGGGGAGGAATGCCAGGAAAACCTCATCAAGATCAACATTATGAAC
ATGAACAAGCAGAGCAAGCTGTATTCCAGGGCATGGCCCCCTTTGTGCGCACACTGCCCCACCCGGCCACGCTGG
GAACGCATTTCAGAGACCGGCCACCTTTGAGATGACAGAGACGCAGTTTGTGTTATCCTTTGTTTCATCGTTTCGTG
GAGGGCCGTGGGGCCACCACCTTCTTCGCCTTCTGCTACCCCTTCTCCTACAGTGACTGCCAGGAACTGCTAAAC
CAGCTAGACCAGCGCTTTCCGGAGAACCACCTACCCATAGCAGCCCCCTGGATACCATCTATTACCATCGGGAG
CTCCTTTGCTATTCTCTGGATGGACTTCGTGTAGATCTGCTGACGATCACTTCCTGCCATGGGCTTCGAGAAGAT
CGAGAGCCCCGTCTAGAGCAGCTATTTCTGATACCAGCACCCTCGACCATTCCGTTTCGAGGCAAGAGGATA
TTCTTCTTAAGCAGTAGAGTACACCCAGGGGAGACTCCATCTAGCTTTGTCTTCAATGGCTTTCTGGACTTCATC
CTCCGACCTGATGATCCCCGGGCCCAAACCTCCGTGCGCTCTTCGTCTTTAAGCTGATTCCCATGTTGAACCC
GATGGTGTGGTCCGGGGACACTACCGCACAGACTCACGTGGAGTGAATCTGAACCGTCAGTACCTGAAGCCTGAT
GCCGTCTGCACCCGGCCATCTATGGGGCCAAAGCTGTGCTTCTTACCACCATGTGCACTCTCGTCTGAACCTC
CAGAGTTCTCTGAGCACCAGCCAGTTCTGTCTCCCTCCTGATGCTCCTGTTTCTGACCTGGAGAAAGCCAAC
AATCTCCAAATGAAGCTCAGTGTGGGCACTCAGCTGACAGGCATAACGCTGAAGCCTGGAACAAACAGAGCCA
GCAGAACAGAAGCTCAACAGTGTGTGGATTATGCCACAACAGTCTGCGGGGCTTGAAGAGTCAGCCCCGTGATACC
ATCCCCCCCCAAGAGAGTGGCGTTGCTTACTATGTGGACCTGCATGGACATGCTTCCAAAAGGGGCTGCTTCATG
TACGGAAACAGCTTTAGTGATGAGAGCACCAGGTGGAACATGCTATATCCAAAGCTCATCTCCTTGAATTCA
GCCCACCTTCGACTTCAGGGCTGCAATTTCTCAGAGAAGAATATGTATGCCCGAGACCGTAGAGATGGCCAGTCT
AAAGAGGGAAGCGGCCGTGTTGCAATCTACAAAGCCTCAGGGATAATCCACAGCTACACACTTGAATGCAACTAC
AACACTGGACGCTCAGTAAACAGCATCCCTGCTGCCTGCCATGACAATGGGCGTGCCAGCCCCCTCCCCGCCG
GCTTTCCCTCCAGATACACTGTGGAATATTTGAGCAGGTGGGACGAGCTATGGCCATTGACAGCCCTGGACATG
GCGGAATGTAATCCGTGGCCCCGAATTGTACTGTGAGACACAGCAGCCTTACTAATCTACGGGCCTGGATGCTG
AAACATGTACGCAACAGCCGAGGCCTAAGCAGCACTCTGAATGTGGGTGTCAACAAGAAGGGGCCCTTCGAACT
CCACCCAAAAGTCACAATGGGTGCTCTCCTGCTCCGAAAACACCTTGAGTCGGGCACGAAGTTTTAGCACC
GGCACAAGTGCCGGTGGTAGCAGCAGCAGCCAACAAATTCTCCACAGATGAAGAATTCCCCCAGCTTTCCTTTT
CATGGCAGTCGGCCTGCAGGGCTGCCAGGCCTGGGCTCTAGTACCCTAACAAAGGTACCCACCGGGTGCTGGGCCCC
GTCAGAGAGCCCCGAAGCCAGGACAGGAGACGGCAGCAGCAGCCCTGAACCATCGTCCTGCAGGCAGCCTCGCT
CCATCCCCAGCTCCTACTAGTTCTGGCCAGCCTCCTCACACAAGCTGGGCTCCTGTCTACTGCCTGATTCAATC
AACATACCAGGGAGCAGTTGCTCACTCTTGTCTCTGAGACAAACCAGAGGCTGTGATGGTAATCGGGAAAGGT
CTGCTAGGGACTGGAGCTCGGATGCCCTGCATCAAGACTCGATTGACAGCCTGTCCGAGGAGAGTTTCCGCCAGG
AGGGGTCCCGGATTCCCCAGGCTAGGCCAGGTTGGGCCGGGGCTCACCGCCGACTCGCAGAGGGATGAAGGCT
CTTCAGGCCCCACATCCCCTACCCCCCGGACCAGGGAGAGCAGTGAGCTGGAGCTGGGATCCTGCTCTGCTACAC
CAGGGCTGCCTCAGGCCAGGCCCCACGGCCCCGCTCTGCCCCCTGCCTTTTCTCCTATATCCTGTAGTCTATCTG
ACTCCCCATCCTGGAATTGTTACAGCAGGGGTCCCTTGGGCCAACCTGAGGTTTGTTTTGTCCCTAAATCTCCCC
CACTGACTGTTTCTCCCCGGGTCTGATAATGCCTTTATGTTCAATCCAGGATATAGCCCCAAGATGGGGTAACA
GTGGGAAATATGCTAGTTCCCCTCCAGGCCGCTGATTCCATGTGACAGCCGTTAAGTCCTTGGAAATGCCAGCCAC
GCTGTCCAAGGCATTACAGAGTATCACCTTGAGACAGAACAAAACAGGGACCTGCCACCCCTTCCCTCCCTCCGC
AGCACAAGATTTTGGGACCACAAAAAAGTCTATATTTTATATTGGGGGGAGGGAGTAGAAAAGCAAGCCCCCT
ATACTGGGCCCTATTTCAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGAGGAAATAAAAGTTGTTTG
GAAAAATCCAAAAA

WO 2004/030615

PCT/US2003/028547

758/6881
FIGURE 708

MNMNKQSKLYSQGMAPFVRTLPTRPRWERIRDRTFEMTETQFVLSFVHRFVEGRGATTFFAFCYPFSYSDCQEL
LNQLDQRFPENHPHTHSSPLDTIYYHRELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPFRFAGK
RIFFLSSRVHPGETPSSFVFNGLDFILRPDDPRAQTLRRLEVFVKLIPMLNPDGVVRGHRDTSRGVNLNRQYLK
PDAVLHPAIYGAKAVLLYHHVHSRLNSQSSSEHQPSCLPPDAPVSDLEKANNLQNEAQCGHSADRHNAEAWKQT
EPAEQKLNSVWIMPQQSAGLEESAPDTIPPKESGVAYYVDLHGASKRGCFMYGNSFSDESTQVENMLYPKLISL
NSAHFDFQGCNFSEKNMYARDRRDQSQKEGSGRVAIYKASGIIHSYTLECNNTGRSVNSIPAACHDNGRASPPP
PPAFPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNLRAWMLKHVRNSRGLSSTLNVGVNKKRGL
RTPPKSHNGLPVSCSENTLSRARSFSTGTSAGGSSSSQNSPQMKNSESPFFHGSRPAGLPGLGSSTQKVTHRVL
GPVREPRSQDRRRQQQLNHRPAGSLAPSPAPTSSGPASSHKLGSCLLPDSFNIPGSSCSLLSSGDKPEAVMVIG
KGLLGTGARMPCIKTRLQTCPRRVSAARRGPGFPRLGPGWAGAHRRRLAEG

WO 2004/030615

PCT/US2003/028547

759/6881
FIGURE 709

CCCCCCCCACTCTGGACTCCCGCGCTGGGCGCGCTGAGGCGGCCCCCGAGCGAGCGCGCTGCAGCCGCCGCCG
CCCCGAGCACCCGCGAGCTCCGGCGCCGCGGCGAGACGGAGACGGACCGAGCCACGGGCCCCCGCGGCCGAGCATC
TCGGAGGAGAACATCGCTTGCCAACTCAGCCAGCGTGAGGATCCTCATCAAGGGAGGCAAGGTGGTGAACGATGAC
TGCACCCACGAGGCTGACGTCTACATCGAGAATGGCATCATCCAGCAGGTGGGCCGCGAGCTCATGATCCCTGGC
GGGGCCAAGGTGATTGATGCCACAGGAAAAGTGGTGATCCCTGGTGGCATCGACACCAGCACCCACTTCCACCAG
ACCTTCATGAATGCCACGTGCGTGGACGACTTCTACCATGGGACCAAGGCAGCACTCGTCGGAGGCACCACCATG
ATCATCGGCCACGTCTCGCCGACAAGGAGACCTCCCTTGTGGACGCTTATGAGAAGTGCCGAGGTCTGGCCGAC
CCCAAGGTCTGCTGTGATTACGCCCTCCACGTGGGGATCACCTGGTGGGCACCCAAGGTGAAAGCAGAAATGGAG
ACACTGGTGAGGGAGAAGGTGTCAACTCGTTCAGATGTTTCATGACCTACAAGGACCTGTACATGCTTCGAGAC
AGTGAGCTGTACCAAGTGTTGCACGCTTGCAAGGACATTGGGGCAATCGCCCGCGTCCATGCTGAAAATGGGGAG
CTTGTGGCCGAGGGTGCTAAGGAGGCACTGGATTGGGGATCACAGGCCCAGAAGGAATCGAGATCAGCCGTCCA
GAGGAGCTGGAAGCTGAAGCCACTCATCGTGTATCACCATTGCAAACAGGACTCACTGTCCAATCTACCTGGTC
AACGTGTCCAGTATCTCGGCTGGTGACGTTATCGCAGCTGCTAAGATGCAAGGGAAGGTTGTGCTGGCGGAGACC
ACCACTGCACATGCCACGCTGACAGGCTTACACTACTACCACCAGGACTGGTCCCACGCGGCTGCCTATGTACAG
GTGCCTCCCCTGAGACTGGACACCAACCTCAACCTACCTCATGAGCCTGCTGGCCAATGACACTCTGAACATC
GTGGCATCAGATCACCAGCCTTTCACCACAAAGCAGAAAGCTATGGGCAAGGAAGACTTCACCAAGATCCCACAT
GGAGTGAGTGGCGTGACAGGACCGCATGAGCGTCACTGGGAGAGAGGAGTGGTTGGAGGAAAGATGGATGAGAAC
CGTTTTGTGGCCGTTACCAGTTCCAACGCAGCTAAGCTTCTGAACCTGTATCCCCGCAAGGGCCGCATTATTCCC
GGAGCCGATGCTGATGTGGTGGTGTGGGACCCAGAAGCCACAAAGACCATCTCAGCCAGCACGCAGGTCCAGGGA
GGAGACTTCAACCTGTATGAGAACATGCGCTGCCACGGCGTGCCACTGGTCACCATCAGCCGGGGGCGCGTCGTG
TATGAGAACGGCGTCTTCATGTGCGCCGAGGGCACCGGCAAGTTCTGTCCCCTGAGGTCTTCCCAGACACTGTG
TACAAGAAGCTGGTCCAGAGAGAGAAGACTTTAAAGGTTAGAGGAGTGGACCGCACTCCCTACCTGGGGGATGTC
GCTGTTGTGCTGCACCCCTGGGAAAAAAGAGATGGGAACCCCACTCGCAGACACTCCTACCCGGCCCGTCAACCCGG
CATGGGGGATGAGGGACCTTCACGAATCCAGCTTCAGCCTCTCTGGCTCTCAGATCGATGACCATGTTCCAAAG
CGAGCTTCAGCTCGGATCCTCGCTCCTCCCGAGGCAGGTTCAGTGCCATTGTTGGTAAAGGCATTGCCAAGCCCC
CGAGTGAGGACGCACCGCCGCCACCAGCCCGCAACTCTCCAGCCGAAGCTGCAGGGGCAGGAGAGGCTGGGCTGG
GTGGCACACCACCCGAGGGGGGCCCCGGGACCCACGGAGCCCTCCCTATGTCTGCAAAGTGATTCACTGTGCTTC
GAGCCAACTCTAACAGGCATTTGAGATGTGTTCTCTCTGTAGTCTTCTGCTTGGCCTTGGCCTCGGCGGGCTTT
TCTGGGGCCAGGAAGCCACACTATGCACAGAGCCCAATGCATAGAGCCCTGGCCAGCCCTTCTCTCACTCCT
GCCTCCGCTGGCTTTGGGAAAGCCCAGACTTTAGTGCCCTGCCCTGGCTGACTGGCCAGTTGCCAGAGCACT
TTAGCAGATGTGGTTTCAAAGTAAAGGCCTCCTCCCCACCCCTTAGGCCCGTGGTGACATTTCCCAAGTCAGA
CAGATGTGAGCTTCCCAGCCATGCCAGGACGTCTATCTCCCCAACCCACCTCTGGCCCTGTGTAGGGGCAGG
GATGGGGGTGGCTGGGACTCCTGGTGCCCTCGCCAGCTTCTCCTGCGCCCCGCCACACCCCTCGGGGGGGTTCAC
AGGCCCAGAAGGGTAGCTGGGCGGGGCTCGAGGCTGGTGCCAGGCGCGTGTAATGGTTTTGTTTTGCACGTTTG
GTTTTGCGCAGTAGTTTTGTTTTGACTTGTGTTGTGTCATCCTGTGAAAAATAACGGTGCTTGTGTCACTAGCATAGAA
TAGCGACAGGAATAGATGTGGTCTTTAGGAGACGCTGCACCTTGACACCAACCAGACAGCACAGGGCAGGGGTGGT
GGAGGGGGCTGGGCTCACAGGCTCTCTTTTCCCCGCTGCAGTCTTCTGGGCTGCGGGAGGCCCTGGCCCTTTC
CCCTTCCCCTCCCCTCCTTGTCTAGTTTTCCACATTCCAAAAGGGGGCTGGGATGCTAGCCCCAGAGATGCCAG
CCCTTCAGGAAGCAGGTGTCTTTTCCCCTCTCTGCCCTGATCACTCCCAGCACTCCCCTTGCCTTCCCCTGTCT
TCACCTGCCACCACACACACACACACACACACACACACACACATGGCTTCTTATACTTCTTCTCTGCTG
GACAGAGACTCAGCGCTCCTCCTGTGTGACTGGCAAGAGGCCTCATGCCTGCTGAGAGAGGGTCGACGCGGCCG

WO 2004/030615

PCT/US2003/028547

760/6881
FIGURE 710

MLANSASVRILIKGGKVVNDCTHEADVYIENGIIQQVGRELMIPGGAKVIDATGKLVIPGGIDTSTHFHQTFMN
ATCVDDFYHGTAAALVGTTMII GHVLPDKETSLVDAYEKCRGLADPKVCCDYALHVGITWWAPKVKAEMETLVR
EKGVNSFQMFMTYKDLYMLRDSELYQVLHACKDIGAIARVHAENGELVAEGAKEALDLGITGPEGIEISRPEELE
AEATHRVITIANRTHCPIYLVNVSSISAGDVIAAAKMQGKVLAETTTAHATLTGLHYHQDWSHAAAYVTVPPPL
RLDTNTSTYLSLLANDTLNIVASDHRPFTTKQKAMGKEDFTKIPHGVSQVDRMSVIWERGTVGGKMDENRFVA
VTSSNAAKLLNLYPRKGRIIPGADADVVDPEATKTISASTQVQGGDFNLYENMRCHGVPLVTISRGRVYENG
VFMCAEGTGKFCPLRSFPDTPVYKKLVQREKTLKVRGVDRTPYLGDAVAVVHPGKKEMGTPLADTPTRPVTRHGGM
RDLHESSFSLSGSQIDDHVPKRASARILAPPGRRSSGIW

PCT/US2003/028547

CTTGCTCCGAGAGGGAGTCTCTGCGGACGTGAGCCAGATTCCGAAATGACTATCTTTGACTTACCCCTTTAAAAA
TCTTCCCACCTGCATCAAAATGGGCCCTCAGATTTTCCATAAGACCTCTGAGCTGTTCCCTCCCAGCTACGAGCTGC
CCCAGCTGTCCAGACCAAAACGAAGAAGACGTTAGCCAAACCAATATAAGGAATGTTGTGGTGGTGGATGGTGT
TCGCACTCCATTTTTGCTGTCTGGCACTTCATATAAAGACCTGATGCCACATGATTTGGCTAGAGCAGCGCTTAC
GGGTTTGTTCATCGGACCAAGTGTCCCTAAGGAAGTAGTTGATTATATCATCTTTGGTACAGTTATTACAGGAAGT
GAAAACAAGCAATGTGGCTAGAGAGGCTGCCCTTGGAGCTGGCTTCTCTGACAAGACTCCTGCTCACACTGTAC
CATGGCTTGTATCTCTGCCAACCAAGCCATGACCACAGGTGTTGGCTTGATTGCTTCTGGCCAGTGTGATGTGAT
CGTGGCAGGTGGTGTGAGTTGATGTCCGATGTCCCTATTTCGTCACTCAAGGAAAATGAGAAAACCTGATGCTTGA
TCTCAATAAGGCCAAATCTATGGGCCAGCGACTGTCTTTAATCTCTAAATTCCGATTTAATTTCTAGCACCTGA
GCTCCCTGCGGTTTCTGAGTTCTCCACCAGTGAGACCATGGGCCACTCTGCAGACCGACTGGCCGCTGCCTTTGC
TGTTTCTCGGCTGGAACAGGATGAATATGCACCTGCGCTCTCACAGTCTAGCCAAGAAGGCACAGGATGAAGGACT
CCTTTCTGATGTGGTACCCTTCAAAGTACCAGGAAAAGATACAGTTACCAAAGATAATGGCATCCGTCCTTCCCTC
ACTGGAGCAGATGGCCAAACTAAAACCTGCATTTCATCAAGCCCTACGGCACAGTGACAGCTGCAAATTCTTCTTT
CTTGACTGATGGTGCATCTGCAATGTTAATCATGGCGGAGGAAAAGGCTCTGGCCATGGGTTATAAGCCGAAGGC
ATATTTGAGGGATTTTATGTATGTGTCTCAGGATCCAAAAGATCAACTATTACTTGGACCAACATATGCTACTCC
AAAAGTTCTAGAAAAGGCAGGATTGACCATGAATGATATTGATGCTTTTGAATTTTCATGAAGCTTTTCTCGGGTCA
GATTTTGGCAAATTTTAAAGCCATGGATTCTGATTGGTTTGCAGAAAACCTACATGGGTAGAAAAACCAAGGTGG
ATTGCCCTCCTTTGGAGAAGTTTAAATAACTGGGGTGGATCTCTGTCCCTGGGACACCCATTTGGAGCCACTGGCTG
CAGGTTGGTCATGGCTGCTGCCAACAGATTACGGAAAGAAGGAGGCCAGTATGGCTTAGTGGCTGCGTGTGCAG
TGGAGGGCAGGGCCATGCTATGATAGTGGAAGCTTATCCAAAATAGATCCAGAAGAAGTGACCTGAAGTTTCT
TGTGCAACACTCACACTAGGCAATGCCATTTCAATGCATTACTAAATGACATTTGTAGTTTCTAGCTCCTCTTAG
GAAAACAGTTCTTGTGGCCTTCTATTAAATAGTTTGCACCTTAAGCCTTGCCAGTGTCTGAGCTTTTCAATAATC
AGTTTACTGCTCTTTCAGGGATTTCTAAGCCACCAGAATCTCACATGAGATGTGTGGTGGTGTGTTTTTGGTCTC
TGTGTGCTACTAAAGACTAAATGAGGGTTTGCAGTTGGGAAAGAGGTCAACTGAGATTTGGAAATCATCTTTGTAA
TATTTGCAAATTATACTTGTCTTATCTGTGTCTTAAAGATGTGTTCTCTATAAAATACAAACCAACGTGCCTAA
TTAATTATGAAAAATAATTACAGAACTTAAACACCACTGAAAACCTTATAAAAAATGTTTAGATACATAAATATGG
TGGTCAGCGTTAATAAAGTGGAGAAATATTGGAAAAA

WO 2004/030615

PCT/US2003/028547

762/6881
FIGURE 712

MTILTYPFKNLPTASKWALRFSIRPLSCSSQLRAAPAVQTKTKKTLAKPNIRNVVVVDGVRTPFLLSGTSYKDL
PHDLARAALTGLLHRTSVPKEVVDYIIIFGTVIQEVKTSNVAREAAAGAGFSDKTPAHTVTMACISANQAMTTGVG
LIASGQCDVIVAGGVELMSDVPIRHSRKMRLMLDLNKAQSMGQRLSLISKFRFNFLAPELPAVSEFSTSETMGH
SADRLAAAFAVSRLEQDEYALRSHSLAKKAQDEGLLSDVVPFKVPGKDTVTKDNGIRPSSLEQMAKLKPAFIKPY
GTVTAANSFSLTDGASAMLIMAEKALAMGYKPKAYLRDFMYVSQDPKDQLLLGPTYATPKVLEKAGLTMNDIDA
FEFHEAFSGQILANFKAMDSDFWFAENYMGRTKVGLPPELEKFNWGGSLSLGHPFGATGCRLVMAAANRLRKEGG
QYGLVAACAAGGQGHAMIVEAYPK

WO 2004/030615

PCT/US2003/028547

763/6881
FIGURE 713

GGCACGAGGCCACTGCTGTCTCTTCAGCTCAAGATGGTGGCCTGCCGGGCGATTGGCATCCTCAGCCGCTTTTC
TGCCTTCAGGATCCTCCGCTCCCGAGGTTATATATGCCGCAATTTTACAGGGTCTTCTGCTTTGCTGACCAGAAC
CCATATTAACATATGGAGTCAAAGGGGATGTGGCAGTTGTTTGAATTAACCTCTCCCAATTCAAAGGTAAATACACT
GAGTAAAGAGCTACATTCAGAGTTCTCAGAAATTATGAATGAAATCTGGGCTAGTGATCAAATCAGAAGTGCCGT
CCTTATCTCATCAAAGCCAGGCTGCTTTATTGCAAGTGCTGATATCAACATGTTAGCCGCTTGCAAGACCCTTCA
AGAAGTAACACAGCTATCACAAGAAGCACAGAGAATAGTTGAGAACTTGAAAAGTCCACAAAGCCTATTGTGGC
TGCCATCAATGGATCCTGCTGGGAGGAGGACTTGAGGTTGCCATTTTCATGCCAATACAGAATAGCAACAAAAGA
CAGAAAAACAGTATTAGGTACCCCTGAAGTTTTGCTGGGGGCTTACCAGGAGCAGGAGGCACACAAAGGCTGCC
CAAAATGGTGGGTGTGCTGCTTTGGACATGATGCTGACTGGTAGAAGCATTTCGTGCAGACAGGGCAAAGAA
AATGGGACTGGTTGACCAACTGGTGGAAACCCCTGGGACCAGGACTAAAACCTCCAGAGGAACGGACAATAGAATA
CCTAGAAGAAGTTGCAATTACTTTTGCCAAAGGACTAGCTGATAAGAAGATCTCTCCAAAGAGAGACAAGGGATT
GGTGGAAAAATTGACAGCGTATGCCATGACTATTCCATTTGTGAGGCAACAGGTTTACAAAAAAGTGGAAGAAAA
AGTGCGAAAAGCAGACTAAAGGCCCTTATCCTGCACCTCTGAAAAATAATTGATGTGGTAAAGACTGGAATTGAGCA
AGGGAGTGATGCCGGTTATCTCTGTGAATCTCAGAAATTTGGAGAGCTTGTAATGACCAAAGAATCAAAGGCCTT
GATGGGACTCTACCATGGTCAGGTCTGTGCAAGAAGAATAAAATTTGGAGCTCCACAGAAGGATGTTAAGCATCT
GGCTATTCTTGGTGCAGGGCTGATGGGAGCAGGCATCGCCCAAGTCTCCGTGGATAAGGGGCTAAAGACTATACT
TAAAGATGCCACCCCTCACTGCGCTAGACCGAGGACAGCAACAAGTGTTCAAAGGATTGAATGACAAAGTGAAGAA
GAAAGCTCTAACATCATTTGAAAGGGATTCCATCTTCAGCAACTTGACTGGGCAGCTTGATTACCAAGGTTTTGA
AAAGGCCGACATGGTGATTGAAGCTGTGTTTGAGGACCTTAGTCTTAAGCACAGAGTGCTAAAGGAAGTAGAAGC
GGTGATTCCAGATCACTGTATCTTTGCCAGTAACACATCTGCTCTCCCAATCAGTGAAATCGCTGCTGTGAGCAA
AAGACCTGAGAAGGTGATTGGCATGCACTACTTCTCTCCCGTGGACAAGATGCAGCTGCTGGAGATTATCAGCAG
CGAGAAAACTTCCAAAGACACCAGTGCTTCAGCTGTAGCAGTTGGTCTCAAGCAGGGGAAGGTATCATCTGGT
TAAGGATGGACCTGGCTTCTATACTACCAGGTGTCTTGCGCCCATGATGTCTGAAGTCATCCGAATCCTCCAGGA
AGGAGTTGACCCGAAGAAGCTGGATTCCCTGACCACAAGCTTTGGCTTTCTGTGGGTGCCGCCACACTGGTGGA
TGAAGTTGGTGTGGATGTAGCGAAACATGTGGCGGAAGATCTGGGCAAAGTCTTTGGGGAGCGGTTTGAGGTTGG
AAACCCAGAACTGCTGACACAGATGGTGTCCAAGGGCTTCCTAGGTCGTAAATCTGGAAGGGCTTTTACATCTA
TCAGGAGGGTGTGAAGAGGAAGGATTGAATTCTGACATGGATAGTATTTTAGCGAGTCTGAAGCTGCCTCCTAA
GTCTGAAGTCTCATCAGACGAAGACATCCAGTTCCGCTGGTGACAAGATTTGTGAATGAGGCAGTCATGTGCCT
GCAAGAGGGGATCTTTGGCCACACCTGCAGAGGGAGACATCGGAGCCGTCTTTGGGCTTGGCTTCCCGCCTTGTCT
GGGAGGGCCTTTCCGCTTTGTGGATCTGTATGGCGCCAGAAAGATAGTGGACCGGCTCAAGAAATATGAAGCTGC
CTATGGAAAAACAGTTACCCCCATGCCAGCTGCTAGCTGACCATGCTAACAGCCCTAACAAAGAAGTTCTACCAGTG
AGCAGGCCTCATGCCTCGCTCAGTCAGTGCACTAACCCAGCTGCCGGCAGTGCTGGTTCTCCAACAGAGTGGTG
TCTAGATTTATCAGAGTAACGAGAAGACAAACTCCGGCACTGGGTTTGTCTCCCTGATTAAAGTGCCTTCAGCCAA
GACCATCTCTCCCTCCTGGTGAAGTGTGACTTTCGAATTAGTTTGCATTTCTATTGGAAGGTAGAGCCCACTGCT
CATTGTATAAGCCCCGAGGCCTAGAGTGGCAGCCAAGAGCCATCTGAAGCCACCTCTCTGCCTGTTCTCTCCCAAG
AGGCCAGGGTGGCCAGGGGTGGTGAGGGCAGTTCTGCACCCAGCCAAACACATAACAATAAAAACCAAACCTCTGT
GTCAGCATCTTTGCCCTTCTGGTTTAAACGCCTCCTTCAAAAAGCAATCTGGAAGAAAGCCCTGTGCTTTGGGGG
AGTAAGAATGTGTGTGAGAATTCTAGGCAGCACCTTAGGGAGGGACTGGGATGAGAGAAAGTGGGACCTGGTGG
GCTCAACCACACACACCTGTCTGTGAGATGCTTTGCCAGGCTTCTCACCACGGTGTACCGGGATATTAAACCT
CTTTCCCGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

764/6881
FIGURE 714

MVACRAIGILSRFSAFRILRSRGYICRNFTGSSALLTRTHINYGVKGDVAVVRINSPNSKVNTLSKELHSEFSEV
MNEIWASDQIRSAVLISSEKPGCFIAGADINMLAACKTLQEVTLQSQAQRIVEKLEKSTKPIVAAINGSCLGGL
EVAISCQYRIATKDRKTVLGTPEVLLGALPGAGGTQRLPKMVGVPALDMMMLTGRSIRADRAKKMGLVDQLVEPL
GPGLKPPEERTIEYLEEVAITFAKGLADKKISPKRDKGLVEKLTAYAMTIPFVRQQVYKKVEEKVRKQTKGLYPA
PLKIIDVVKTGIEQGS DAGYLCESQKFGE LVMTKESKALMG LYGQVLCCKNKF GAPQKDVKHLAILGAGLMGAG
IAQVSVDKGLKTI LKDATLTALDRGQQQVFKGLNDKVKKKALTSFERDSIFSNLTGQLDYQGF EKADMVIEAVFE
DLSLKHRLVKEVEAVIPDHCIFASNTSALP ISEIAAVSKRPEK VIGMHYFSPVDKMQLLEIITTEKTSKDTASA
VAVGLKQGKVII VVKDGP GFYTT RCLAPMMSEVIRILQEGVDPKKLDSLTSFGFPVGAATLVDEVGVDVAKHVA
EDLGKVFGERFGG NPELLTQMVS KGFLGRKSGKGFYIYQEGVKRDLNSDMDSILASLKLPPKSEVSSDEDIQF
RLVTRFVNEAVMCLQEGILATPAEGDIGAVFGLGFPPCLGGPFRFVDLYGAQKIVDRLKKYEAAYGKQFTPCQLL
ADHANSPNKKFYQ

WO 2004/030615

PCT/US2003/028547

765/6881
FIGURE 715

TTCTGTTTTTCTCTCTCATTCTCCAGTGGCGGCGGCGGGGAAGGCGGAGGCAGAGGCAGCAGCAGCCGCGCTGGC
TGCAATGAATGATCCCCAGCTTGGGGGGAGGACTCCAGGTGAGCCTCTGCCCTCGGGAGGCCCGGGACCCCCGG
CCGCCCACGACCGGCAGCCACGCTATGGATCCCTAGAGGAAGGAGGAGAAGACAGCTCGCCGCCACCCCCATC
CCATTTTCCTCTTCCTTTATCTCATTGTTGCCGAAGCTGTTTACGGCAGCGCTCCCTCTGCTCCAGGACTCCCTG
GGGGGGAATGCCAAGACCATCATGGTAGCCACACTGGGGCCAGCTTCTCACAGCTACGATGAGAGCCTCTCCACC
TTGCGCTTTGCCAACCAGGCCAAGAACATCAAGAACAAGCCCCAGGTGAACGAGGACCCCAAGGACACACTGCTG
CGGGAATTCCAAGAGGAGATTGCCCCCCTGAAGGCCAGCTGGAGAAGAGGGGGATGCTGGGGAAGCGGCCCCGG
AGGAAGAGCAGCCGCAGGAAGAAGGCCGTGTCCGCCCCGCTGGGTACCCTGAGGGCCCAGTGATTGAGGCCTGG
GTGGCAGAAGAGGAGGATGACAACAACAACCACCGCCCCGCCAGCCATCCTGGAGTCAGCCTTGGAAGAAG
AACATGGAGAATTACCTGCAGGAACAGAAGGAGCGGCTGGAGGAGGAGAAGGCAGCCATCCAGGATGACCGCA

PCT/US2003/028547

766/6881

GCTGGAGGTGGCCTCCCTCCGCCCCAGACAAGAAGAGGCCCTCAGCCCTCCCCGGTCTCAGAGAGCCCTTGAGA
GGAGGCCCAGTCCAGAGCTCTTCTCCGTTCCAGTCCAATTCTCTAGGGCCAGTAGCAGACACCAGCCAGTATG
CCGAGGAACCAGGGCTTCTCCGAGCCCGAATACTCGGCCAGTACTACTGACCCGAGTACTCCGTCAGCCTGCCCTCC
GACCCTGACCGCGGGGTGGGCCGACCCATGAAATGTAACCACTCTACCAGACCTACTTCAAAAGGCAGCGCCACGAG
TTCATGCGGCTGACTTTCGTGCCGGAGTCTTGGAGAACCTCTACCAGACCTACTTCAAAAGGCAGCGCCACGAG
ACCTGTCTGGTGCTGGTGGTCTTTGACGCCCTTTGACTGCTACGTGGTGGTTCATGTGTGCTGTGGTCTTCTCC
AGCGACAAGCTGGCTTCCCTCGCGCTGGCTGGAATTGGACTGGTGTGGACATCATCTCTTCTGTGCTCTGCAA
AAGGGGCTGTCCCGGACCGGGTACCCGACAGAGTGCTGCCCTACGTGCTGTGGCTGCTCATAACCGCCAGATC
TTCTCTTACCTGGGCCTGAACCTCGCGCGTGCCACGCGGCTAGTGACACGGTGGGCTGGCAGGTCTTCTTTGTG
TTCTCTTCTTCTACATCAGCTGCCCCCTCAGCCTCAGCCCCATCGTGATCATCTCCGTGGTCTCCTGTGTGGTGCAC
ACGTGTGGTCTTGGGGGTACCGTGGCCAGCAGCAGCAGGAGGAGCTCAAGGGGATGCAGCTGCTGCGGGAGATC
CTGGCCAACTGCTTCTCTTACCTGTGCGCCATCGCTGTGGGCATCATGTCTTACTACATGGCTGACCGCAAGCAC
CGCAAGGCCCTTCTTGGAGGCCCGCCAGTCTGCTGGAGGTGAAGATGAACCTGGAAGAGCAGAGCCAGCAGCAGGAG
AACCTCATGCTTCTCATCTGCCCCAAGCACGTGGCTGACGAGATGCTGAAAGACATGAAGAAAGACGAGAGCCAG
AAGGACCAGCAGCAGTTC AACACCATGTACATGTACCGTCACGAGAACGTGACATCTCTTTGCCGACATCGTG
GGCTTTACCCAGCTGTCTTCTGCCTGCAGTGCCAGGAGCTTGTGAAGCTGCTCAACGAGCTCTTTGCCCGCTTT
GACAAGCTGGCAGCTAAATACCACAGCTGCGGATTAAGATCCTGGGCGACTGCTACTACTGCATCTGCGGCTTG
CCGACTACCGGGAGGACCACGCCGTCTGCTCCATCTCATGGGGCTGGCCATGGTGGAGGCCATCTCGTATGTG
CGGGAGAAGACCAAGACTGGGGTGGACATGCGTGTGGGGGTGCACACGGGCACCGTCTGGGGGGCGTCTCGTGGG
CAGAAGCGCTGGCAGTACGACGTGTGGTGCAGTGTACTGTAGCCACAAGATGGAGGCCGGCGGCATCCCT
GGGCGCGTGCACATCTCCAGAGCACCATGGACTGCCTGAAAGGGGAGTTTGAATGTGGAGCCAGGCGATGGGGG
AGCCGCTGTGATTACCTAGAAGAGAAGGGTATTGAAACCTACCTCATCATTTGCCCTCCAAGCCAGAGGTGAAGAAA
ACAGCCACCCAGAATGGCCTCAATGGCTCGGCCCTGCCCAATGGAGCACCAGCTTCTCTCAAAGTCCAGCTCCCT
GCCCTCATTTGAGACCAAGGAGCCCAACGGGAGTGCCACACAGCAGTGGGTCCACGTCCGAGAGAGCCCGGAGGAGCAG
GATGCCAGGCGGACAACCCCTCATTTCCCAACCCACGCCGGAGGCTGCGCCTGCAGGACCTGGGTGACCGAGTG
GTGGATGCCTCTGAAGATGAGCACGAGCTCAACCAGCTGCTCAACGAGGCCCTGCTTGAGCGAGAGTCCGCCCAA
GTGTAAAGAAGAGAAACACCTTCTTGTCCATGCGGTTTATGGACCCCGAGATGGAACCCGCTACTCGGTGG
AGAAGGAGAAGCAGAGTGGGGCTGCCTTACGCTGCTCCTGCGTCTGCTCTGCACGGCCCTGGTCGAGATAC
TCATCGACCCCTGGCTAATGACAACTATGTGACCTTCATGGTGGGGGAGATTCTGCTCCTCATCTGACCATCT
GCTCCCTGGCTGCCATCTTTCCCCGGGCCCTTCTTAAGAAGCTTGTGGCCTTCTCAACTTGGATTGACCGGACCC
GCTGGGCCAGGAACACCTGGGCCATGCTCGCCATCTTCATCCTGGTGATGGCAAATGTCGTGGACATGCTCAGCT
GTCTCCAGTACTACACGGGACCCAGCAATGCAACGGCAGGGATGGAACGGAGGGCAGCTGCCTGGAGAACCCCA
AGTATTACAACATATGTGGCCGTGCTGTCCCTCATCGCCACCATCATGCTGGTGCAGGTGAGCCACATGGTGAAGC
TCACGCTCATGCTGCTCGTCGACGGCGCCGTGGCCACCATCAACCTCTATGCCTGGCGTCCCGTCTTTGATGAAT
ACGACCACAAGCGTTTTTCGGGAGCACGACTTACCTATGGTGGCCTTAGAGCAGATGCAAGGATTCAACCCCTGGGC
TCAATGGCACTGACAGGCTGCCCCCTGGTGCCTTCCAAGTACTCTATGACGGTGATGGTGTCTCTCATGATGCTCA
GCTTCTACTACTTCTCCCGCCACGTAGAAAACTGGCAGGGACACTTTTCTTGTGGAAGATTGAGGTCCACGAC
AGAAGGAACGTGTCTATGAGATGCGACGCTGGAACGAGGCTTGGTACCAACATGTTGCCTGAGCAGCTGGCAC
GCCATTTCTTGGGGTCCAAGAAGAGAGATGAGGAGCTGTATAGCCAGACGTATGATGAGATTGGAGTCATGTTTG
CTCCCTGCCCAACTTTGCTGACTTCTACACAGAGGAGAGCATCAACAATGGTGGTATTGAGTGTCTGCGTTTTCC
TCAATGAAATCATCTCAGATTTTGTACTCTCTCCTGGACAATCCCAAGTTCGGGGTGATACCAAGATCAAAACCA
TTGGCAGCAGTATATGGCGGCTTTCAGGAGTACCCCCGATGTCAACACCAATGGCTTTGCCAGCTCCAACAAG
AAGACAAGTCCGAGAGAGAGCGCTGGCAGCACCTGGCTGACCTGGCCGACTTCGCGCTGGCCATGAAGGATACGC
TGACCAACATCAACAACCAGTCTTCAATAACTTCATGCTGCGCATAGGCATGAACAAAGGCGGGTTCTGGCTG
GGGTGATCGGAGCCCGGAAACCACACTACGACATCTGGGGCAATACAGTCAATGTAGCCAGCAGGATGGAGTCCA
CGGGGGTTCATGGGCAACATTTCAGGTATGTCCAGTGGCACAGCTGGCACGTGCTCAGACTCGGCATGAGAACAAAA
CCGGAACAGTGCTTTCCACGTGCCCCCTGCCTCCACCCTGGCCCTGAACAGTAAGTCCAGAGGCAGAGACGTGG
GGCAAGTGGAAAAGAATCTCTGCAATAGCTAGCCTCAGCACAGGAAGAAACACTTCCACCCATCCACAAAATCTG

WO 2004/030615

PCT/US2003/028547

767/6881
FIGURE 716B

GGCTGAAGTTCTAGATGCATATGGCCTACCTTTGGGTATGAACCTTCTAATACCTTGTGATCTGTCTCAGTGGCG
TCTGGCAGAAAAGCTCCACGAAAGGGGCAAAGGGACAGAAGAGCAGGCAGTGGCAGTTTCCAGGTAACAGTGCTG
CCACCCAGGTGACCATGGCCATCCTAGGAGAGAAAGTCTCTGGATGAGAGGAGGCCCCCAGCCAGTCACTCCAGGG
TTCTCCTTCCCACCCGCTGCTCGCCACGGGTGGAAGGGCTTGGCCC

WO 2004/030615

PCT/US2003/028547

768/6881
FIGURE 717

GCCGCGGCACCAGGGCGCGCAGCCGGGCGGGCCGACCCACCGGCCATACGGTGGAGCCATCGAAGCCCCACC
CACAGGCTGACAGAGGCACCGTTACACAGAGGGCTCAACACCGGGATCTATGTTTAAGTTTAACTCTCGCCTCC
AAAGACCACGATAATTTCCTTCCCCAAAGCCAGCAGCCCCCAGCCCCGCGCAGCCCCAGCCTGCCTCCCGGCGC
CCAGATGCCCGCCATGCCCTCCAGCGGGCCCCGGGGACACCAGCAGCTCTGCTGCGGAGCGGGAGGAGACCGAAA
GGACGGAGAGGAGCAGGAGGAGCCGCGTGGCAAGGAGGAGCGCCAAGAGCCCAGCACCACGGCAGGAAGGTGGG
GCGGCCTGGGAGGAAGCGCAAGCACCCCCCGGTGGAAAGCGGTGACACGCCAAAGGACCCTGCGGTGATCTCCAA
GTCCCCATCCATGGCCCAGGACTCAGGCGCCTCAGAGCTATTACCCAATGGGGACTTGGAGAAGCGGAGTGAGCC
CCAGCCAGAGGAGGGGAGCCCTGCTGGGGGGCAGAAGGGCGGGGCCCCAGCAGAGGGAGAGGGTGACGCTGAGAC
CCTGCCTGAAGCCTCAAGAGCAGTGGAATGGCTGCTGCACCCCCAAGGAGGGCCGAGGAGCCCTGCAGAAGC
GGGCAAAGAACAGAAGGAGACCAACATCGAATCCATGAAAATGGAGGGCTCCCGGGGCCGGCTGCGGGGTGGCTT
GGGCTGGGAGTCCAGCCTCCGTGACGCGGCCATGCCGAGGCTCACCTTCCAGGCGGGGACCCCTACTACATCAG
CAAGCGCAAGCGGGACGAGTGCGTGGCAGCTGGAAAAGGGAGGCTGAGAAGAAAGCCAAAGTCAATGACAGGAAT
GAATGCTGTGGAAGAAAACAGGGGGCCCGGGAGTCTCAGAAGGTGGAGGAGGCCAGCCCTCCTGTGTGAGCA
GCCCCACTGACCCCGCATCCCCACTGTGGCTACCACGCTGAGCCCGTGGGGTCCGATGCTGGGGACAAGAAATGC
CACCAAAGCAGGCGATGACGAGCCAGAGTACGAGGACGGCCGGGGCTTTGGCATTGGGGAGCTGGTGTGGGGGAA
ACTGCGGGGCTTCTCCTGGTGGCCAGGCCGCAATTGTGTCTTGGTGGATGACGGGGCCGAGCCGAGCAGCTGAAGG
CACCCGCTGGGTGATGTGGTTCGGAGACGGCAAATTCTCAGTGGTGTGTGTGAGAAGCTGATGCCGCTGAGCTC
GTTTTGCAGTGCGTTCCACAGGCCACGTACAACAAGCAGCCCATGTACCGCAAAGCCATCTACGAGGTCTGCA
GGTGGCCAGCAGCCGCGCGGGGAAGCTGTTCCCGGTGTGCCACGACGAGCGATGAGAGTGACACTGCCAAGGCCGT
GGAGGTGCAGAACAAAGCCCATGATTGAATGGGCCCTGGGGGGCTTCCAGCCTTCTGGCCCTAAGGGCCTGGAGCC
ACCAGAAGAAGAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGGGTGGAACCTGAGGCAGCTGCCTACGC
ACCACCTCCACAGCCAAAAAGCCUCGGAAGAGCAGCAGCGAGAAGCCCAAGGTCAAGGAGATTATTGATGAGCG
CACAAGAGAGCGGCTGGTGTACGAGGTGCGGCAGAAGTGCCGAACATTGAGGACATCTGCATCTCCTGTGGGAG
CCTCAATGTTACCCTGGAACACCCCCCTCTTCGTTGGAGGAATGTGCCAAACTGCAAGAAGCTGCTTCTGGAGTG
TGCGTACCAGTACGACGACGACGGCTACCAGTCTACTGCACCATCTGCTGTGGGGGCCGTGAGGTGCTCATGTG
CGGAAACAACAAGTGTGTCAGGTGCTTTTGGCTGGAGTGTGTGGACCTCTTGGTGGGGCCGGGGGCTGCCAGGC
AGCCATTAAGGAAGACCCCTGGAAGTGTACATGTGCGGGCACAAGGGTACCTACGGGCTGCTGCGGCGGCGAGA
GGACTGGCCCTCCCGGCTCCAGATGTTCTTCGCTAATAACCACGACCAGGAATTTGACCCTCCAAAGGTTTACCC
ACCTGTCCAGCTGAGAAGAGGAAGCCCATCCGGGTGCTGTCTCTCTTTGATGGAATCGCTACAGGGCTCCTGGT
GCTGAAGGACTTGGGCATTACAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCAGGTGGGCAT
GGTGGCGCACCAAGGGGAAGATCATGTACGTGCGGGACGTCCGACGCTCACACAGAAGCATATCCAGGAGTGGGG
CCCATTCGATCTGGTGATTGGGGGACGTCCCTGCAATGACCTCTCCATCGTCAACCCTGCTCGCAAGGGCCTCTA
CGAGGGCACTGGCCGGCTCTTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGGAGATGATCG
CCCTTCTTCTGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCGCGATTTCTCGA
GTCCAACCTGTGATGATTGATGCCAAAGAAGTGTGAGCTGCACACAGGGCCCGCTACTTCTGGGGTAACCTTCC
CGGTATGAACAGGCCGTTGGCATCCACTGTGAATGATAAGCTGGAGCTGCAGGAGTGTCTGGAGCATGGCAGGAT
AGCCAAGTTCAGCAAAGTGAGGACCATTACTACGAGGTCAAACCTCCATAAAGCAGGGCAAAGACCAGCATTTTCC
TGTCTTCATGAATGAGAAAAGAGGACATCTTATGGTGCAGTGAATGGAAAGGGTATTTGGTTTCCAGTCCACTA
TACTGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGGTCAAGGAGCGTGCCAGTCAATCCG
CCACCTCTTCGCTCCGCTGAAGGAGTATTTTGGTGTGTGTAAAGGACATGGGGGCAAAGTGGGTAGCGACACA
AAGTT

WO 2004/030615

PCT/US2003/028547

769/6881
FIGURE 718

MPAMPSSGPGDTSSSAEREEDRKDGEEQEPRGKEERQEPSTTARKVGRPGRKRKHPPVESGDTPKDPAVISKS
PSMAQDSGASELLPNGDLEKRSEPQPEEGSPAGGQKGGAPAEEGEGAAETLPEASRAVENGCCPTKEGRGAPAEAG
KEQKETNIESMKMEGSRGRLRGGLGWESSLRQRPMPRLTFQAGDPYYISKRKRDEWLARWKREAEKKAKVIAGMN
AVEENQGPGESQKVEEASPPAVQQPTDPASPTVATTPEPVGSDAGDKNATKAGDDEPEYEDGRGFGIGELVWGKL
RGFSWWPGRIVSWWMTGRSRAAEGTRWVMWFWDGKFSVVCVEKLMPLSSFCSAFHQATYNKQPMYRKAIYEV LQV
ASSRAGKLFVPVCHDSDESDTAKAVEVQNKPMIEWALGGFQPSGPKGLEPPEEEKNPYKEVY TDMWVEPEAAAYAP
PPPAKKPRKSTAEKPKVKEIIDERTRERLVYEV RQKCRNIEDICISCGSLNVTL EHP L FVGGMCQNCKNCFLECA
YQYDDDGYQSYCTICCGGREVL MCGNNNCCRCFCVECVDLLVGP GAAQAAIKEDPWNCYMC GHKGT YGLLRRED
WPSRLQMF FANNHDQEFDPK VYPPVPAEK RKP IRVLSLFDGIATGLLV LKDLGIQVDRI IASEVCEDSITVGMV
RHQKIMYVG DVRSVTQKH IQEWGPF DLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRLLHDARPKEGDDRP
FFWLFENVVAMGVSDKRDISRFL ESNPVMIDAKEVSA AHRARYFWGNLP GMNRPLASTVNDKLELQECLEHGRIA
KFSKVRTITTRSNSIKQGKDQHFPVFMNEKEDILWCTEMERVFGFPVHYTDVSNMSRLARQRL LGRSWSVPVIRH
LFAPLKEYFACV

WO 2004/030615

PCT/US2003/028547

770/6881
FIGURE 719

CTGACCGCCGGGGGGTGCCCCGGGACGTAGCGCCGCGGAGAGGAAGCGGCCAAAGGGGACCATGCGGCGCCTGAC
TCGTGCGGCTGGTTCTGCCAGTCTTCGGGGTGCTCTGGATCACGGTGCTGCTGTTCTTCTGGGTAACCAAGAGGAA
GTTGGAGGTGCCGACGGGACCTGAAGTGCAGACCCCTAAGGTTTGGTCCTTGTTTTTCAAGGTGGCTGGGATGAG
CCCTTGGGCGCCTCAGGTGCCTGTATCACCCACTCCTCCCTACCAAAGAGGGGCATCTTCCTACAGGAGGACACCT
TGCTGTATGTCATTTCCCATGTCTCTTGCAAGAAGCTCAGTTCCATTTGCAGACTCAGGTCTTTCTTCAAGTCAG
ATGCACACTGCTGGTGTATTGCACGGACCTTCCACCCACTAGCATCATCATCACCTTCCACAACGAGGCCCGCTC
CACGCTGCTCAGGACCATCCGCAGTGTATTAAACCGCACCCCTACGCATCTGATCCGGGAAATCATATTAGTGGA
TGACTTCAGCAATGACCCTGATGACTGTAAACAGCTCATCAATTGCCCAAGGTGAAATGCTTGCGCAATAATGA
ACGGCAAGGTCTGGTCCGGTCCCGGATTTCGGGGCGCTGACATCGCCCAGGGCACCACTCTGACTTTCTCGACAG
CCACTGTGAGGTGAACAGGGGACTGGCTCCAGCCTCTGTTGCACAGGGTCAAAGAGGACTACACGCGGGTGGTGTG
CCCTGTGATCGATATCATTAACTGGACACCTTCACTACATCGAGTCTGCCTCGGAGCTCAGAGGGGGGTTTGA
CTGGAGCCTCCACTTCCAGTGGGAGCAGCTCTCCCCAGAGCAGAAGGCTCGGCGCCTGGACCCACGGAGCCCAT
CAGGACTCCTATCATAGCTGGAGGGCTCTTCGTGATCGACAAAGCTTGGTTTGATTACCTGGGGAAATATGATAT
GGACATGGACATCTGGGGTGGGGAGAACTTTGAAATCTCCTTCCGAGTGTGGATGTGCGGGGGCAGCCTAGAGAT
CGTCCCCCTGCAGCCGAGTGGGGCACGTCTTCCGGAAGAAGCACCCCTACGTTTTCCCTGATGGAAATGCCAACAC
GTATATAAAGAACACCAAGCGGACAGCTGAAGTGTGGATGGATGAATACAAGCAATACTATTACGCTGCCCCGCC
ATTGCCCCCTGGAGAGGCCCTTTCGGGAATGTTGAGAGCAGATTGGACCTGAGGAAGAATCTGCGCTGCCAGAGCTT
CAAGTGGTACCTGGAGAATATCTACCCTGAACTCAGCATCCCCAAGGAGTCTCCATCCAGAAAGGGCAATATCCG
ACAGAGACAGAAGTGCCTGGAATCTCAAAGGCAGAACCAAGAAACCCCAAACCTAAAGTTGAGCCCCGTGTC
CAAGGTCAAAGGCGAAGATGCAAAGTCCCAGGTATGGGCCTTACATACACCCAGCAGATCCTCCAGGAGGAGCT
GTGCTGTGAGTCATCACCTTGTTCCCTGGCGCCCCAGTGGTTCTTGTCCTTTGCAAGAATGGAGATGACCGACA
GCAATGGACCAAACTGGTTCCCACATCGAGCACATAGCATCCACCTCTGCCTCGATACAGATATGTTCCGGTGA
TGGCACCGAGAACGGCAAGGAAATCGTCGTCAACCCATGTGAGTCCTCACTCATGAGCCAGCACTGGGACATGGT
GAGCTCTTGAGGACCCCTGCCAGAAGCAGCAAGGGCCATGGGGTGGTGCTTCCCTGGACCAGAACAGACTGGAAA
CTGGGCAGCAAGCAGCCTGCAACCACCTCAGACATCTGGACTGGGAGGTGGAGGCAGAGCCCCCAGGACAGGA
GCAACTGTCTCAGGGAGGACAGAGGAAAACATCACAAGCCAATGGGGCTCAAAGACAAATCCCACATGTTCTCAA
GGCCGTTAAGTTCCAGTCTTGCCAGTCATTCCCTGATTGGTATCTGGAGACAGAAACCTAATGGGAAGTGTTTA
TTGTTCTTTTCTACAAAGGAAGCAGTCTCTGGAGGCCAGAAAGAAAGCCTTCTTTTTCACTAGGCCAGGACT
ACATTGAGAGATGAAGAATGGAGGTGTTTCCAAAAGAAATAAAGAGAACTTAGAAGTTGTCTCTGG

WO 2004/030615

PCT/US2003/028547

771/6881
FIGURE 720

MRRLLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKVWSLFFKVAGMSPWAPQVPVSPTPPYQRGHL
TGGHLAVCHFPCLLQEAQFHLQTQVFLQVRCTLLVYCTDLPPTSIIITFHNEARSTLLRTIRSVLNRTPTHIRE
IILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADIAQGTTLTFLDSHCEVNRDWLQPLLHRVKEDY
TRVVCVIDIINLDTFTYIESASELRGGFDWSLHFQWEQLSPEQKARRLDPTPIRTPIIAGGLEVIDKAWFDYL
GKYDMDMDIWGGENFEISFRVWMCSSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDYKQYY
YAARPFALERPFNGVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLSQRQNNQETPNLK
LSPCAKVKGEDAKSQVWAFYTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTKTGSHIEHIAHLCLDT
DMFGDGTENGKEIVVNPCESSLMSQHWDVSS

WO 2004/030615

PCT/US2003/028547

772/6881
FIGURE 721

GGTGTTCACTCAACTTGGATCTGTGCTGAAAAATTGTGACATTTTCAGTACATCTGGTAGAGGGTACAGCTTTTAT
CTTGACATGAATTTTTTGGATGTTCTTCCGTGTCATAAATTTTCAGAAAAACACCACAGGGATGGCGAGAAGTATTT
GTTGACATTGATCCACAGGTTTCTGATAAACTGAGGTTTGTTTTGGCACCTTCTGCCACCCCAGCAGAAGCCTTC
ATACAACATGACGAAACAAGGGATCATGTTGAAGTGTGTCTGATGCTGGTGTATCATCGAGGAACTTTCTCAA
CGCATTGCATTAACTGGAGGTGCTGCACTGGTTGCTGATTATGGTCATGATGGAACAAAGACAGATACCTTCAGA
GGGTTTTGCGACCACAAGCTTCATGATGTCTTAATTGCCCCAGGAACAGCAGATCTAACAGCTGATGTGGACTTC
AGTTATTTGCGAAGAATGGCACAGGGAAAAGTAGCCTCTCTGGGCCCAATAAAACAACACACATTTTTAAAAAAT
ATGGGTATTGATGTCCGGCTGAAGGTTCTTTTAGATAAATCAAATGAGCCATCAGTGAGGCAGCAGTTACTTCAA
GGATATGATATGTTAATGAATCCAAAGAAGATGGGAGAGAGATTTAACTTTTTTGCCCTTGCTACCTCATCAGAGA
CTTCAAGGTGGAAGATATCAGAGGAATGCACGTCAGTCAAACCCTTTGCATCCGTTGTAGCTGGGTTTAGTGAA
CTTGCTTGGCAGTGATATTTTCAGCTTGGACATTTTACCCTTCAGTCGGGCCCAAGAAATCAAATAAAGGAAACAC
ATTTCATATACTGCAGGTAACAAAAGTCAAAGTATTTTATCTTTTCACAGCAAGAACAGTCCATGTTGTATATAA
TACAACCAACATTATAGAACTTTTAGGGTTGTGACTGGCTTTGGTGCAAATGTGTGCTCAAGCTAATAAGTTATT
GTGAACTGAGTTTCCTTTAACTTACAAAGCTAGTTGCCATATTTCTATTTTATTTTAAAAAGTAAACATGCGGC
TGGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCATATCACCTGAGGTCAGCAGT
TAAAGACCAGCCTGACCAAAATGGAGAAACCCCATCTCTACTAAAAATACAAACTAGCCGGGTATGGTGGTACA
TGCCTGTAATCCCAGC

WO 2004/030615

PCT/US2003/028547

773/6881
FIGURE 722

MAQGKVASLGPIKQHTFLKNMGIDVRLKVLLDKSNEPSVRQQLQGYDMLMNPCKMGERFNFFALLPHQRLQGGR
YQRNARQSKPFASVVAGFSELAWQ

WO 2004/030615

PCT/US2003/028547

774/6881
FIGURE 723

CTTCTCTCGCCAGGCATCCTCGTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGT
GATGCCCCAGGGAAGACAGGGCGACCTGGAAGTCCAACCTACTTCCTTAAGATCATCCAACCTATTGGATGATTATCC
AAAATGTTTCATCGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAA
GGTCGTGGTGCTGATGGGCAAGAACACCATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCT
GGAGAACTGCTGCCTCATATCTGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGAGATCAGGGA
CATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGC
CCAGAACACTGGTCTCGGGCCCCGAGAAGACCTCCTTTTTCCAGGCTTTAGGTATCACCCTAAAATCTCCAGGGG
CACCATTGAAATCCTGAGTGATGTGCAGCTGATCAAGACTGGAGACAAAGTGGGAGCCAGCGAAGCCACGCTGCT
GAACATGCTCAACATCTCCCCCTTCTCCTTTGGGCTGGTTCATCCAGCAGGTATTGACAATGGCAGCATCTACAA
CCCTGAAGTGCTTGATAAAACAGAGGAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGT
CTGTCTGCAGACTGGCTACCCAACCTGTTGCATCAGTACCCCATTTCTATCATCAACGGGTACAAACGAGTCCTGGC
CTTGCTGTGGAGACGGATTACACCTTCCCACTTGCTGAAAATGTCAAGGCCTTCTTGGCTGATCCATCTGCCTT
TGTGGCTGCTGCCCCCTGTGGCTGCTGACACCACAGCTGCTCCTGCTGCTGCTGCAGCCCCAGCTAAGGTTGAAGC
CAAGGAAGAGTCGGAGGAGTCGGACGAGGATATGGGATTTGGTCTCTTTGACTTAATCACCAAAAAGCAACCAACT
TAGCCAGCTTTATTTGCAAAACAAGGAAATAAAGGCTTACTTCTTT

WO 2004/030615

PCT/US2003/028547

775/6881
FIGURE 724

MPREDRATWKSNYFLKIIQLLDDYPKCFIVGADNVGSKQMQQIRMSLRGKVVLGMKNTMMRKAIRGHLENNPAL
EKLLPHIWGNVGFVFTKEDLTEIRDMLLANKVPAAARAGAIAPCEVTVPAQNTGLGPEKTSFFQALGITTKISRG
TIEILSDVQLIKTGDKVGASEATLLNMLNISPFSFGLVIQQVFDNGSIYNPEVLDKTEETLHSRFLEGVRNVASV
CLQTGYPTVASVPHSIINGYKRVLALSVETDYTEFLAENVKAFLADPSAFVAAAPVAADTTAAPAAAAAPAKVEA
KEESESEDEDMGFGFLFD

WO 2004/030615

PCT/US2003/028547

776/6881
FIGURE 725

GTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCCAGGGAAGACAGGGCGACCTGGAAGTCCA
ACTACTTCCTTAAGATCATCCAACCTATTGGATGATTATCCAAAATGTTTCATCGTGGGAGCAGACAATGTGGGCT
CCAAGCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAAGGTCGTGGTGCTGATGGGCAAGAACACCATGATGC
GCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATATCTGGGGGAATGTGG
GCTTTGTGTTACCAAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCC
GTGCTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGGCCCCGAGAAGACCTCCT
TTTTCCAGGCTTTAGAGTGATGTGCAGCTGATCAAGACTGGAGACAAAGTGGGAGCCAGCGAAGCCACGCTGCTG
AACATGCTCAACATCTCCCCCTTCTCCTTTGGGCTGGTCATCCAGCAGGTATTGACAATGGCAGCATCTACAAC
CCTGAAGTGCTTGATAAAACAGAGGAAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGTC
TGTCTGCAGACTGGCTACCCAACCTGTTGCATCAGTACCC

WO 2004/030615

PCT/US2003/028547

777/6881
FIGURE 726

CTGCGTGGCAATCCCTGACGCACCGCCGTGATGCCCAGGGAAGACAGGGCGACCTGGAAGTCCAACCTACTTCCTT
AAGATCATCCAACCTATTGGATGATTATCCAAAATGTTTCATCGTGGGAGCAGACAATGTGGGCTCCAAGCAGATG
CAGCAGATCCGCATGTCCCTTCGCGGGAAGGTTCGTGGTGCTGATGGGCAAGAACACCATGATGCGCAAGGCCATC
CGAGGGCACCTGGAACAACCCAGCTCTGGAGAACTGCTGCCTCATATCTGGGGGAATGTGGGCTTTGTGTTT
ACCAAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCCGTGCTGGTGCC
ATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGGCCCCGAGAAGACCTCCTTTTTCCAGGCT
TTAGGTATCACCCTAAAATCTCCAGGGGCACCATTTGAAATCCTGACAGGTATTCGACAATGGCAGCATCTACAA
CCCTGAAGTGCTTGATAAAACAGAGGAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGT
CTGTCTGCAGACTGGCTACCCAACCTGTTGCATCAGTACCCCATTCATCATCAACGGGTACAAACGAGTCCTGGC

WO 2004/030615

PCT/US2003/028547

778/6881
FIGURE 727

CCTCTAGCTTAGCGAGCGCTGGAGTTTGAAGAGCGGGCAGTGGCTGCACACGCCAAACTTTCCCTATGGCTTCGG
TGACCAGGGCCGTGTTTGGAGAGCTGCCCTCGGGAGGAGGGACAGTGGAGAAGTTCCAGCTGCAGTCAGACCTCT
TGAGAGTGGACATCATCTCCTGGGGCTGCACGATCACAGCCCTAGAGGTCAAAGACAGGCAGGGGAGAGCCTCGG
ACGTGGTGCTTGGCTTCGCCGAGTTGGAAGGATACCTCCAAAAGCAGCCATACTTTGGAGCAGTTATTGGGAGGG
TGGCCAACCGAATCGCCAAAGGAACCTTCAAGGTGGATGGGAAGGAGTATCACCTGGCCATTAACAAGGAACCCA
ACAGTCTGCATGGAGGAGTCAGAGGGTTTGATAAAGTGCTCTGGACCCCTCGGGTGCTGTCAAATGGCGTCCAGT
TCTCGCGCATCAGTCCAGATGGTGAAGAAGGCTACCCCGGAGAGTTAAAAGTCTGGGTGACATACACCCTGGATG
GCGGAGAGCTCATAGTCAACTACAGAGCACAAGCCAGTCAGGCCACACCAGTCAACCTGACCAACCATTCTTACT
TCAACCTGGCAGGCCAGGCTTCCCCAAATATAAATGACCATGAAGTCACCATAGAAGCGGATACTTATTTGCCTG
TGGATGAAACCCTGATTCTACAGGAGAAGTTGCCCCAGTGCAAGGCACTGCATTTCGACCTGAGAAAGCCAGTGG
AGCTTGAAAAACACCTGCAGGACTTCCATCTCAATGGTTTTTGACCACAATTTCTGTCTGAAGGGATCTAAAGAAA
AGCATTTTTGTGCAAGGGTGTCATCATGCTGCAAGCGGGCGGGTACTAGAAGTATACACCACCCAGCCCGGGTCC
AGTTTTACACGGGCAACTTCTTGATGGCACATTAAAGGGCAAGAATGGAGCTGTCTATCCCAAGCACTCCGGTT
TCTGCCTGGAGACTCAGAACTGGCCTGATGCAGTCAATCAGCCCCGCTTCCCTCCTGTGCTGCTGAGGCCTGGTG
AGGAGTATGACCACACCACCTGGTTCAAGTTTTCTGTGGCTTTAAGGAAGTGTGAAGATATGATCCAGTCCAGGGC
TAGGCTCAGCCACCTGTCTCCTGTCCAGAAAAAAGGTGAAGATTAAAGAAGCTTTCAGAATGATTCTATGGATTAA
AATCATACAAATGGTGGCTGTTCTGAGAATCAGTCTGGGTATTGATTTCTTTTTCCAGTGACTGGCTCCAGGCCA
TGTCTAATGACCAGCTCGATTCCCTGTGCAGTTCAGAGAGCAAGTGAACCCAACCAACAATGTCGTCATCTAAGC
CCTGACCCTAGCCAGGGACTCCCATGCTGCTGTTGGCTCCATCTCTCCACACTGCCTCTTTCTTTTCAACTTTTT
GCCCTTCCCTTTCTTTAAAGCTATTCTCACATTGCTTTTATTTCTCCTCCTTCACCTCCAACCACTGTGAGCAGC
ACTCTGGAGTTTTCAAATGTCACATTAGCCTCACCTGCATGCTAGGAGATGGACCTGTCTCTATACAGCAGTAG
ATGATTGATAAGTGAGGAACTGAGGCTTACAGAGGTTGAAGACCAACAAGCTAATAAATAAAAAGTTGAGGCCG
GGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGAGGCAGGCGGATCACGAGGTCAGGAGATCGA
GACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACATAAAAAATTAGCTGGGTGTGGTAGCACGCACCCGTAG
TTCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGCTTGAACCTGGGAGGTGGAGGTGCAGTGAGCCGAGATCA
TGCCACTGCACTGGGCAACAGAGCAAACTCGATCTCAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

779/6881
FIGURE 728

MASVTRAVFGELPSGGGTVEKFQLQSDLLRVDIISWGCTITALEVKDRQGRASDVVLGF AELEGYLQKQPYFGAV
IGRVANRIAKGTFKVDGKEYHLAINKEPNSLHGGVVRGFDKVLWTPRVLSNGVQFSRISPDGEEGYPGELKVWVTY
TLDGGELIVNYRAQASQATPVNLTNHSYFNLAGQASPNINDHEVTIEADTYLPVDETLIPTGEVAPVQGTAFDLR
KPVELGKHLQDFHLNGFDHNFCLKGSKEKHFCARVHHAASGRVLEVYTTQPGVQFYTGNF LDGTLKGKNGAVYPK
HSGFCLETQNWPD AVNQPRFPPVLLRP GEEYDHTTWFKFSVA

WO 2004/030615

PCT/US2003/028547

780/6881
FIGURE 729

GACTTCAGGAAAAATCAACCCAGCACCAGCAGCTACCAACCACCATTCCATCTCTTCACTTGAACAGCATTAGTT
AAGTCCAGATGTGGGAACCCCTTCTCTTGGAAGAAGTTCCCTAATTGTGTCTCAGACCGGTGTAAACAAACCAGCCA
GCCGCCACCTTGCTAAACCTATAAGCTTTTTTAAAAATCCAATATATTCTGCCAAGAAATATGCCTTGATAGTTAGCC
CTCAGCCCATAGGTGTTTTTTGTTTTTAAACAGAATTATATATGTCTGGGGGTGAAAAAACCCCTTGCATTCCAAA
GGTCCATACTGGTTACTTGGTTTCATTGCCACCACCTTAGTGGATGTTTCAGTTTAGAACCATTTTGTCTGCTCCCT
CTGGAAGCCTTGCGCAGAGCTTACTTTGTAATTGTTGGAGAATAACTGCTGAATTTTGTAGCTGTTTTGAGTTGAT
TCGCACCACTGCACCACAACCTCAATATGAAAACCTATTTAACTTATTTATTATCTTGTGAAAAGTATACAATGAAA
ATTTTGTTCATACTGTATTTATCAAGTATGATGAAAAGCAATAGATATATATTCTTTTATTATGTTAAATTATGA
TTGCCATTATTAATCGGCAAAATGTGGAGTGTATGTTCTTTTACAGTAATATATGCCTTTTGTAACTTCACTTG
GTTATTTTATTGTAAATGAGTACAAAATTCCTAATTTAAGAGATTGTATGTAATATTTATTTCAATTAATTTCTTT
CCTTGTTTACGTAAATTTTGAAGATTGCATGATTTCTTGACAGAAATCGATCTTGATGCTGTGGAAGTAGTTTG
AGGAACATCCTATGAGTTTTCTTAGAATGTATAAAGGTTGTAGCCCATCCAACCTCAAAGAAAAAATGACCACA
TACTTTGCAATCAGGCTGAAATGTGGCATGCTTTTCTAATTCCAACTTTATAAACTAGCAAAAAAGTGTGTGCTT
ATTCCACCAGTTCTACTGTGACATACTCGAGTATAAAGACATGTAGCAATAACGGGGAGTGGGGGGGAGTCTCA
CAGTGCCTTTGGAAGGGCCCGAACTTGCCTTAAATCTTCCTCAACCAATAAGTATTTTATTAGTGCTTGAGAGA
ATCTGAATGTAGGATGGGTTCAACTGCACAAAAGGAAAAGATTTTACCACCTTTTTTATATAGATATAAAGTGA
AGCAACCGCCTTAGTGCTGAAATATGTAGTACATGAATATGCCTTGTTTAATTACAGAAAATTCCTTCCGGACA
GCAGATGAATGAGCGGTAGCTTTAGTTTGTACGTAGGTACAGTTGGAGCACTATATGTACTCTCTGGACTACTTT
GGACAGAAGTAGGTTTTTGAATGTAACAAGATAAGTCAACTTGAGTTGTAATATATTTTGGGGAATCAGCTCACT
ACAAATTGTGACTGTAAACATTGTAAGTAAATGTTTTGTAGTT

WO 2004/030615

PCT/US2003/028547

781/6881
FIGURE 730

MWEPFSWKKFLIVSQTGVNKPASRHLAKPISFLKSNIFCQEYALIVSPQPIGVFCFLTELYMSGGEKTLAFQRSI
LVTWFHCHHLVDVQFRTILSAPSGSLAQSLCNCWRITAEFLAVLS

WO 2004/030615

PCT/US2003/028547

782/6881
FIGURE 731

CCTGATTCTAGGCTGGTCACTACTCCGAGCCTGTGACGTTTGCGGCAGCCAGGCCGTGACGATGCCAGTGAAA
CTCTCTGGGAAATTGCAAAAGCTGAAGTGAAAAAAGGGGAATTAATGGAAGTGAAGGTGATGGAGCTGAAATTG
CAGAAAAATTTGTTTTCTTCATTGGCAGTAAAAATGGGGGAAAGACTACTATTATTCTAAGGTGTCTTGACAGAG
ATGAACCACCAAAACCAACCTTAGCTTTGGAATATACATATGGAAGAAGAGCAAAAGGGCACAACACACCAAAAG
ATATCGCTCACTTTTGGGAACCTGGTGGAGGAACCTCTTTATTGGACTTAATCAGCATACCCATCACAGGTGACA
CCTTACGGACGTTTTCTCTTGTTCCTGTTCTGGATCTTTCAAAACCTAATGATCTCTGGCCCACCATGGAAAATC
TCTTGCAAGCCACAAAAAGCCATGTAGACAAAGTGATAATGAAACTGGGAAAAGACAAATGCTAAAGCAGTTTCTG
AAATGAGACAGAAGATCTGGAATAATATGCCGAAGGATCATCCTGATCATGAATTAATTGACCCATTTCCGGTAC
CTCTGGTCATAATTGGAAGTAAATATGATGTTTTTCAGGATTTTGAGTCTGAGAAGAGAAAGGTAATATGCAAGA
CACTTCGATTTGTTGCACATTATTATGGAGCATCATTAAATGTTTACCAGTAAATCAGAAGCTCTATTACTAAAAA
TACGTGGAGTTATCAACCAGTTGGCATTGTCATTGACAAAAGCAAATCAATATGTGTGGATCAGAATAAACCGC
TGTTTTATCACAGCAGGATTGGATTCTTTCCGGTCAAATAGGATCTCCTCCTGTTCCCTGAAAATGACATTGGAAAGC
TTCATGCCCACTCACCTATGGAGTTGTGGAAAAAGTGTATGAAAAGCTCTTCCACCAAAGAGTATTAACACGC
TGAAAGATATCAAGGACCCTGCGAGAGATCCTCAGTATGCTGAAAATGAAGTCGATGAGATGAGAATTCAGAAGG
ATCTGGAAGTGAACAGTACAAAAGAAGTTCTTCCAAGTCTTGGAACAAATCGAGCTTGATTCTTGAAACCTATT
TCAATTATTGTATATTTATTTCTTTTCCAAATACAAATAAGATTATACTGTGAATTAACCTATTGTGGCAATA
TGTGAAGAAAGTTAACTGTATAATTTGTTAAAGGACAAGCTGGATTTCTTGGAAGTAGTGCATCTCCCTGTATAT
CTTGAAGCTTTTTAAAGGAAAAATTATTGTAGAACCACGTGTAATTTTTTTTAAATAAAAGAATCTTCTACTA
CCTACCTCT

WO 2004/030615

PCT/US2003/028547

783/6881
FIGURE 732

MPSETLWEIAKAEVEKRGINGSEGDGAEIAEKVFFFIGSKNGGKTTIILRCLDRDEPPKPTLALEYTYGRRAKGH
NTPKDIAHFWEELGGGTSLLDLISIPITGDTLRTFSLVLVLDLSKPNDLWPTMENLLQATKSHVDKVIMKLGKTNA
KAVSEMRQKIWNMPKDHDPHELIDFPVPLVIGSKYDVFQDFESEKRKVICKTLRFVAHYYGASLMFTSKSEA
LLLKIRGVINQLAFGIDKSKSICVDQNKPLFITAGLDSFGQIGSPPVPENDIGKLHAHSPMELWKKVYEKLFPPK
SINTLKDIKDPARDPQYAENEVDEMRIQKDLELEQYKRSSSKSWKQIELDS

WO 2004/030615

PCT/US2003/028547

784/6881
FIGURE 733A

ACATGCTCCTCCTGTCTTCTGGCGGAGCGTGCTTCCCGCTGCGGGGACGTTTCGAGCAATGGCAGCCCTGCTGAG
ATCCGCGCGTTGGTTGCTGCGTGCCGGGGCGGCCCCGCGCTCCCGCTCTCCCTGCGCCTCCTCCCTGGCGGGCC
GGGCGGCTGCATGCCGCTCCTATCTGCCCCGCGCTCGCGCCGGGCCCCGTGGCCGGAGGACTACTGAGCCCAGC
CAGGCTGTATGCCATTGCTGCCAAGAAAAAGATATTCAAGAGGAGTCCACTTTTTCTTCTAGGAAGATTCCAA
TCAGTTTGATTGGGCTCTAATGAGACTAGATCTTTCTGTTTGAAGAACTGGCCGCATTCCAAAGAAGCTTCTACA
AAAAGTTTTTAATGATACCTGCCGCTCAGGTGGCCTAGGTGGTAGTCATGCCTTGCTTCTACTACGTAGTTGTGG
TTCTCTCTTGCTGAAGCTTGAAGAGAGAACAAGATTTGCTCATAGGATATGGGACACACTTCAGAAATT
AGGTGCTGTGTATGATGTGAGTCACTATAATGCTTTACTTAAAGTCTATCTTCAAATGAATATAAATTCTCACC
AACTGATTTCTGGCAAAAATGGAGGAAGCAACATTCAACCAATCGAGTGACATACCAGAGATTGATTGCTTC
TTATTGTAATGTAGGAGATATTGAAGGTGCCAGCAAGATTCTTGGATTTATGAAAATAAGGATCTCCCAGTTAC
AGAGGCAGTATTCAGTGCCCTTGTGACAGGGCATGCCAGAGCTGGTGATATGGAGAATGCAGAAAACATTCTCAC
AGTGATGAGAGATGCCGGAATTGAGCCTGGTCCAGACACATACCTCGCATTATTGAATGCATATGCTGAGAAGGG
CGACATTGACCATGTTAAGCAGACTCTGGAGAAGGTGGAGAAGTCCGAGCTTACCTTATGGACCGTGATTTACT
GCAAAATTATTTTAGCTTCAGTAAAGCTGGGTATCCTCAGTATGTCTCAGAAATTTTGGAAAAAGTTACATGTGA
AAGAAGATATATTCCAGATGCAATGAACCTCATTTTACTTTTAGTCACTGAAAAATTGGAAGATGTAGCGTTGCA
AATTTTACTAGCATGCCCCGTATCAAAGGAAGATGGCCCCAAGTGTCTTTGGCAGTTTCTTTTACAACACTGTGT
GACTATGAATACGCCTGTGGAGAAGCTAACAGACTACTGTAAGAAGTTAAAGGAAGTCCAGATGCACTCCTTTCC
TCTGCAGTTCACCTCCATTGTGCTTTACTCGCCAATAAACTGATTTGGCAAAAGCCTTAATGAAGGCTGTGAA
GGAGGAAGGTTTTCTATCAGACCTCACTATTTCTGGCCATTGCTAGTTGGACGTCGGAAGGAAAAAATGTTCA
AGGTATAATTGAAATCCTCAAAGGAATGCAAGAATTGGGAGTACATCCTGATCAGGAAACATATACAGATTATGT
GATTCATGCTTTGATAGTGTAAGTCACTCAGCAGAGCCATTTTGCAGGAAAATGGATGTCTGTCTGATAGTGATAT
GTTTTCTCAAGCTGGATTGAGAAGTGAAGCAGCAAAATGGGAACCTTAGACTTTGTATTATCATTTTGAATCAAA
TACATTGCCCATCTCGCTGCAGTCTATAAGAAGTAGCCTACTGCTAGGCTTCAGGAGGTCTATGAATATAAATCT
TTGGAGCGAGATAACAGAATTGTTGTACAAGGATGGACGTTATTGCCAGGAGCCTCGAGGACCGACGGAAGCTGT
TGGCTATTTTCTTTATAACTTGATTGACAGCATGAGTGACTCAGAGGTACAGGCCAAGGAGGACATTGAGACA
ATACTTCCATCAGCTGGAGAAGATGAATGTAAAAATTCCTGAAAATATCTACAGAGGCATTCTGTAATCTCCTGGA
AAGCTACCATGTTCTGAATTGATTAAGGATGCTCACTTGTGGTTGAGAGTAAGAATTTAGACTTTCAAAAAAC
TGTGCAACTTACATCATCTGAATTGGAGTCCACACTTGAAACACTAAAAGCTGAAAATCAACCTATAAGAGATGT
CCTAAAGCAACTCATATTAGTGCTTTGTTTCAAGAGAATATGCAAAAAGCCCTTGAATTGAAAGCAAAATATGA
ATCCGACATGGTTACTGGTGGCTATGCAGCTTTAATAAATTTATGCTGTGCGACATGATAAAGTAGAAGATGCCTT
GAACCTGAAAGAAGAATTTGACCGCTTAGATTCACTGCTGTCTTACACCGCAAGTATGTAGGCCTTGTAAAG
AGTATTGGCAAAGCATGGCAAGCTCCAAGATGCTATTAACATTCTGAAGGAGATGAAAGAGAAGGATGTTCTTAT
CAAAGATACAACAGCCTTGTCTTTTCCACATGCTAAATGGCGCAGCTTTAAGAGGTGAAATTGAAACAGTAAA
ACAGTTGCATGAAGCCATCGTGACTCTAGGGTTAGCAGAACCATCCACCAACATAAGTTTCCCATTGGTCACTGT
ACACTTGGAAAAGGGCGACCTATCTACTGCTCTTGAGGTGCGCCATTGACTGCTATGAAAAGTATAAAGTATTACC
AAGGATTCATGATGTCTTGTGTAAGTGGTAGAGAAAGGCGAGACTGATCTAATTCAGAAAGCAATGGACTTTGT
GAGCCAAGAACAAGGTGAAATGGTGATGCTCTATGATCTCTTCTTTGCTTCTACAAACAGGAAATTACAAAGA
GGCCAAGAAGATCATTGAGACTCCAGGGATTAGAGCTCGATCTGCAAGGCTTCAGTGGTTTTGTGACAGATGTGT
TGCAAAATAATCAGGTTGAAACTCTGGAATAATTAGTGGAGCTGACACAGAAGCTATTTGAATGTGATAGAGACCA
GATGTACTACAATCTGTAAAACCTGTATAAAATAAACGGTGACTGGCAAGAGCTGATGCAGTCTGGAATAAAT
CCAAGAAGAAAAATGTTATTCCTCGTGAAAAAGACATTAAGATTATTAGCAGAAATCCTTAGAGAGGGTAACCAGGA
AGTTCGTTTGACGTACCTGAGTTGTGGTATGAAGATGAAAAACATTCCCTGAATTCTTCGTCAGCCTCAACCAC
AGAACCTGATTTCAGAAAGATATATTGATTGCCTGCCGATTGAACCAAAAAAAGGGGCATATGATATTTTCTT
GAATGCAAAAGAGCAAAACATTGTGTTAATGCTGAAACCTACAGCAATCTCATTAATTAATGATGTGAGAAGA
TTATTTTACACAAGCAATGGAAGTGAAAGCATTGCGGGAGACCCACATCAAGGGCTTCACACTGAACGATGCTGC
CAACAGCCGCTCATCATAAACGCAAGTTAGGCGGGATTATTTGAAAGAGGCTGTGACAACACTGAAAACAGTATT
GGATCAGCAGCAGACCCCTTCTAGGTTAGCAGTGACCCGTGTATCCAGGCATTGGCCATGAAGGGTGATGTTGA
AAACATAGAAGTAGTTCAGAAGATGTTAAATGGACTCGAAGACTCCATTGGACTTTCAAAAATGGTTTTTCATCAA

WO 2004/030615

PCT/US2003/028547

785/6881
FIGURE 733B

TAACATTGCTTTGGCTCAAATAAAGAATAATAACATAGATGCCGCAATAGAAAACATTGAAAATATGCTTACTTC
AGAGAATAAAGTCATTGAACCCCAATACTTCGGCTTGGCATACTTATTTCAGAAAAGTAATAGAGGAGCAGTTGGA
ACCAGCAGTTGAAAAGAGTAACATCATGGCGGAGAGATTGGCCAATCAGTTTGCAATTTATAAACCTGTCACCTGA
TTTTTTCCTTCAACTTGTGGATGCAGGCAAGGTGGATGATGCCAGAGCTCTCCTACAGAGATGTGGTGCAATTGC
TGAACAAACCCCGATTTTGTGTTGTTTCCTCCTTAGGAATTCTAGGAAACAAGGAAAGGCATCAACTGTGAAATC
TGTGTTAGAATTGATTCCTGAATTAATGAAAAGGAAGAAGCATACAATTCCCTCATGAAAAGCTATGTCTCAGA
GAAAGATGTCACATCTGCTAAAGCACTGTATGAACATTTGACTGCAAAGAATACAAAATTGGATGATCTGTTTCT
AAAGCGTTACGCATCTTTGCTGAAGTATGCTGGAGAGCCTGTCCCTTTCATTGAACCCCTGAAAGCTTTGAATT
TTATGCACAGCAGCTAAGAAAATTGAGGGAAAACCTCTTCTTGAAATAACCAGGCGATACTTTGTTTTGTATATAT
TTGTGATTCTGTGTCTACATGTTATTTTGAAGTATATCTGAGGGAAAAATAAATGAAAATTTTCTTTATGTACTT
ATGTATGTGTGATGCATGTTCAAAGTCTTATTGACCATAACTCTGTGCACTTGGTTATTGGACATTTTGGAGTT
TTTTTCTCTGGGAAAAATCGATAGTGTTCCTTCAATGCTGCTGCTGTGTGAAGCCATACTTTTTCAGGATTCTT
CCCCTAATTGGCTCTTTGGTTTCCCTGCTCTGTTTCATTTATTTTATTAAATGTTATTCCTTTATTTAAGATT
ACTTATTAGTCTGCTGTTTCTCTGAAAAATTTTAGAGCTAGGTATAGTGACCGTGAACCTTTCTAACGCATAATAT
TCTGTGATACAGCCATTCCGTACATGTGTGAAGTCTGCTGATACTTTTCGAACCTTTGTTAAATGTTGGCACTAGGA
GTCATCAGATCTAGGCTTCATCATTTTCCAGTGAGAAGCAGAGACCCAAAGGGCCTGTTACTTGTGCTTGGTCAG
GGGACTGTCTGTCATGCCTGGAGGCTCTTCGGCACACTTCCCCATCTTTCCCTTCTGCCACTGTGGCTTCAAGCA
CCTCTGTTTCATAGAGCGTCTCTGAAATTGAGTCTCGGTCATGACTTATCCCGAAGTAGAGCAATGTGTTTCTCT
CATTGTAGTTTTCAGGACTTTGTGAGTACAAGCTCTGCCCTAGGCTTGTTACTTTTATACTCATATCCTGAAAAGAT
GTGATTTTCATCTATGAAGGGGTAAAATATTGGTTTGTATTTAATTGTTTGAATAAAAAGTGATCCCTATATTG

WO 2004/030615

PCT/US2003/028547

786/6881
FIGURE 734

ATGGGCTCAGGCTACACCAAGGCCGTGTACCGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTG
GACTTTAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAGCTCTATGGCTACTGC
TACCAGGACAGCGAGGACATCCCAGACACCCTGACCACCATCACGGAGCTGGGCGCCCCTGTAGAAATGATCCAG
CTGCTGCAAACCTTCCTGGGAGGATCGATTCCGAATCTGCCTGAGCCTGGGCGCCCTCCTCCACCACCTGGCCAC
TCCCCACTGGGCTCCGTCACCTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATACTCGAGTTTCCGGCC
AGGAACTTCACCCTGCCCTGCTCAGCCCAGGGCTGGTGCGAGGGCATGAACGAGAAGCGGAACCTCTATAATGCC
TACAGGTTTTTCTTACATACCTCCTGCCTCACAGTGCCCCGCCCTTCACTGCGTCCTCTGCTGGACAGCATCGTC
AACGCCACAGGAGAGCTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAGACAGCACCATCCCC
CAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCCTCCTTTCAGTGTCAACCTGGCTGAGGCT
GTGGATGTCGTGAGAGCCATGCCAGTGTGGGCCCTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGCAG
CTGGTCTTTTTCAAGACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGA

WO 2004/030615

PCT/US2003/028547

787/6881
FIGURE 735

MGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAAHKLLKEMVLLERLRHPNVLQLYGYC
YQDSEDIPDTLTTITELGAPVEMIQLLQTSWEDRFRICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKV
TDLDDARVEETPCAGSTDCILEFPARNFTLPCSAQGWCEGMNEKRNLNAYRFFFTYLLPHSAPPSLRPLLD SIV
NATGELAWGVDETLAQLEKVLHLYRSGQYLQNSTASSSTEYQCIPDSTIPQEDYRCWPSYHHGSCLLSVFNLAEA
VDVCESHAQCRAFVVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

WO 2004/030615

PCT/US2003/028547

788/6881
FIGURE 736

GCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCA
GCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGT
AAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACT
GTGTTCAATAGTGTGAGAATGTAGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACA
GGAGACTTGGCGGGAGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAGG
GGACACTCCCAGGCCAGCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCAAGACTGGGGTCAGGGA
GCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGTGGGGCCGGGGCCTTTCTGCCTCATTGCTTTCAATGAAA
GCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTG
GTTAAATTGTTTATTTTTGTAAAAATAAAATAAAATTAGTTAATAA

WO 2004/030615

PCT/US2003/028547

789/6881
FIGURE 737

MWVILYLGRSLTSRQGTLPQGPRGQQRCTPQHEPRLGSGSRCGLSQDLGRGWGRGLSASFANESLKAAKTRL
SPFLEFEYPESFVLLVG

WO 2004/030615

PCT/US2003/028547

790/6881
FIGURE 738A

AGATGACTTTGGGAAATTGCTGCTGGCTGAGGCCCTCCTGGAGCAGTGTTTGAAGGAGAACCATGCCAAAATAAA
AGACTCCATGCTTTGCTGGAGAAGAATGAGCCGAAGATGAGCGAAGCCAAAAATTATCTAAGCAGTATCCTTAA
CCATGGGAGGCTCTCGCCACAGTACATGTGTGAGGCCATGCTGATCCTGGGCAAACCTGCATTACGTGGAGGGCTC
ATACCGAGATGCCATCAGCATGTACGCACGGGCCGGGATTGATGACATGTCCATGGAGAACAAGCCCCTGTATCA
GATGCGGCTGCTGTGCGGAGGCTTTTGTATCAAAGGCCTCTCTCTGGAACGCCTACCCAACCTCATCGCCTCCCG
CTTCCGCTGACAGAGAGGGAGGAGGAAGTGATCACCTGTTTTGAGAGGGCCTCCTGGATCGCTCAGGTGTTCCCT
GCAGGAATTGGAGAAGACCACAAATAACAGCACGTGAGGCATCTGAAAGGCTGTCACCCGCTTGACTATGAGCT
CACCTACTTCTGGAAGCTGCCCTCCAGAGCGCCTATGTGAAAACTGAAGAAGGGGAACATCGTGAAGGGCAT
GAGAGAGCTCCGGGAGGTGCTGCGGACTGTGGAGACCAAGCAACTCAGAACTTCAAAGTGATGGCGGCCAAGCA
CCTGGCGGGGCTCTGCTGCACTCCCTGAGTGAGGAGTGCTACTGGAGCCCCCTGTCCACCCCTCTGCCTGAGTT
CATGGGCAAGGAGGAGAGTTCTTTGCGCACTCAGGCCCTGCGGAAACCTCACCTCTATGAAGGAGACAACCTCTA
CTGCCCCAAGGACAACATCGAGGAAGCCCTCCTGCTCCTCCTCATCAGCGAATCCATGGCAACTCGAGATGTTGGT
GCTGAGCCGGGTGCCGGAGCAGGAGGAGGACCGGACAGTGAGCTTGCGAATGCCGAGCCATCTATGACCTGCCCT
GAGCATCACGTTGGGCAGAAAGGGGACAGTACGTGCTCTCGGAGTGCTGAGCGAGCCATGAAGTTTGCGTT
TGGAGAATTTACCTTTGGTACCAGGTGGCCCTCTCCATGGTGGCTTGTTGGGAAGTCAGCCTACGCTGTGTCCCT
GCTGCGGGAGTGTGTGAAGTTGCGGCCCTCGGACCCACCGTGCCCTGATGGCCGCGAAGGTCTGCATCGGGTC
CCTTCGCTGGCTAGAGGAAGCAGAGCACTTTGCCATGATGGTGATCAGCCTCGGAGAGGAAGCCGGGGAGTTCTCT
CCCCAAGGGCTACCTGGCTCTGGGTCTCACCTATAGCCTGCAGGCCACCGACGCCACCTGAAGTCCAAGCAAGA
TGAATTGCACCGGAAGGCACTGCAGACGCTGGAGAGGGCTCAGCAGCTGGCGCCAGTACCCCCAGGTATCCT
CTATGTCTCGCTGCAGCTGGCCCTCGTCCGACAGATCTCCAGTGCCATGGAGCAGCTGCAGGAGGCCCTGAAGGT
ACGCAAGGATGATGCCACGCCCTCCACCTGCTGGCACTGCTCTTCTCTGCCCAGAAGCACCACCAGCATGCCCT
GGATGTTGTCAACATGGCCATCACCGAGCACCCCTGAGAACTTCAACCTGATGTTACCAAGGTGAAGCTGGAGCA
GGTGCTGAAAGGCCAGAGGAAGCCCTCGTGACCTGCAGACAAGTGCTGAGGCTGTGGCAGACCCTGTACAGCTT
CTCCCAGCTGGGAGGCCTAGAAAAGGATGGCAGCTTCGGTGAGGGCCTCACCATGAAGAAGCAGAGTGGCATGCA
CCTGACTTTGCTGATGCCCATGATGCAGACTCTGGCTCCCGCGGGCTTCGTCCATCGCCGCTCCCGGCTGGA
GGAGGCCATGTGAGAGCTGACTATGCCCTCTTCGGTCTTGAAGCAGGGCCCCATGCAGCTGTGGACCACGCTGGA
ACAGATCTGGCTGCAGGCTGCTGAGCTGTTGATGAGCAGCAGCACCTCAAGGAAGCAGGTTTCTGCATCCAGGA
GGCGGCGGGCCTCTTCCCACTTCTCACTCAGTACTCTATATGCGGGGCCGGCTGGCTGAGGTGAAGGGCAACCT
GGAGGAGGCCAAGCAGCTGTACAAGGAGGCGCTCACGGTGAACCCAGATGGCGTGCGCATCATGCATAGCCTGGG
TCTGATGCTGAGTCGGCTGGGCCACAAGAGCTTGGCCAGAAAGGTGCTTCGTGATGCCGTGGAGAGGCAGAGTAC
GTGCCACGAGGCTGGCAGGGCCTGGGCGAGGTGCTGCAGGCCCAGGGCCAGAACGAGGCTGCCGTTGACTGCTT
CCTCACCGCCCTTGAGCTGGAGGCCAGCAGCCCTGTACTGCCCTTCTCCATCATCCCCAGAGAGCTCTGACGACG
CTGCAGCCCGCAGGGAGGGAGGGGCTGGCCAGAGGGAGAGGCAGCAGGGAACGTGGGTGAGGGTGGGGCAACAGTG
GCATCAGGTGCGGGGCCCTCAGGGAATAACATCTTTAGTGAACGCCTCTGCAGCTGCAGCCCTCGTTCTCTTGGCT
GGGCCAAGAGGGCCTTCTGGATTTCTTTGTTGGTGCCCTTGGGAAACAGTCTGACTTGAACCCTAAGTGCCTTTG
GAGAGTTTTGTGGTGACCAGACTTGCTCCCCAAGAGCTGGGCAGCGGGGAGCCTCACAGCTGTCTTACCCTCA
CCCATGCCCTCTGGCTTGGAGTCTGGGTGGGGGTTCTCACTCCCCACTCTCAGCACAGTACAGACTTCTGGATCT
CTCTCAGGTCTTGCCAGGGCGGTACAAATGTGAAGAACTGCGGGCAAGTGGGAAGACTATGAGATTTCTGGGT
TCCCTTCTCAGACTTGGAGTTAGTAGATGATTCCTGCATTGCCCTGCTTGCCCTCTGAGACCAGCTGGGCCCCA
CCTTGCTCTTTCCCCCTGCTACCAAGTGCTTTGGGGTCTGACCAGGGGTACTGAGCACCGGCCCTAACACTTCC
ATCTCCACCCACCCATCTCCCTGGCGATGTGCTCCAGCCCAAGCAGCCTCCGTAGGCTTTAGATCCTGTGGTTG
CTAGATCCAGTCTTTCTAATACCCTGAGTCAACACATTACTCTGCAGGTCTTAGGCTACAATGCAGGTCCCTT
GAGGGCCACCAACATGGAGGTAGGCAGTTTCTAGGACTGTCCCCAGTACATCTACCACCACAGCCCTTTTTTT
GCCTTGATTGAGCCTCACCTGGCCTTTTGGCTTCCCTGCCTGAGAGAGACCTGAGGAGGGGACAGAGCCAG
CCCCTCTCCTGTGGCTGAGCAGGCCTCTGTGTCCATGACACCTGTCTCCGGGCTGGGGCTGTGGGTGTATGT
CCTCCCTACTGGCTTCCCCGGCCCTGCTGCATGATGCTCTTGGAACCTTCTCCAAGGAGTCAGTCCCCCAGGC
CTATCAGGGGATCCTTTTGTATCTGCACCTTGGGTTTTAGTTTTCAAAGCTCCATCAGGTACAGCTTGCATTTAG
GATGTGTGGAAGCTCGGGTGAAGGCTGCCCTGGTTTCATCATAGCTCCACCTTCTCGGAAGGAGTGGGCTGTTG

WO 2004/030615

PCT/US2003/028547

791/6881
FIGURE 738B

GAGACCCCCCATCCATGGCACACTAGCTCAGCACTGCATTTCCCGAGATGATTCCCAAGACAGCTGGTGCCTCCT
GGCTTTTCCTGTGCCAGGCCAAGGGGCACCACAGAGGACCCTGGATCCTTTGCCTCTTCTTGTTGAAGGATCTCT
ATGTATGTGTGTATATAAATATAGTTTTTTATCTATATATATAAAATAGAGATCTATTTTTTTTCTGGAATTCTG
TTAGAAAAGTAAAGAAAAAGCAAATGCTGTTGGTTTATCTCAGGGTGCCCAAAGTGGTTATAGTCAATTTTGGT
ACTAGGAAAGGCACCCAATGCATTTCTGACTTTTAAGCATTTCTTGTGGAAGCAGCAGAGGGCCAGGCCAAG
TTGCTGACAGTGACTTTGCAGGTTGAATAAAGAAACCCCTGGAGGGGAAGCAGGCTTGTCTGAAGCAGCATGTAT
ATTCAGTGGGCATGTAGCTCCACACCAGCCTTGAGCCAGGCCCTGGACAGGAGGGGCTGTTGCAGGATGAGGGA
GGCCAGAGAAGGCATCGAAGCCAAGACCTGGGCCACCTGGGGAGGGATGTGGGAAAGGAAGGATGGGAGGGAGG
ACCTCTGGGAAAATGTGGATTTGAGCTGGTGAGAGTGTGCTAAGGCTGGGCTAAAGCCTGGAGAGGGTAGGAG
GAGGCAAGAGGGGTCCAGGCAGGGCTGATCCTGGCCTCTGACCTGTCCAGGGCGACCCCTGAAGCCCCTGCTGCC
TCTGGGCATTGCTGGGAGAGGCCAAGGCAGGACTCACGTCTGAACAGAGATCCCCTCGGGCATTGCTGATGGGCC
ACCTTCAGCTGCAGGGAAGAAGCCTAGGAGAGGAGGCATGGGAGGGACCTGGGCCTTGTTTCAGATTGGCCACCTC
TGCTGAGAAGTCCATACCAGTACACCCCTAATAAGTTATGCCACATACCAACGTACTGTGGATATTATAACCTGC
ATTAAACAACCTCTAAAGAACGCTGCTCATT

WO 2004/030615

PCT/US2003/028547

792/6881
FIGURE 739

MAAKGAHGSYLKVESELERCRAEGHWDRMPQLVRLQTLSPGGGGNRRGSPSAAFTFPDITDDFGKLLLAEEALLE
QCLKENHAKIKDSMPLLEKNEPKMSEAKNYLSSILNHGRLSPQYMCEAMLILGKLHYVEGSYRDAISMYARAGID
DMSMENKPLYQMRLLSEAFVIKGLSLERLPNSIASRFLTEREEVITCFERASWIAQVFLQELEKTNNSTSRH
LKGCHPLDYELTYFLEAALQSAYVKNLKKGNIVKGMRELREVLRTVETKATQNFKVMAAKHLAGVLLHSLSEECY
WSPLSHPLPEFMGKEESSFATQALRKPHLYEGDNLYCPKDNIEEALLLLISESMATRDVVLRSRVPEQEEDRTVS
LQNAAIYDLLSITLGRRGQYVMLSECLERAMKFAFGEFHLWYQVALSMVACGKSAYAVSLLRECVKLRPSDPTV
PLMAAKVCIGSLRWLEEAHFAMMVISLGEEAGEFLPKGYLALGLTYSLQATDATLKSQDELHRKALQTLERAQ
QLAPSDPQVILYVSLQALVLRQISSAMEQLQEALKVRKDDAHALLALLFSAQKHHQHALDVVNMAITEHPENF
NLMFTKVKLEQVLKGPEEALVTCRQVRLWQTLYSFSQLGGLEKDGSGFGEGLTMKKQSGMHLTLPDAHDADSGSR
RASSIAASRLEEAMSELTMPSSVLKQGPMLWTTLQIWLQAAELFMEQQHLKEAGFCIQEAAGLFPTSHSVLYM
RGRLAEVKGNNLEEAKQLYKEALTVNPDGVRIMHSLGLMLSRLGHKSLAQKVLDAVERQSTCHEAWQGLGEVLQA
QGQNEAAVDCFLTALELEASSPVLPFSIIPREL

WO 2004/030615

PCT/US2003/028547

793/6881
FIGURE 740

AGTCCGAGTGGAGAGAGCGAGCTGAGTGGTTGTGTGGTCGCGTCTCGGAAACCGGTAGCGCTTGCAGCATGGCTG
ACCAACTGACTGAAGAGCAGATTGCAGAATTCAAAGAAGCTTTTCACTATTTGACAAAGATGGTGATGGAAC TA
TAACAACAAAGGAATTGGGAACTGTAATGAGATCTCTTGGGCAGAATCCACAGAAGCAGAGTTACAGGACATGA
TTAATGAAGTAGATGCTGATGGTAATGGCACAATTGACTTCCCTGAATTTCTGACAATGATGGCAAGAAAAATGA
AAGACACAGACAGTGAAGAAGAAATTAGAGAAGCATTCCGTGTGTTTGATAAGGATGGCAATGGCTATATTAGTG
CTGCAGAACTTCGCCATGTGATGACAAACCTTGGAGAGAAGTTAACAGATGAAGAAGTTGATGAAATGATCAGGG
AAGCAGATATTGATGGTGATGGTCAAGTAACTATGAAGAGTTTGTACAAATGATGACAGCAAAGTGAAGACCTT
GTACAGAATGTGTTAAATTTCTTGTACAAAATTGTTTATTTGCCTTTTCTTTGTTTGTAACTTATCTGTAAAAGG
TTTCTCCCTACTGTCAAAAAAATATGCATGTATAGTAATTAGGACTTCATTCCCTCCATGTTTTCTTCCCTTATCT
TACTGTCAATTGTCCTAAACCTTATTTTAGAAAATTGATCAAGTAACATGTTGCATGTGGCTTACTCTGGATATA
TCTAAGCCCTTCTGCACATCTAACTTAGATGGAGTTGGTCAAATGAGGGAACATCTGGGTTATGCCTTTTTTAA
AGTAGTTTTCTTTAGGAACTGTCAGCATGTTGTTGTTGAAGTGTGGAGTTGTAACCTCGCGTGGACTATGGACAG
TCAACAATATGTACTTAAAAGTTGCACTATTGCAAAACGGGTGTATTATCCAGGTACTCGTACACTATTTTTTG
TACTGCTGGTCCTGTACCAGAAACATTTTCTTTTATTGTTACTTGCTTTTTAACTTTGTTTAGCCACTTAAAT
CTGCTTATGGCACAATTTGCCTCAAAATCCATTCCAAGTTGTATATTTGTTTTCCAATAAAAAAATTACAATTT

WO 2004/030615

PCT/US2003/028547

794/6881
FIGURE 741

GGCGGGAAACAGCTTAGTGGGTGTGGGGTCGCGCATTTTCTTCAACCAGGAGGTGAGGAGGTTTCGACATGCGCGG
TGCAGCCGAAGGAGACGCTGCAGTTGGAGAGCGCGGCCGAGGTTCGTGCGCTTCTTTCAGGGCATGCCGG
AGAAGCCGACCACCACAGTGCGCCTTTTCGACCGGGGCGACTTCTATACGGCGCACGGCGAGGACGCGCTGCTGG
CCGCCCCGGGAGGTGTTCAAGACCCAGGGGGTGATCAAGTACATGGGGCCGGCAGGAGCAAAGAATCTGCAGAGTG
TTGTGCTTAGTAAATGAATTTTGAATCTTTGTAAAAGATCTTCTTCTGGTTCGTCAGTATAGAGTTGAAGTTT
ATAAGAATAGAGCTGGAAATAAGGCATCCAAGGAGAATGATTGGTATTTGGCATATAAGGCTTCTCCTGGCAATC
TCTCTCAGTTTGAAGACATTCTCTTTGGTAACAATGATATGTCAGCTTCCATTGGTGTGTGGGTGTTAAATGT
CCGCAGTTGATGGCCAGAGACAGGTTGGAGTTGGGTATGTGGATTCCATACAGAGGAACTAGGACTGTGTGAAT
TCCCTGATAATGATCAGTTCTCCAATCTTGAGGCTCTCCTCATCCAGATTGGACCAAAGGAATGTGTTTTACCCG
GAGGAGAGACTGCTGGAGACATGGGGAAACTGAGACAGATAATTCAAAGAGGAGGAATTCGATCACAGAAAGAA
AAAAAGCTGACTTTTCCACAAAAGACATTTATCAGGACCTCAACCGGTTGTTGAAAGGCAAAAAGGGAGAGCAGA
TGAATAGTGCTGTATTGCCAGAAATGGAGAATCAGGTTGCAGTTTCATCACTGTCTGCGGTAATCAAGTTTTTAG
AACTCTTATCAGATGATTCCAACCTTTGGACAGTTTGAAGTACTACTTTTGAAGTTCAGCCAGTATATGAAATTGG
ATATTGCAGCAGTCAGAGCCCTTAACCTTTTTCAGGGTCTGTTGAAGATAACCACTGGCTCTCAGTCTCTGGCTG
CCTTGCTGAATAAGTGTAAGAACCCCTCAAGGACAAAGACTTGTTAACCAGTGGATTAAGCAGCCTCTCATGGATA
AGAACAGAAATAGAGGAGAGATTGAATTTAGTGGAAGCTTTTGTAGAAGATGCAGAATTGAGGCAGACTTTACAAG
AAGATTTACTTCGTGCGATTCCAGATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAG
ATTGTTACCGACTCTATCAGGGTATAAATCAACTACCTAATGTTTATACAGGCTCTGGAAAAACATGAAGGAAAAAC
ACCAGAAATTAATTGTTGGCAGTTTTTGTGACTCCTCTTACTGATCTTCGTTCTGACTTCTCCAAGTTTTCAGGAAA
TGATAGAAACAACCTTTAGATATGGATCAGGTGGAAGAACCATGAATTCCTTGTAAGAACCTTCATTTGATCCTAATC
TCAGTGAATTAAGAGAAATAATGAATGACTTGGAAGAAAGATGCAGTCAACATTAATAAGTGCAGCCAGAGATC
TTGGCTTGGAACCTGGCAAACAGATTAACTGGATTCCAGTGCACAGTTTGGATATTACTTTTCGTGTAACCTGTA
AGGAAGAAAAAGTCTTCGTAACAATAAAACCTTTAGTACTGTAGATATCCAGAAGAATGGTGTAAATTTACCA
ACAGCAAATTGACTTCTTTAAATGAAGAGTATACCAAAAAATAAAACAGAATATGAAGAAGCCCAGGATGCCATTG
TTAAAGAAATTGCAATATTTCTTCAGGCTATGTAGAACAATGCAGACACTCAATGATGTGTTAGCTCAGCTAG
ATGCTGTTGTCAGCTTGTCTACGTGTCAAATGGAGCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAG
GACAAGGAAGAATTATATAAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTTATTCCTA
ATGACGTATACTTTGAAAAAGATAAACAGATGTTCCACATCATTACTGGCCCAATATGGGAGGTAAATCAACAT
ATATTCGACAACTGGGGTGATAGTACTCATGGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGT
CCATTGTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAGTCAATTGAAAGGAGTCTCCACGTTTCATGGCTG
AAATGTTGGAAACTGCTTCTATCCTCAGGTCTGCAACCAAAGATTCAATTAATAATCATAGATGAATTGGGAAGAG
GAACCTTCTACCTACGATGGATTGGGTTAGCATGGGCTATATCAGAATACATTGCAACAAAGATTGGTGTCTTTT
GCATGTTTGCAACCCATTTTCATGAACCTTACTGCCTTGCCCAATCAGATACCAACTGTTAATAATCTACATGTCA
CAGCACTCAACACTGAAGAGACCTTAACTATGCTTTATCAGGTGAAGAAAGGTGTCTGTGATCAAAGTTTTGGGA
TTCATGTTGCAGAGCTTGCTAATTTCCCTAAGCATGTAATAGAGTGTGCTAAACAGAAAGCCCTGGAACCTGAGG
AGTTTCAGTATATTGGAGAATCGCAAGGATATGATATCATGGAACCAGCAGCAAAGAAGTGCTATCTGGAAAGAG
AGCAAGGTGAAAAAATTATTAGGAGTTTCTGTCCAAGGTGAAACAAATGCCCTTTACTGAAATGTCAGAAGAAA
ACATCACAATAAAGTTAAAAACAGCTAAAAGCTGAAGTAATAGCAAAGAATAATAGCTTTGTAAATGAAATCATT
CACGAATAAAGTTACTACGTGAAAAATCCCAGTAATGGAATGAAGGTAATATTGATAAGCTATTGTCTGTAATA
GTTTTATATTGTTTTATATTAACCTTTTTCCATAGTGTTAACTGTCAGTGCCCATGGGCTATCAACTTAATAAG
ATATTTAGTAATATTTTACTTTGAGGACATTTTCAAAGATTTTTATTTTGAAGAAATGAGAGCTGTAAGTGGAGC
TGTTTGCAATTGACATAGGCAATAATAAGTGATGTGCTGAATTTTATAAATAAATCATGTAGTTTGTGG

WO 2004/030615

PCT/US2003/028547

795/6881
FIGURE 742

MAVQPKETLQLESAAEVGFVRFFQGMPEKPTTTVRLFDRGDFYTAHGEDALLAAREVFKTQGVIKYMGPAGAKNL
QSVVLSKMNFEFVKDLLVRQYRVEVYKNRAGNKASKENDWYLAYKASPGNLSQFEDILFGNNDMSASIGVVG
KMSAVDQQRQVGVGYVDSIQRKLGCEFPDNDQFSNLEALLIQIGPKECVLPGETAGDMGKLRQIIQRGGILIT
ERKKADFSTKDIYQDLNRLKGGKGEQMNSAVLPEMENQVAVSSLSAVIKFLELLSDDSNFGQFELTTDFDSQYM
KLDIAAVRALNLFQGSVEDTTGSQSLAALLNKCKTPQGQRLVNQWIKQPLMDKNRIEERLNLVEAFVEDAELRQT
LQEDLLRRFPDLNRLAKKFQQAANLQDCYRLYQGINQLPNVIQALEKHEGKHQKLLAVFVTPLTDLRSDFSKF
QEMIETTLDMQVENHEFLVKPSFDPNLSELREIMNDLEKKMQSTLISAARDLGLDPGKQIKLDSSAQFGYYFRV
TCKEEKVLRNNKNFSTVDIQKNGVKFTNSKLTSLNEEYTKNKTEYEEAQDAIVKEIVNISSGYVEPMQTLNDVLA
QLDAVVSFAHVSNGAPVPYVRPAILEKGQGRILKASRHACVEVQDEIAFIPNDVYFEKDKQMFHIIITGPNMGGK
STYIRQTGVIVLMAQIGCFVPCESAEVSIVDCILARVGAGDSQLKGVSTFMAEMLETASILRSATKDSLIIIDEL
GRGTSTYDGFGLAWAISEYIATKIGAFCMFATHFELTALANQIPTVNNLHVLTALTTEETLTMLYQVKKGVCDQS
FGIHVAELANFPKHVIECAKQKALELEEFQYIGESQGYDIMEPAAKKCYLEREQGEKIIQEFLSKVKQMPFTEMS
EENITIKLKQLKAEVIAKNNSFVNEIISRIKVT

WO 2004/030615

PCT/US2003/028547

796/6881
FIGURE 743

CTTTTTCGGGTGGCGGCGAACGCGGAGAGCACGCCATGAAGGCCTCGGGCACACTACGAGAGTACAAAGTAGTGG
GTCGCTGCCTGCCCACCCCAAATGCCACACACCACCCCTCTACCGCATGCGAATCTTTGCGCCTAATCATGTGCG
TCGCCAAGTCCCGCTTCTGGTACTTCGTATCTCAGTTAAAGAAGATGAAGAAGTCTTCAGGGGAGATTGTCTACT
GTGGGCAGGTGTTTGAGAAGTTCCCCTTGCGGGTGAAGAACTTCGGGATCTGGCTGCGCTATGACTCCCGGAGCG
GCACCCACAACATGTACCGGGAATACCGGGACCTGACCACCGCAGGCGCTGTCACCCGGTGCTACCGAGACATGA
GCGCCCGGCACGGCGGCCGGGCCCACTCCATTTCAGATCATGAAGGTGGAGGAGATCGCGGCCAGCAAGTGCCGCC
GGCCGGCTGTCAAGCAGTTCCACGACTCCAAGATCAAGTTCCCGCTGCCCCACCGGGTCCTGCGCCGTCAGCACA
AGCCACGCTTCACCACCAAGAGGCCCAACACCTTCTTCTAGGTGCAGGGCCCTCGCCCGGTGTGCCCCAAATAA
ACTCAGGAACGCCCC

WO 2004/030615

PCT/US2003/028547

797/6881
FIGURE 744A

ATTTCCCGCCAGCAGGAGCCGCGCGGTAGATGCGGTGCTTTTAGGAGCTCCGTCCGACAGAACGGTTGGGCCTTG
CCGGCTGTGCGGTATGTGCGGACAGAGCACCCTGTACAGCTTCTTCCCCAAGTCTCCGGCGCTGAGTGATGCCAAC
AAGGCCTCGGCCAGGGCCTCACGCGAAGGCGGCCGTGCCGCGCTGCCCCGGGGCCTCTCCTTCCCCAGGCGGG
GATGCGGCCTGGAGCGAGGCTGGGCCTGGGCCAGGCCCTTGGCGCGATCCGCGTCACCGCCCAAGGCGAAGAAC
CTCAACGGAGGGCTGCGGAGATCGGTAGCGCCTGCTGCCCCACCAGTTGTGACTTCTCACCAGGAGATTTGGTT
TGGGCCAAGATGGAGGGTTACCCCTGGTGGCCTTGTCTGGTTTACAACCACCCCTTTGATGGAACATTCATCCGC
GAGAAAGGGAAATCAGTCCGTGTTTATGTACAGTTTTTTGATGACAGCCCAACAAGGGGCTGGGTTAGCAAAAGG
CTTTTAAAGCCATATACAGGTTCAAATCAAAGGAAGCCAGAAGGGAGGTCATTTTACAGTGCAAAAGCCTGAA
ATACTGAGAGCAATGCAACGTGCAGATGAAGCCTTAAATAAGACAAGATTAAGAGGCTTGAATTGGCAGTTTGT
GATGAGCCCTCAGAGCCAGAAGAGGAAGAAGAGATGGAGGTAGGCACAACCTACGTAACAGATAAGAGTGAAGAA
GATAATGAAATTGAGAGTGAAGAGGAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGTAGCCGCCAAATAAAA
AAACGAAGGGTCATATCAGATTCTGAGAGTGACATTGGTGGCTCTGATGTGGAATTAAGCCAGACACTAAGGAG
GAAGGAAGCAGTGATGAAATAAGCAGTGGAGTGGGGGATAGTGAGAGTGAAGGCCTGAACAGCCCTGTCAAAGTT
GCTCGAAAGCGGAAGAGAATGGTGACTGGAATGGCTCTCTTAAAGGAAAAGCTCTAGGAAGGAAACGCCCTCA
GCCACCAACAAGCAACTAGCATTTCATCAGAAACCAAGAATACTTTGAGAGCTTCTCTGCCCTCAAATTTCT
GAATCCCAAGCCCACGTTAGTGGAGGTGGTGATGACAGTAGTCGCCCTACTGTTTGGTATCATGAACTTTAGAA
TGGCTTAAGGAGGAAAAGAGAAGAGATGAGCACAGGAGGAGGCCTGATCACCCTGATTTTGATGCATCTACACT
TATGTGCCTGAGGATTTCTCAATTCTTGTACTCTGGGATGAGGAAGTGGTGGCAGATTAAGTCTCAGAACCTT
GATCTTGTCTATCTGTTACAAGGTGGGGAATTTTATGAGCTGTACCACATGGATGCTCTTATTGGAGTCAGTGAA
CTGGGGCTGGTATTTCATGAAAGGCAACTGGGCCATTCTGGCTTCTGAAATTGCATTTGGCCGTTATTCAGAT
TCCCTGGTGCAGAAGGGCTATAAAGTAGCACGAGTGGAACAGACTGAGACTCCAGAAATGATGGAGGCACGATGT
AGAAAGATGGCACATATATCCAAGTATGATAGAGTGGTGAGGAGGAGATCTGTAGGATCATTACCAAGGGTACA
CAGACTTACAGTGTGCTGGAAGGTGATCCCTCTGAGAACTACAGTAAGTATCTTCTTAGCCTCAAAGAAAAGAG
GAAGATTCTTCTGGCCATACTCGTGCATATGGTGTGTGCTTTGTGATACTTCACTGGGAAAGTTTTTCATAGGT
CAGTTTTTCAGATGATCGCCATTGTTTCGAGATTTAGGACTCTAGTGGCACACTATCCCCAGTACAAGTTTTATT
GAAAAAGGAAATCTCTCAAAGGAACTAAAACAATTCTAAAGAGTTTCAATTGTCTGTTCTCTTCAGGAAGGTCTG
ATACCCGGCTCCCAGTTTTGGGATGCATCCAAAACCTTGAAGACTCTCCTTGAGGAAGAATATTTTAGGGAAAAG
CTAAGTGATGGCATTGGGGTGATGTTACCCAGGTGCTTAAAGGTATGACTTCAGAGTCTGATTCCATTGGGTTG
ACACCAGGAGAGAAAAGTGAATTGGCCCTCTCTGCTCTAGGTGGTTGTGTCTTCTACCTCAAAAATGCCTTATT
GATCAGGAGCTTTTATCAATGGCTAATTTTGAAGAATATATTCCCTTGGATTCTGACACAGTCAGCACTACAAGA
TCTGGTGCTATCTTACCAAAGCCTATCAACGAATGGTGCTAGATGCAGTGACATTAAACAACCTTGGAGATTTT
CTGAATGGAACAAATGGTTCTACTGAAGGAACCTACTAGAGAGGGTTGATACTTGCCATACTCTTTTGGTAAG
CGGCTCCTAAAGCAATGGCTTTGTGCCCACTCTGTAACCATTATGCTATTAATGATCGTCTAGATGCCATAGAA
GACCTCATGGTTGTGCTGACAAAATCTCCGAAGTTGTAGAGCTTCTAAAGAAGCTTCCAGATCTTGAGAGGCTA
CTCAGTAAAATTATCAATGTTGGGTCTCCCTGAAGAGTCAGAACCACCCAGACAGCAGGGCTATAATGTATGAA
GAAACTACATACAGCAAGAAGAAGATTATTGATTTTTCTTCTGCTCTGGAAGGATTCAAAGTAATGTGTAAAATT
ATAGGGATCATGGAAGAAGTTGCTGATGGTTTTAAGTCTAAAATCCTTAAGCAGGTCTCTCTCTGCAGACAAAA
AATCCTGAAGGTCGTTTTCTGATTTGACTGTAGAATTGAACCGATGGGATACAGCCTTTGACCATGAAAAGGCT
CGAAAGACTGGACTTATTACTCCCAAAGCAGGCTTTGACTCTGATTATGACCAAGCTCTTGTGACATAAGAGAA
AATGAACAGAGCCTCCTGGAATACCTAGAGAAACAGCGCAACAGAATTGGCTGTAGGACCATAGTCTATTGGGG
ATTGGTAGGAACCGTTACCAGCTGGAATTTCTGAGAATTTCAACACTCGCAATTTGCCAGAAGAATACGAGTTG
AAATCTACCAAGAAGGGCTGTAAACGATACTGGACCAAACTATTGAAAAGAAGTTGGCTAATCTCATAAATGCT
GAAGAACGGAGGGATGTATCATTGAAGGACTGCATGCGGCGACTGTTCTATAACTTTGATAAAAATTACAAGGAC
TGGCAGTCTGCTGTAGAGTGTATCGCAGTGTGGATGTTTTACTGTGCTGGCTAACTATAGTCGAGGGGGTGAT
GGTCTATGTGTGCGCCAGTAATTCTGTTGCCGGAAGATACCCCCCTTCTTAGAGCTTAAAGGATCACGCCAT
CCTTGCAATTACGAAGACTTTTTTGGAGATGATTTTATCTAATGACATTCTAATAGGCTGTGAGGAAGAGGAG
CAGGAAAATGGCAAAGCCTATTGTGTGCTTGTACTGGACCAAAATATGGGGGGCAAGTCTACGCTTATGAGACAG
GCTGGCTTATTAGCTGTAATGGCCAGATGGGTTGTTACGTCCCTGCTGAAGTGTGCAGGCTCACACCAATTGAT

WO 2004/030615

PCT/US2003/028547

798/6881
FIGURE 744B

AGAGTGTTTACTAGACTTGGTGCCTCAGACAGAATAATGTCAGGTGAAAGTACATTTTTTGTGAATTAAGTGAA
ACTGCCAGCATACTCATGCATGCAACAGCACATTCTCTGGTGCTTGTGGATGAATTAGGAAGAGGTACTGCAACA
TTTGATGGGACGGCAATAGCAAATGCAGTTGTTAAAGAACTTGCTGAGACTATAAAATGTCGTACATTATTTTCA
ACTCACTACCATTCATTAGTAGAAGATTATTCTCAAAATGTTGCTGTGCGCCTAGGACATATGGCATGCATGGTA
GAAAATGAATGTGAAGACCCCAGCCAGGAGACTATTACGTTCTCTATAAATTCATTAAGGGAGCTTGTCTAAA
AGCTATGGCTTTAATGCAGCAAGGCTTGCTAATCTCCAGAGGAAGTTATTCAAAGGGACATAGAAAAGCAAGA
GAATTTGAGAAGATGAATCAGTCACTACGATTATTTGGGAAGTTTGCCTGGCTAGTGAAAGGTCAACTGTAGAT
GCTGAAGCTGTCCATAAATTGCTGACTTTGATTAAGGAATTATAGACTGACTACATTGGAAGCTTTGAGTTGACT
TCTGACCAAAGGTGGTAAATTCAGACAACATTATGATCTAATAAACTTTATTTTTTAAAAATGA

WO 2004/030615

PCT/US2003/028547

799/6881
FIGURE 745

MSRQSTLYSFFPKSPALSDANKASARASREGGRAAAAPGASPSPGGDAWSEAGGPRPLARSASPPKAKNLNGG
LRRSVAPAAPTSCDFSPGDLVWAKMEGYPPWPCLVYNHPFDGTFIREKGKSVRVHVQFFDDSPTRGWVSKRLLKP
YTGSKSKEAQKGGHFYSAKPEILRAMQRADEALNKDKIKRLELAVCDEPSEPEEEEEEMEVTYVTDKSEEDNEI
ESEEEVQPKTQGSRRSSRQIKKRRVISDSESDIGGSDVEFKPDTKEEGSSDEISSGVGDSESEGLNSPVKVARRR
KRMVTGNGLKRKSSRKETPSATKQATSISSETKNTLRAFSAPQNSSEQAHVSGGGDDSSRPTVWYHETLEWLKE
EKRRDEHRRRPDHPDFDASTLYVPEDFLNSCTPGMRKWWQIKSQNFDLVICYKVGKIFYELYHMDALIGVSELGLV
FMKGNWAHSGFPEIAFGRYSDSLVQKGKVARVEQTETPEMMEARCRKMAHISKYDRVVRREICRIITKGTQYTYS
VLEGDPSENYSKYLSSLKEKEEDSSGHTRAYGVCFVDTSLGKFFIGQFSDDRHC SRFRTLVAHYPPVQVLFKNGN
LSKETKTILKSSSLCSLQEG LIPGSQFWDASKTLRTLLEEEYFREKLSDGIGVMLPQVLKGMTSESDSIGLTPGE
KSELALSALGGCVFYLLKKCLIDQELLSMANFEEYIPLSDTVSTTRSGAIFTKAYQRMVLDVTLNLEIFLNGT
NGSTEGTLLERVDTCHTPFGKRLKQWLCAPLCNHYAINDRLDAIEDLMVVPDKISEVVELLKKLPDLERLLSKI
HNVGSPLKSQNHPSRAIMYEETYSKKKIIDFLSALEGFKVMCKIIGIMEEVADGFKSKILKQVISLQTKNPEG
RFPDLTVELNRWDTAFDHEKARKTGLITPKAGFSDYDQALADIRENEQSLLEYLEKQRNRIGCRTIVYWGIGRN
RYQLEIPENFTTRNLPEEYELKSTKKGCKRYWTKTIEKKLANLINAEERRDVSLKDCMRRLFYNFDKNYKDWQSA
VECIAVLVDVLLCLANYSRGGDGPMCRPVILLPEDTPPFLELKGSRHPCITKTFFGDDFIPNDILIGCEEEEQENG
KAYCVLVTGPNMGGKSTLMRQAGLLAVMAQMGCVPAEVCRLTPIDRVFTRLGASDRIMSGESTFFVELSETASI
LMHATAHSLVLVDELGRGTATFDGTAIANAVVKELAETIKCRTLFSTHYHSLVEDYSQNVAVRLGHMACMVENEC
EDPSQETITFLYKFIKGACPKSYGFNAARLANLPEEVIQKGRKAREFEKMNQSLRLFREVCLASERSTVDAEAV
HKLLTLIKEL

WO 2004/030615

PCT/US2003/028547

800/6881
FIGURE 746A

GTGAGCTGAAGCAGGGCAGGGCATCAACTCACCCAGGAAGTGCAAGGGGTTTGGGGATTTTCCTTTCTAGCCAA
GGGAAGGCATGACAGACTGTACCTGGAAAAACAGGACACTCTTGCCCAAATACTGCACTTTTTGCACAGTCTTAG
CAACTGGCAGACCAGGAGATTCTCTCTGTGCTTGATTGATTGGGTCCCACACCCATAGGGCCTTGCTTACTGCC
AGTGCAGCAGTCTGAGATTAAACACCCCATCCCCGGGAGAAGCTCTAAGAAGGAGCTGATGTGGAGGAGCAGCTGAG
ACAGTTCAAGATGACGACCACAGTAGCCACAGACTATGACAACATTGAGATCCAGCAGCAGTACAGTGATGTCAA
CAACCGCTGGGATGTCGACGACTGGGACAATGAGAACAGCTCTGCGCGGCTTTTTGAGCGGTCCCGCATCAAGGC
TCTGGCAGATGAGCGTGAAGCCGTGCAGAAGAAGACCTTCACCAAGTGGGTCAATTCCCACCTTGCCCGTGTGTC
CTGCCGGATCACAGACCTGTACACTGACCTTCGAGATGGACGGATGCTCATCAAGCTGCTGGAGGTCTCTCTGG
AGAGAGGCTGCCTAAACCCACCAAGGGACGAATGCGCATCCACTGCTTAGAGAATGTGGACAAGGCCCTTCAGTT
CCTGAAGGAGCAGAGAGTCCATCTTGAGAACATGGGGTCCCATGACATCGTGGATGGAAACCACGGCTGACCTT
TGGCCTCATCTGGACCATCATCCTGCGCTTCCAGATCCAGGATATCAGTGTGGAAACTGAAGACAACAAAGAGAA
GAAATCTGCCAAGGATGCATTGCTGTTGTGGTGCCAGATGAAGACAGCTGGGTACCCCAATGTCAACATTACAA
TTTACCACCTAGCTGGAGGGACGGCATGGCTTCAATGCACTGATACACAAACACCGGCCTGACCTGATAGATTT
TGACAAACTAAAGAAATCTAACGCACACTACAACCTGCAGAATGCATTTAATCTGGCAGAACAGCACCTCGGCCT
CACTAAACTGTTGGACCCCGAAGACATCAGCGTGGACCATCCTGATGAGAAGTCCATAATCACTTATGTGGTGAC
TTATTACCCTACTTCTCTAAGATGAAGGCTTAGCTGTTGAAGGAAAACGAATTGGAAAGGTGCTTGACAATGC
TATTGAAACAGAAAAATGATTGAAAAGTATGAATCACTTGCTCTGACCTTCTGGAATGGATTGAACAAACCAT
CATCATTCTGAACAATCGCAAATTTGCCAATTCAGTGGTTCGGGGTTCAACAGCAGCTTCAGGCATTCAACACTTA
CCGCACTGTGGAGAAACCACCCAAATTTACTGAGAAGGGGAACTTGGAAGTGTGCTCTTACCATTTCAGAGCAA
GATGAGGGCCAAACAACCAGAAGGTCTACATGCCCGGGAGGGGAAGCTCATCTCTGACATCAACAAGGCCTGGGA
AAGACTGGAAAAAGCGGAACACGAAAGAGAACTGGCTTTGCGGAATGAGCTCATAAGACAGGAGAACTGGAACA
GCTCGCCCGCAGATTTGATCGCAAGGCAGCTATGAGGGAGACTTGCTGAGCGAAAACAGCGTCTGGTGTCTCA
GGACAACTTTGGGTTTGACCTTCTGCAAGTTGAGGCGCCACAAAAAGCACGAGGCCATTGAGACAGACATTGC
CGCATACGAGGAGCGTGTGCAAGGCTGTGGTAGCCGTGGCCAGGGAGCTCGAGGCCGAGAATTACCACGACATCAA
GCGCATCACAGCGAGGAAGGACAATGTATCCGGCTCTGGGAATACCTACTGGAAGTGTCTAGGGCCCGGAGACA
GCGGCTCGAGATGAACCTGGGGCTGCAGAAGATATTCAGGAAATGCTCTACATTATGGACTGGATGGATGAAAT
GAAGGTGCTAGTATTGTCTCAAGACTATGGCAAACACTTACTTGGTGTGGAAGACCTGTACAGAAGCACACCCT
GGTTGAAGCAGACATTGGCATCCAGGCAGAGCGGGTGAGAGGTGTCAATGCCTCCGCCAGAAAGTTCGCAACAGA
CGGGGAAGGTTACAAGCCCTGTGACCCCAAGGTGATCCGAGACCGCGTGGCCACATGGAGTTCTGTTATCAAGA
GCTTTGCCAGCTGGCGGCTGAGCGCAGGGCCGCTGGAAGAGTCCCGCCGCTCTGGAAGTTCTTCTGGGAGAT
GGCAGAAGAGGAAGGCTGGATACGGGAGAAGGAGAAGATCCTGTCTCGGACGATTACGGGAAGACGATTGACCAG
CGTCATGCGCCTGCTCAGCAAGCACCGGGCGTTCGAGGACGAGATGAGCGGCCGAGTGGCCACTTTGAGCAGGC
CATCAAGGAAGGCGAAGACATGATCGCGAGGAGCACTTCGGGTCGGAGAAGATCCGTGAGAGGATCATTACAT
CCGGGAGCAGTGGGCCAACCTAGAGCAGCTCTCGGCCATTCCGGAAGAAGCGCCTGGAGGAGGCCTCCCTGCTGCA
CCAGTTCCAGGCAGATGCTGATGACATTGATGCCTGGATGCTGGACATCCTCAAGATTGTCTCCAGCAGCGACGT
GGGCCACGATGAGTATTCACACAGTCTCTGGTCAAGAAACACAAGGACGTGGCGGAAGAGATCGCCAATTACAG
GCCACCCCTTGACACGCTGCACGAACAAGCCAGCGCCCTCCCCAGGAGCATGCCGAGTCTCCAGACGTGAGGGG
CAGGCTGTGCGGCATCGAGGAGCGGTATAAGGAGGTGGCAGAGCTGACGCGGCTGCGGAAGCAGGCACTCCAGGA
CACTCTGGCCCTGTACAAGATGTTGAGCGAGGCTGATGCCTGTGAGCTCTGGATCGACGAGAAGGAGCAGTGGCT
CAACAACATGCAGATCCAGAGAAGCTGGAGGATCTGGAGGTGATCCAGCACAGATTTGAGAGCCTAGAACCAGA
AATGAACAACCAGGCTTCCCGGTTGCAAGGTGAACCAGATTGCACGCCAGCTGATGCACAGCGGCCACCCAAG
TGAGAAGGAAATCAAGCCAGCAGGACAACTCAACACAAGGTGGAGCCAGTTTCAGAGAAGTGGTTGACAGGAA
GAAGGATGCCCTCCTGTCTGCCCTGAGCATCCAGAATAACACCTCGAGTGCAATGAAACCAAATCCTGGATTGCG
GAAAAAGACCAAGGTCTATCGAGTCCACCCAGGACCTGGGCAATGACCTGGCTGGCGTCATGGCCCTGCAGCGCAA
GCTGACCGGCAATGGAGCGGACTTGGTGGCCATTGAGGCAAGCTGAGTGACCTGCAGAAGGAGGCGGAGAAGCT
GGAGTCCGAGCACCCCGACAGGCCAGGCCATCCTGTCTCGGCTGGCCGAGATCAGCGACGTGTGGGAGGAGAT
GAAGACCACCCTGAAAAACCGAGAGGCCTCCCTGGGAGAGGCCAGCAAGCTGCAGCAGTTCTACGGGACTTGGA
CGACTTCCAGTCCCTGGCTCTCTAGGACCCAGACAGCGATCGCTCGGAGGACATGCCAAACACCCTGACCGAGGC

WO 2004/030615

PCT/US2003/028547

801/6881
FIGURE 746B

TGAGAAGCTGCTCACGCAGCACGAGAACATCAAGAATGAGATCGACAACACTACGAGGAGGACTACCAGAAGATGAG
GGACATGGGCGAGATGGTCACCCAGGGGAGACCGATGCCCAGTACATGTTTCTGCGGCAGCGGCTGCAGGCCCT
GGACACTGGATGGAACGAGCTCCACAAGATGTGGGAGAACAGACAAAATCTCCTATCCCAGTCACATGCCTACCA
GCAGTTCTCAGAGACACGAAGCAAGCCGAAGCCTTTCTTAACAACAGGAGTATGTTCTGGCTCACACTGAAAT
GCCTACCACCTTGAAGGAGCTGAAGCAGCAATTAAAAAGCAAGAGGACTTCATGACCACCATGGACGCCAATGA
GGAGAAGATCAATGCTGTGGTGGAGACTGGCCGGAGGCTGGTGAGCGATGGGAACATCAACTCAGATCGCATCCA
GGAGAAGGTGGACTCTATTGATGACAGACATAGGAAGAAATCGTGAGACAGCCAGTGAACCTTTTGATGAGGTTGAA
GGACAACAGGGATCTACAGAAATTCCTGCAAGATTGTCAAGAGCTGTCTCTCTGGATCAATGAGAAGATGCTCAC
AGCCCAGGACATGTCTTACGATGAAGCCAGAAATCTGCACAGTAAATGGTTGAAGCATCAAGCATTATGGCAGA
ACTTGCATCCAACAAAGAATGGCTTGACAAAATCGAGAAGGAAGGAATGCAGCTCATTTCAGAAAAGCCTGAGAC
GGAAGCTGTGGTGAAGGAGAACTCACTGGTTTACATAAAATGTGGGAAGTCCTTGAATCCACTACCCAGACAAA
GGCCCAGCGGCTCTTTGATGCAAACAAGGCCGAACCTTTTACCCAGAGCTGTGCAGATCTAGACAAATGGCTGCA
CGGCTGGAGAGTCAGATTCACTGTGATGACTATGGCAAAACACCTGACCAGTGTCAATATCCTGCTGAAAAAGCA
ACAGATGCTGGAGAATCAGATGGAGTGCGGAAGAAGGAGATCGAAGAGCTCCAAAGCCAAGCCCAGGCCCTGAG
TCAGGAAGGGAAGAGCACCGACGAGGTAGACAGCAAGCGCTCACCGTGCAGACCAAGTTCATGGAGTTGCTGGA
GCCCTTGAACGAGAGGAAGCATAACCTGCTGGCCTCCAAAGAGATCCATCAGTTCAACAGGGATGTGGAGGACGA
GATC1TGTGGGTTGGAGAGAGGATGCCCTTGGCAACTTCCACGGATCATGGCCACAACCTCCAGACTGTGCAGCT
GTTAATAAAGAAAAATCAGACCCCTCCAGAAAGAAAATCCAGGGGACACAGCCTCGCATTGACGACATCTTTGAGAG
GAGCCAAAACATCGTCACTGACAGCAGCAGCCTCAGCGCTGAGGCCATCAGACAGAGGCTTGCCGACCTGAAGCA
GCTGTGGGGTCTCCTCATTGAGGAGACAGAGAAACGCCACAGGCGGCTGGAGGAGGCGCACAGGGCCCAGCAGTA
CTACTTTGACGCTGCTGAGGCCGAAGCCTGGATGAGCGAGCAGGAGCTGTACATGATGTGAGGAGAGAAGGCCAA
GGATGAGCAGAGTGTGTCTCCATGTTGAAGAAGCACCAGATCTTAGAACAAGCTGTGGAGGACTATGCAGAGAC
CGTGATCAGCTCTCCAAGACCAGCCGGGCCCTGGTGGCCGACAGCCATCCTGAAAGTGAGCGCATTAGCATGCG
GCAGTCCAAGTGGATAAACTGTACGCTGGTCTGAAAGACCTTGCTGAAAGAGAGAAGAGGCAAGCTGGATGAGAG
ACACAGGTTATTCCAGCTCAACCGGAGGTGGACGACCTGGAGCAGTGGATCGCTGAGAGGGAGGTGGTCGCAGG
GTCCCATGAACTGGGACAGGACTATGAGCATGTACGATGTTACAAGAACGATTCCGGGAGTTTGCCCGAGACAC
CGGGAACATTGGGACAGGAGCGGTGGACACGGTCAATCACCTGGCAGATGAGCTCATCAACTCTGGACATTGAGA
TGCCGCCACCATCGTGAATGGAAGGATGGCCTCAATGAAGCCTGGGCCGACCTCCTGGAGCTATTGACACAAG
AACACAGATTCTTGCCGCTTCTATGAACTGCACAAGTTTACCACGATGCCAAGGAGATCTTTGGGCGTATACA
GGACAAACACAAGAACTCCCTGAGGAGCTTGGGAGAGATCAGAACACAGTGGAGACCTTACAGAGAATGCACAC
TACATTTGAGCATGACATCCAGGCTCTGGGCACACAGGTGAGGCAGCTGCAGGAGGATGCAGCCCGCCTCCAGGC
GGCCTATGCGGGTGACAAGGCCGACGATATCCAGAAGCGGAGAACGAGGTCTTGAAGCCTGGAAGTCCCTCCT
GGACGCCGTGAGAGCCGACGGTGCGGCTGGTGACACAGGGGACAAGTTCCGCTTCTTACAGCATGGTGCGCGA
CCTCATGCTCTGGATGGAGGATGTCATCCGGCAGATCGAGGCCACGAGAAGCCAAGGGATGTATCATCTGTTGA
ACTCTTAATGAATAATCATCAAGGCATCAAAGCTGAAATTGATGCACGTAATGACAGTTTACAACCTGCATTGA
ACTTGGGAAATCCCTGTTGGCGAGAAAACACTATGCATCTGAGGAGATCAAGGAAAAATTAAGTGCAGTTGACGGA
AAAGAGGAAAGAAATGATCGACAAGTGGGAAGACCGATGGGAATGGTTAAGACTGATTCTGGAGGTCCATCAGTT
CTCAAGAGACGCCAGTGTGGCCGAGGCTGGCTGCTTGGACAGGAGCCGTACCTATCCAGCCGAGAGATAGGCCA
GAGCGTGGACGAGGTGGAGAAGCTCATCAAGCGCCACGAGGCATTTGAAAAGTCTGCAGCAACCTGGGATGAGAG
GTTCTCTGCCCTGGAAAGGCTGACTACATTGGAGTTACTGGAAGTGCGCAGACAGCAAGAGGAAGAGGAGAGGAA
GAGGCGGCGCCCTTCTCCCGAGCCGAGCACGAAGGTTTACAGAGGAAGCCGAGTCCAGCAGCAGTGGGATACTTC
AAAAGGAGAAACAAGTTTCCCAAAACGGTTTGCCAGCTGAACAGGGATCTCCACGGATGGCAGAAACGGTGGACAC
AAGCGAAATGGTCAACGGCGCTACAGAACAAAGGACGAGCTCTAAAGAGTCCAGCCCCATCCCCTCCCCGACCTC
TGATCGTAAAGCCAAGACTGCCCTCCAGCCAGAGTGCCGCCACCTTACCAGCCAGAACCAGGAGACACCTTC
GGCCAGATGGAAGGCTTCTCAATCGGAAACACGAGTGGGAGGCCCAATAAGAAAGCCTCAAGCAGGTCTTG
GCACAAATGTTTATTGTGTATAAATAACCAAGAAATGGGTTTCTACAAAGATGCAAAGACTGCTGCTTCTGGAAT
TCCCTACCACAGCGAGGTCCCTGTGAGTTTGAAGAAGCTGTCTGCGAAGTGGCCCTTGATTACAAAAAGAAGAA
ACACGTATTCAAGCTAAGACTAAATGATGGCAATGAGTACCTCTTCCAAGCCAAAGACGATGAGGAAATGAACAC

WO 2004/030615

PCT/US2003/028547

802/6881
FIGURE 746C

ATGGATCCAGGCTATCTCTTCCGCCATCTCCTCTGATAAACACGAGGTGTCTGCCAGCACCCAGAGCACGCCAGC
ATCCAGCCGCGCGCAGACCTCCCCACCAGCGTCGTCACCATCACCAGCGAGTCCAGTCCCGGCAAGCGGGAAAA
GGACAAAGAGAAAAGACAAAGAGAAGCGGTTTCAGCCTTTTTGGCAAAAAGAAATGA~~ACT~~CTCTTCCTTCACCTCCT
GCCCTTCTCTTACCTTTTCAGTGAAATTCCAGCATGCAAGCTCAGAACCAACACATTACTCTCTGTGCCTAATGT
TCCTCAATGTGGTTGATTTATTTTTTTTTTTAATTTATAGAGCATTTCTGGGGGGGGTGGGG

WO 2004/030615

PCT/US2003/028547

803/6881
FIGURE 747

MTTTVATDYDNIEIQQQYSDVNNRWDVDDWDNENSSARLFERSRIKALADEREAVQKKFTTKWVNSHLARVSCRI
TDLYTDLRDGRMLIKLLEVLSSGERLPKPTKGRMRIHCLENVDKALQFLKEQRVHLENMGSHDIVDGNHRLTLGLI
WTIILRFQIQDISVETEDNKEKKSADALLLWCMKTAGYPNVNIHNFTTSWRDGMFALIHKHRPDLIDFDKL
KKSNAHYNLQNAFNLAEQHLGLTKLLDPEDISVDHPDEKSIITYVVITYHYFSKMALAVEGKRIGKVLDNAIET
EKMIKEYESLASDLEWIEQTIIILNNRKFANSLVGVQQQLQAFNTYRTVEKPPKFTEKGNLEVLLFTTIQSKMRA
NNQKVYMPREGKLISDINKAWERLEKAEHERELALRNELIRQEKLEQLARRFDRKAAMRETWLSNQRLVSQDNF
GFDLPAVEAATKKHEAIEDIAAYEERVQAVVAVARELEAENYHDIKRITARKDNVIRLWEYLLELLRARRQRLE
MNLGLQKIFQEMLYIMDWMDEMKVVLVSQDYGKHLGVEDLLQKHTLVEADIGIQAERVGVNASAQKFATDGEG
YKPCDPQVIRDRVAHMEFCYQELCQLAAERRARLEESRRLWKFFWEMAE EEGWIREKEKILSSDDYGKDLTSVMR
LLSKHRAFEDEMSGRSGHFEQAIKEGEDMIAEEHFGESEKIRERIIYIREQWANLEQLSAIRKKRLEEASLLHQFQ
ADADDIDAWMLDILKIVSSSDVGHDEYSTQSLVKKHKDVAEEIANYPRTLDTLHEQASALPQEHASPOVRGRLS
GIEERYKEVAELTRLRKQALQDITLALYKMFSEADACELWIDEKEQWLNMMQIPEKLEDLEVIQHRFESLEPEMNN
QASRVAVVNQIARQLMHSGHPSEKEIKAQQDKLNTRWSQFRELVDKRDALLSALSQNYHLECNETKSWIREKT
KVIESTQDLGNDLAGVMALQKRLTGMRDLVAIEAKLSDLQKEAEKLESEHPDQAQAILSRALIESDVWEEMKTT
LKNREASLGASKLQQFLRDLDLDFQSWLSRTQTAIASEDMPNTLTAEKLLTQHENIKNEIDNYEEDYQKMRDMG
EMVTQGGTDAQYMFRLRQLQALDTGWNELHKMWENRQNLSSQSHAYQQFLRDTKQAEAFLLNNQYVLAHTEMPTT
LEGAEAAIKKQEDFMTTMDANEEKINAVVETGRRLVSDGNINSRIQEKVDSIDDRHRKNRETASELLMRLKDNR
DLQKFLQDCQELSLWINEKMLTAQDMSYDEARNLHSHKWLKHQAFMAELASNKEWLDKIEKEGMQLISEKPETEAV
VKEKLTGLHKMWEVLESTTQTKAQLRFDANKAELFTQSCADLDKWLHGLESQIQSDDYGKHLTSVNILLKKQQML
ENQMEVRKKEIEELQSQQAALSQEGKSTDEVDSKRLTVQTKFMELLEPLNERKHNLLASKEIHQFNRDVEDEILW
VGERMPLATSTDHGHNLQTVQLLIKKNQTLQKEIQGHQPRIDDIFERSQNIIVTDSSSLSAEAIQRQLADLKQLWG
LLIEETEKRRHRLLEEAHRAQQYYFDAAEAEAWMSEQELYMMSEEKAKDEQSAVSMLKKHQILEQAVEDYAETVHQ
LSKTSRALVADSHPESEIRISMRQSKVDKLYAGLKDLAEERRGKLDERHRLFQLNREVDDLEQWIAEREVVAGSHE
LGQDYEHVTMLQERFREFARDTGNIGQERVDTVNHLEDELINSGHSDAATIAEWKDGLNEAWADLLELIDTRTQI
LAASYELHKFYHDAKEIFGRIQDKHKKLPEELGRDQNTVETLQRMHTTFEHDIQALGTQVRQLQEDAARLQAAYA
GDKADDIQKRENEVLEAWKSLLDACESRRVRLVDTGDKFRFFSMVRDLMLWMEDVIRQIEAQEKPRDVSSVELLM
NNHQGIKAEIDARNDSTTCIELGKSLLARKHYASEEIKEKLLQLTEKRKEMIDKWEDRWELRLILEVHQFSRD
ASVAEAWLLGQEPYLSREIGQSVDEVEKLIKREHAEFEKSAATWDERFSALERLTLELLEVRQQEERKRPP
PSPEPSTKVSEEAESQQQWDTSKGEQVSQNGLPAGEQSPRMAETVDTSEMVGATEQRTSSKESSPIPSPTSDRK
AKTALPAQSAATLPARTQETPSAQMEGFLNRKHWEAHNKKASSRSWHNVYCVINNQEMGFYKDAKTAASGIPYH
SEVPVSLKEAVCEVALDYKKKKHVFKLRLNDGNEYLFQAKDDEEMNTWIQAISSAISSDKHEVSASTQSTPASSR
AQTLPTSQVTTITSESSPGKREKDKKDKKRFSLFGKKK

WO 2004/030615

PCT/US2003/028547

804/6881
FIGURE 748

CACAACCGCCCGCGGCTCTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATCTCCACCCTCCAGC
CATGGAAGACGAGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCT
GGAGAGGAAGCCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCCCACCGCCCCCTGCCGCCGGCGCGCCCCCTGATGGA
CTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCGCTCGCCCCGGAGCGGCA
GCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCC
CTCCAAGCTCCCTGAGGACGACGAGCCTCCGGCCCCGG

WO 2004/030615

PCT/US2003/028547

805/6881
FIGURE 749

TTCTTCCTTTTCGATCCGCCATCTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGA
AGACCATCACCCCTCGAGGTTGAACCCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAA
TTCTTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGGACGTACTTTGTCTGACTACAATA
TTCAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACA
CCACTCCCAAGAAGAATAAGCACAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGA
ATGGCAAAATTAGTCGCCTTCGTGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGCAAGTCACT
TTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGACAAGTAACTGTATGAGT
TAATAAAAGACATGAACTAACAAAAA

WO 2004/030615

PCT/US2003/028547

806/6881
FIGURE 750

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYNIQKESTLHLVLRRLRG
GAKKRRKKKSYTTPKKNKHKKKKVLAFLKYYKVDENGKISRLRRECPSECGAGVFMASHFDRHYCGKCCLTYCF
NKPEDK

WO 2004/030615

PCT/US2003/028547

807/6881
FIGURE 751

GGCACGAGCAGAATCCAGGGGCCCGGGGCTGTAGATTCTTGACAAGGATATCCTAGCGGCGAAACAACACCGTA
CTGGGAGTCAGAACGTCTGGGTTCTAGTCTTGACTGCCATTAACTAGCGGTATGACATTGGAGAAGCTTTTTTGA
CCCTTCTGGATTTCCGTTTCTTTTCTGTAAAATGAGGAGCTTGGAAGATCCGGAAAATGAGGCCCATAGGAAAC
AAGTGACTTGCTGAGTCCAGATAACACTGACTGTCAGAGAGAAACCATGAACCAGAAGCTACTGAAGTTGGAGAAC
TTGCTACGATTTACACTATTTATAGGCAACTGCACAGTCTGTGTCAAAGAAGAGCATTAAAGACAGTGGAGGCAT
GGGTTTTTCATCTGCTTACCCTGTGTGGACAGCTCAACTGTGTGCCCTGGCCCTGGCCAACAGATGTGCTCAATGGG
GCTGCTTTATCTCAGTATAGGCTTCTAGTAACAAAAAAGGAAGAAGGACCATGGAAATCTCAGTTATCTTCAACA
AAATCTAAAAAGGTGGTAGAAGTATGGATTGGAATGACTATTGAGGAACTGGCCAGGGCAATGGAAAAAACACA
GATTATGTATATGAAGCTTTATTGAACACTGATATTGACATAGATTCACTGGAAGCAGACTCACATTTAGATGAA
GTCTGGATCAAAGAAGTGATAACGAAGGCAGGGATGAAGTTAAAGTGGAGTAAATTAAAAACAGGACAAAGTCAGA
AAAAATAAAGATGCTGTAAAGAAGGCCCCAGGCAGATCCAGCTTTATTAAACCCCAAGGTCCCCAGTTGTTACTATA
ATGGGCCATGTTGATCACGGGAAAACGACATTACTTGACAAATTTCGAAAACTCAAGTGGCAGCAGTGGAACT
GGAGGCATCACTCAGCACATTGGTGCCTTTCTTGCTCTCTGCTTCTGGGGAAAAGATAACTTTTCTTGATACT
CCAGGACATGCTGCTTTCTCAGCAATGAGAGCCAGAGGTGCTCAGGTCACTGACATTGTCTGATTGGTTGTAGCT
GCAGATGATGGAGTGATGAAACAACTGTAGAATCTATTGAGCATGCCAAAGATGCACAGGTTCTATTATCCTT
GCCGTAAATAAATGTGACAAAGCTGAGGCTGATCCTGAGAAAGTGAAAAAGAGCTGCTGGCTTACGATGTGGTA
TGTGAAGATTATGGAGGTGATGTTCAAGCAGTGCTGTCTCCGCACTTACGGGCGATAATCTGATGGCTTTGGCA
GAAGCAACAGTTGCTCTTGCAAGAAATGTTAGAATTGAAAGCAGATCCCAATGGTCCAGTGGAAGGAACAGTAATA
GAGTCTTTACAGACAAAGGAAGAGGTCTTGTTACTACAGCTATAATTCAAAGAGGAACTTTAAGAAAAGGCTCT
GTTCTGGTTGCTGGAAATGTTGGGCAAAAGTACGCTTAATGTTTGATGAAAATGGAAAAACAATTGATGAGGCC
TATCCCAGCATGCCAGTGGGAATTACAGGCTGGAGAGACCTTCTTCTGCAGGAGAAGAAATCTTGAAGTAGAA
TCTGAGCCAAGGGCACGTGAAGTTGTTGACTGGAGGAAATATGAACAAGAACAGGAGAAAGGTCAGGAGGATCTG
AAAATAATAGAAGAAAAGCGAAAGGAACACAAAGAACATCAGAAAGCCCGTGAGAAGTATGGCCATCTACTG
TGGAAGAAGAGATCAATTCTACGGTTTTTAGAAAGAAAAGAACAAATACCCTTAAAGCCAAAAGAGAAAAGGGAA
AGAGATTCAAATGTACTTTCTGTGATTATTAAAGGTGATGTTGATGGTTCTGTTGAGGCCATTTTGAACATTATA
GATACCTATGATGCTTCACACGAGTGTGAAGTAGAATTAGTACATTTGGAGTGGGTGATATAAGTGCAAATGAT
GTTAACCTTGCTGAAACATTTGATGGTGTATATATGGCTTTAATGTGAATGCAGGCAATGTTATCCAACAGTCA
GCTGCAAAAAAGGAGTAAAAATTAACTTCACAAAATAATTTACCGTCTTGTTGAAGATTGCAAGAGGAACTG
AGCAGCAGATTACCCTGTGCTGTGGAAGAGCACCCAGTAGGTGAGGCATCTATACTAGCTACCTTCTCTGTAAACA
GAAGGGAAGAAAAAGTTCTGTGGCTGGCTGCAGAGTCCAAAAGGGACAGTTAGAAAAACAAAAAAATTTAAA
CTAACCCGTAATGGACATGTAATTTGGAAGGGCTCATTAACTCATTGAAACACCATAAAGATGACATTTCAATT
GTCAAAACGGGAATGGATTGTGGTCTCAGTTTAGATGAAGACAATATGGAATTTCAAGTGGGAGACAGAATTGTT
TGTTATGAAGAAAAGCAAATTCAGCCAAGACTTCTTGGGATCCAGGATTTTTAAAAATTACATTAAAAATGTAAAT
AACTCA

WO 2004/030615

PCT/US2003/028547

808/6881
FIGURE 752

MNQKLLKLENLLRFHTIYRQLHSLCQRRALRQWRHGFSSAYPVWTAQLCAWPWPTDVLNGAALSQYRLLVTKKEE
GPWKSQLSSTKSKKVVEVWIGMTIEELARAMEKNTDYVYEALLNTDIDIDSLEADSHLDEVWIKVITKAGMKLK
WSKLGQDKVRKNKDAVRRPQADPALLTPRSPVVTIMGHVDHGKTLLDKFRKTQVAAVETGGITQHIGAFVSLP
SGEKITFLDTPGHAAF SAMRARGAQVTDIVVLVVAADDGVMKQTVESIQAHAQVPIILAVNKCDKAEADPEKV
KKELLAYDVVCEDYGGDVQAVPVSALTGDNLMALAEATVALAEMLELKADPNPVEGTVIESFTDKGRGLVTTAI
IQRGTLRKGSVLVAGKCWAKVRLMFDENGKTIDEAYPSMPVGITGWRDLPSAGEEILEVESEPRAREVVDWRKYE
QEKEKGQEDLKIIIEKRKEHKEAHQKAREKYGHLLWKKRSILRFLERKEQIPLKPKEKRERDSNVLSVIKGDVD
GSVEAILNIIDTYDASHECELELVHFGVGDISANDVNLAETFDGVIYGFNVNAGNVIQQSAAKKGVKIKLHKIY
RLVEDLQEELSSRLPCAVEEHPVGEASILATFSVTEGKKKVPVAGCRVQKGQLEKQKKFKLTRNGHVIWKGSLTS
LKHHKDDISIVKTGMDCLSLDEDNMEFQVGDRIVCYEEKQIQAKTSWDPGF

WO 2004/030615

PCT/US2003/028547

809/6881
FIGURE 753

GCGTGCCGGGTGTCATGGCGGCCTGCAGGTACTGCTGCTCGTGCCCTCCGGCTCCGGCCCCCTGAGCGATGGTCCTT
TCCTTCTGCCACGGCGGGATCGGGCACTCAGGAGTTGCAAGTGCGAGCACTATGGAGTAGCGCAGGGTCTCGAG
CTGTGGCCGTGGACTTAGGCAACAGGAAATTAGAAATATCTTCTGGAAAGCTGGCCAGATTTGCAGATGGCTCTG
CTGTAGTACAGTCAGGTGACACTGCAGTAATGGTCACAGCGGTGAGTAAACAAAACCTTCCCCTTCCAGTTTA
TGCCTTTGGTGGTTGACTACAGACAAAAGCTGCTGCAGCAGGTAGAATTCCCACAACTATCTGAGAAGAGAGA
TTGGTACTTCTGATAAAGAAATCTAACAAAGTCGAATAATAGATCGTTCAATTAGACCGCTCTTTCCAGCTGGCT
ACTTCTATGATACACAGGTTCGTGTAACTGTTAGCAGTAGATGGTGTAATGAGCCTGATGTCCTAGCAATTA
ATGGCGCTTCCGTAGCCCTCTCATTATCAGATAATCCTTGGAAATGGACCTGTTGGGGCAGTACGAATAGGAATAA
TTGATGGAGAATATGTTGTTAAACCAACAAGAAAAGAAATGCTTCTAGTACTTTAAATTTAGTGGTTGCTGGAG
CACCTAAAAGTCAGATTGTATGTTGGAAGCCTCTGCAGAGAACATTTTACAGCAGGACTTTTGCCATGCTATCA
AAGTGGGAGTGAAATATACCCAAACAAATAATTCAGGGCATTTCAGCAGTTGGTAAAAGAACTGGTGTTACCAAGA
GGACACCTCAGAAAGTTATTTACCCCTTCGCCAGAGATTGTGAAATATACTCATAAACTTGCTATGGAGAGACTCT
ATGCAGTTTTTACAGATTACGAGCATGACAAAGTTTCCAGAGATGAAGCTGTTAAACAAAATAAGATTAGATACGG
AGGAACAACATAAAAGAAAAATTTCCAGAAGCCGATCCATATGAAATAATAGAATCCTTCAATGTTGTTGCAAAGG
AAGTTTTTAGAAGTATTGTTTTGAATGAATACAAAAGGTGCGATGGTCCGGGATTTGACTTCACTTAGGAATGTAA
GTTGTGAGGTAGATATGTTTAAAACCTTCATGGATCAGCATTATTTCAAAGAGGACAAACACAGGTGCTTTGT
CCGTACATTTGATTTCATTAGAATCTGGTATTAAGTCAGATCAAGTTATAACAGCTATAAATGGGATAAAAGATA
AAAATTTTCATGCTGCACTACGAGTTTCCCTCCTTATGCAACTAATGAAATTGGCAAAGTCACTGGTTTAAATAGAA
GAGAACTTGGGCATGGTGCTCTTGCTGAGAAAGCTTTGTATCCTGTTATTTCCCGAGATTTTCCCTTTCACCATAA
GAGTTACATCTGAAGTCCTAGAGTCAAAATGGGTCATCTTCTATGGCATCTGCATGTGGCGGAAGTTTAGCATTAA
TGGATTACAGGGGTTCCAATTTTCATCTGCTGTTGCGAGGCTAGCAATAGGATTGGTCACCAAAACCGATCCTGAGA
AGGGTGAAATAGAAGATTATCGTTTGCTGACAGATATTTTGGGAATTGAAGATTACAATGGTGACATGGACTTCA
AAATAGCTGGCACTAATAAAGGAATAACTGCATTACAGGCTGATATTAATTAACCTGGAATACCAATAAAAATTG
TGATGGAGGCTATTCAACAAGCTTCAGTGGCAAAAAGGAGATATTACAGATCATGAACAAAACCTATTTCAAAC
CTCGAGCATCTAGAAAAGAAAATGGACCTGTTGTAGAACTGTTTCAAGTTCCATTATCAAACGAGCAAAATTTG
TTGGACCTGGTGGCTATAACTTAAAAAACTTCAGGCTGAAACAGGTGTAACCTATTAGTCAGGTGGTAGAAGAA
CGTTTTCTGATTTTGACCAACACCCAGTGCTATGCATGAGGCAAGAGACTTCATTACTGAAATCTGCAAGGATG
ATCAGGAGCAGCAATTAGAATTTGGAGCAGTATATACCGCCACAATAACTGAAATCAGAGATACTGGTGTAATGG
TAAATTTATATCCAAATATGACTGCGGTACTGCTTCATAACACACAACCTTGATCAACGAAAGATTAAACATCCTA
CTGCCCTAGGATTAGAAGTTGGCCAAGAAATTCAGGTGAAATACTTTGGACGTGACCCAGCCGATGGAAGAATGA
GGCTTTCTCGAAAAGTGCTTCAGTCGCCAGCTACAACCGTGGTCAGAACCTTGAATGACAGAAGTAGTATTGTAA
TGGGAGAACCTATTTACAGTCATCATCTAATTTCTCAGTGATTTTTTTTTTAAAGAGAATTCTAGAATTCTATT
TTGTCTAGGGTGATGTGCTGTAGAGCAACATTTTAGTAGTATCTTCCATTGTGTAGATTTCTATATAATATAAAT
ACATTTTAATTATTTGTACTAAAATGCTCATTACATGTGCCATTTTTTTTAAATTCGAGTAACCCATATTTGTTTA
ATTGTATTTACATTATAAATCAAGAAATATTTATTATTAAGTAAGTCATTTATACATCTTAGAAAAAATTACA
TAGTTTTGTTTTTACAATTTGAAATATATGAAAACTTAGATAGAATATGTCATATGTTATTATAACAGATCTC
TTCTACATCTTATTTTTCTTTCTTTGTATACAGTAGTGACAGTTTACCTTCAGTCATCTACAGGTCACCTCTGT
GCCCAACAACCTTTACTTGCCTACAACGGTTTCACAACTGGAACAGGCCATATTCAAAGCCAGTGCCTATTTCTTC
AGAAGTGTAAACAGATATAGTGAGTTGAGGGAGCTAATCTGATACACTTTTGATAATATAATGCCTTTCAAATTA
GTTACCAAAATCATAAACAGAGTGGAATAAATATAAATGAGATTCTAACTAGGATGAATGTGGTAGTAATGATGTA
TATTTTTCAAATTTACCTAAACAGAAAGATTATTGGCTAAGGCAGGCGGATCATGAGATCAGGAGATCGAGACCA
TCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAGTGCAAAAATTAGCCGGGCGTGGTGGCGCATGCCTGTA
ATCCTAGCTACTCAGGAGGCTGAGGCAGAAAGATCACTTCAACCCAGGAGGTGGAGGTTGTAGTGAGCCGAGATT
GCGCCATTGCACTCCAGCTCAGGCAACAAGAGCAAAAACCTCCGTCTC

WO 2004/030615

PCT/US2003/028547

810/6881
FIGURE 754

MAACRYCCSCLRLRPLSDGPFLLPRDRALTQLQVRALWSSAGSRAVAVDLGNRKLEISSGKLARFADGSAVVQS
GDTAVMVTAVSKTKPSPSQFMPLVVDYRQKAAAAGRIPTNYLRREIGTSDKEILTSRIIDRSIRPLFPAGYFYDT
QVLCNLLAVDGVNEPDVLAINGASVALSLSDIPWNGPVGAVRIGIIDGEYVVNPTRKEMSSSTLNLVVAGAPKSQ
IVMLEASAENILQQDFCHAIKVGVKYTQQIIQGIQQLVKETGVTKRTPQKLFTPSPEIVKYTHKLAMERLYAVFT
DYEHDKVS RDEAVNKIRLDTEEQLKEKFPEADPYEIIESFNVVAKEVFRSIVLNEYKRCDGRDLTSLRNVSCVD
MFKTLHGSALFQRGQTQVLCVTTFDSLESGIKSDQVITAINGIKDKNFMLHYEFPPYATNEIGKVTGLNRRELGH
GALAEKALYPVIPRDFPFTIRVTSEVLESNGSSSMASACGGSLALMDSGVPIS SAVAGVAIGLVTKTDPEKGEIE
DYRLTDLILGIEDYNGDMDFKIAGTNKGITALQADIKLPGIPIKIVMEAIQQASVAKKEILQIMNKTISKPRASR
KENGPPVETVQVPLSKRAKFVGGYNLKKLQAETGVTISQVDEETF SVFAPTPSAMHEARDFITEICKDDQEQQ
LEFGAVYTATITEIRD TGVMVKLYPNMTAVLLHNTQLDQRKIKHPTALGLEVGQEIQVKYFGRDPADGRMRLSRK
VLQSPATTVVRTLNDRSSIVMGEPISQSSNSQ

WO 2004/030615

PCT/US2003/028547

811/6881
FIGURE 755

GACAAGATGGCCACACCGGCGGTACCAGCAAGTGCTCCTCCGGCCACGCCAGCCCCAGTCCCGGCGGCGGTCCCA
GCCTCTGCCCCAGCCTCAGTTCCAGCGCCAACGCCAGCACCGGCTGCGGCTCCGGTTCCCGCTGCGGCTCCAGCC
TCATCCTCAGACCCTGCGGCAGCATCGGCTACAAC TGCGGCTCCTGGCCAGACCCCGGCCTCAGCGCAAGCTCCA
GCGCAGACCCAGCGCCCCGCTCTGCCTGGTCTGCTCTTCCAGGGCCCTTCCCCGGCGGCGCGTGGTCAGGCTG
CACCCAGTCATTTTGGCCTCCATTGTGGACAGCTACGAGAGACGCAACGAGGGTGCTGCCCGAGTTATCGGGACC
CTGTTGGGAACTGTCGACAAACACTCAGTGGAGGTCACCAATTGCTTTTTCAGTGCCGCACAATGAGTCAGAAGAT
GAAGTGGCTGTTGACATGGAATTTGCTAAGAATATGTATGAACTGCATAAAAAAGTTTCTCCAAATGAGCTCATC
CTGGGCTGGTACGCTACAGGCCATGACATCACAGAGCACTCTGTGCTGATCCATGAGTACTACAGCCGAGAGGCC
CCCAACCCCATCCACCTCACTGTGGACACAAGTCTCCAGAACGGCCGCATGAGCATCAAAGCCTATGTCAGCACT
TTAATGGGTGTCCCTGGGAGGACCATGGGAGTGATGTTTACACCTCTGACAGTGAAATACGCATACTATGACACT
GAACGCATCGGAGTTGAGCTGATCATGAAGACCTGCTTTAGCCCCAACAGAGTGATTGGACTCTTAAGTGACTTG
CAGCAAGTAGGAGGGGCATCAGCTCGCATCCAGGATGCCCTGAGTACAGTGTTGCAATATGCAGAGGATGTACTG
TCTGGAAAGGTGTCAGCTGACAATACTGTGGGCCGCTTCCTGATGAGCCTGGTTAACCAGGTACCGAAAAATAGTT
CCCGATGACTTTGAGACCATGCTCAACAGCAACATCAATGACCTTTTGATGGTGACCTACCTGGCCAACCTCACA
CAGTCACAGATTGCCCTCAATGAAAACTTGTAACCTGTGAATGGACCCCAAGCAGTACACTTGCTGGTCTAGG
TATTAAACCCAGGACTCAGAAGTGAAGGAGAAATGGGTTTTTGTGGTCTTGAGTCACACTGAGATAGTCAGTTG
TGTGTGACTCTAATAAACGGAGCCTACCTTTTGT

WO 2004/030615

PCT/US2003/028547

812/6881
FIGURE 756

MATPAVPASAPPATPAPVPAAVPASAPASVPAPTPAPAAAPVPAAPASSSDPAAASATTAAPGQTPASAQAPAQ
TPAPALPGPALPGFPFGGRVVRLHPVILASIVDSYERRNEGAARVIGTLLGTVDKHSVEVTNCFSVPHNESEDEV
AVDMEFAKNMYELHKKVSPNELILGWYATGHDITEHSVLIHEYYSREAPNPIHLTVDTSLQNGRMSIKAYVSTLM
GVPGRMTGVMFTPLTVKYAYYDTERIGVELIMKTCFSPNRVIGLLSDLQQVGGASARIQDALSTVLQYAEDVLSG
KVSADNTVGRFLMSLVNRVPKIVPDDFETMLNSNINDLLMVTYLANLTQSQIALNEKLVNL

WO 2004/030615

PCT/US2003/028547

813/6881
FIGURE 757

GTTGGAGACTCGATTGTTGATGACAGCGGAAGAATGATAACAAAATGCGCGGAGCGAGATAGTGAGCCGTTCTCCA
ACCCTTTGGCCCCTGATGGCCACGATGTGGATGATCCTCACTCCTTCCACCAATCAAAACTCACCAATGAAGACT
TCAGGAACTTCTCATGACCCCCAGGGCTGCACCTACCTCTGCACCACCTTCTAAGTCACGTCACCATGAGATGC
CAAGGGAGTACAATGAGGATGAAGACCCAGCTGCACGAAGGAGGAAAAAGAAAAGTTATTATGCTAAGCTACGCC
AACAAGAAATTGAGAGAGAGAGAGAGCTAGCAGAGAAGTACCGGGGTCGTGCCAAGGAACGGAGAGATGGAGTGA
ACAAAGATTATGAAGAAACCGAGCTTATCAACACCACAGCTAACTACAGGGCTGTTGGCCCCACTACTAAGGCGG
ACAAATCAGCTGCAGAGAAGAGAAGACAGTTGATCCAGGAGTCCAAATTCTTGGGTGGTGACATGGAACACACCC
ATTTGGTGAAAGGCTTGGATTTTGCTCTGCTTCAAAGGTACGAGCTGAGATTGCCAGCAAAGAGAAAGAGGAAG
AGGAACTGATGGAAGGCCCGAGAAAGAAACCAAGAAAGATGAGGATCCTGAAAATAAAATTGAATTTAAACAC
GTCTGGGCCGCAATGTTTACCGAGTGCTTTTAAAGAACAAGCATATAAGCGGAATGAGTTGTTCTGCCGGGCCG
CATGGCCTATGTGTAGGCTGGATGATGAGTAAGCTGACACAGATATCCCCACCACTCTTATCCGCAGCAAGGT
TGACTGCCCCACCATGGAGGCCAGACCATACTGACCACAAATGATATTGTCTATTAGCAAGCTTACCCAGTTGCT
TTCATACCTGAGGCAGGGAACCCGTAACAAGAAGCTTAAGAAGAAGGATAAAGGGAAGCTGGAAGAGAAGAAACC
TGCTGAGGCTGACAGGAGTATTTTCGAAGACATTGGGGATTATACACCCTCCACAATCAAGACACCTTGGGACAA
GGAGCGGGAGAGATATCGGGAACGGGAGCGTGATCAGGAGACAGAGACCGTGACCGAGAGCGAGAGCGAGAACGA
GATCAGGAGCGAGAACGAGATCGGGAACGAGAGAGAGAAGAGGAAAAAGAGACACAGCTACTTTGAGAAGCCA
AAAGTACATGATGAGTCCGTGGACGTTGACAAAGGACCTGGGTCCGCCAAGGAGTTGATCAAGTCCATCAATGAA
AAGTTTGCTGGGTCTGCTGGCTGGGAAGGCACAGAATCGCTGAAAATTGCAGAAGACAAAAGCAGCTGAGAGAT
TTCTTTGGCATGTCCAACAGTTATGCAGAGTGCTATCCAGCCACGATGGATGACATGGCTGTGGATAGTGATGAG
GAGGTGGATTATAGCAAAATGGACCAGGGTAACAAGAAGAGAACCTTAAGCCGTTGGGACTTTGATACCCAGGAA
GACTACAGCGAGTATATGAACAACAAGAGGCTTTGCCCAAGGCTGCATTCCAGTATGGTATCAAAATGTCTGAA
GGCGGAAAACCAGACGCTTCAAGGAAACCAATGACAAAGCAGCGCTCGATTGCCAGTGGAAGATTAGTGCAATC
ATTGAGAAGAGGAAGAAGATGGAAGCTGATGGGGTTGAAGTCAAAGACCAAAATACTAA

WO 2004/030615

PCT/US2003/028547

814/6881
FIGURE 758

MPERDSEPF SNPLAPDGHVDVDPHSFHQSKLTNEDFRKLLMTPRAAPTSAPPSKSRHHEMPREYNEDEDPAARRR
KKKSYYAKLRQQEIERERELAEKYRGRAKERRDGVNKDYETELINTTANYRAVGPTTKADKSAAEKRRQLIQES
KFLGGDMEHTHLVKGLDFALLQVRAEIASKEKEEEEELMEKPQKETKKDEDPENKIEFKTRLGRNVYRVLFKNKH
ISGMSCSCRAAWPMW

WO 2004/030615

PCT/US2003/028547

815/6881
FIGURE 759

ATGCCCCGAGAATGTGGCACCCCGGAGCGGGGCGACTGCCGGGGCTGCCGGCGGCCGCGGGAAAGGCGCCTATCAG
GACCGCGACAAGCCAGCCAGATCCGCTTCAGCAACATTTCCGCCGCCAAAGCGGTTGCTGATGCTATTAGAACA
AGCCTTGGACCAAAAGGAATGGATAAAATGATTCAAGATGGAAAAGGTGATGTAACCATTACAAATGATGGTGCT
ACCATTCTGAAACAAATGCAAGTATTACATCCAGCAGCCAGAATGCTGGTGGAGCTGTCTAAGGCTCAAGATATA
GAAGCAGGAGATGGCACCACATCAGTAGTCATCATTGCTGGCTCCCTCTTAGATTCTTGTACCAAGCTTCTTCAG
AAAGGGATTTCATCCAACCATCATTTCTGAGTCATTCCAGAAGGCCCTGGAAAAGGGCATTGAAATCTTGACTGAC
ATGTCTCGACCTGTGGAACCTGAGTGACAGAGAACTTTGTTAAATAGTGCAACCACTTCACTGAACTCAAAGGTG
GTTTCTCAGTATTCAAGTCTGCTTTCTCCAATGAGTGTAATGCAGTGATGAAAGTGATTGACCCAGCCACAGCC
ACCAGTGTAGATCTTAGAGATATTAATAAGTTAAGAAAGCTTGGTGGGACAATTGATGACTGTGAGTTGGTGGAA
GGGCTGGTTCTCACCCAAAAAGTGTCAAATCTGGCATAACCAGAGTTGAAAAGGCCAAGATTGGGCTTATTTCAG
TTTTGCTTATCTGCTCCCAAAACAGACATGGATAATCAAATAGTGGTTTTCTGACTATGCCAGATGGACCGAGTG
CTGCGAGAAGAGAGAGCCATATTTTAAATTTAGTGAAGCAAATTAACAAAAACAGGATGTAATGTCCTTCTCATA
CAGAAATCTATTCTAAGAGATGCTCTTAGTGATCTTGCAATTACACTTTCTGAATAAAATGAAGATCATGGTGATT
AAGGATATTGAAAGAGAAGACATTGAATTCATTTGTAAGACAATTGGAACCAAGCCAGTTGCTCATATTGACCAA
TTTACTGCTGACATGCTGGGTTCTGCTGAGTTAGCTGAGGAGGTCAATTTAAATGGTTCTGGCAAACCTGCTCAAG
ATTACAGGCTGTGCCAGCCCTGGAAAAACAGTTACAATTGTTGTTTCGTGGTTCTAACAACTGGTGATTGAAGAA
GCTGAGCGCTCCATTTCATGATGCCCTATGTGTTATTCGTGTTTAGTGAAGAAGAGGGCTCTTATTGCAGGAGGT
GGTGTCTCAGAAATAGAGTTGGCCCTAGCATTAACTGAATATTCACGAACACTGAGTGGTATGGAATCCTACTGC
GTTCTGTGCTTTTGCAGATGCTATGGAGGTCATTCCATCTACACTAGCTGAAAATGCCGGCCTGAATCCCATTCT
ACAGTAACAGAACTAAGAAACCGGCATGCCAGGGAGAAAAACTGCAGGCATTAATGTCCGAAAGGGTGGTATT
TCCAACATTTTGGAGGAACTGGTTGTCCAGCCTCTGTTGGTATCAGTCAGTGCTCTGACTCTTGCAACTGAACT
GTTTCGGAGCATTCTGAAAATAGATGATGTGGTAAACACTCGATAACTGGATAACTGACTAGCACCATTATGATC
ACCAGTATTGTGGCTGGAATGGAAGAAGATCACCTTGGTGTTCCTTGTTTGGAAGATTATTTCTCTGAATTTCT
GGGCTTGGTCTTCCAGTTGGCATTTCCTGAAGTTGTATTGAAACAATTTAATGAAAATATTAAATATTTGTTT
CAAAAGGCAGATTTATCTTCTCCCAACATTCTGTATTTCTGATACTTTTGAAAACTAATAAAAACTAATAAAA
GAAGCGTA

WO 2004/030615

PCT/US2003/028547

816/6881
FIGURE 760

MPENVAPRSGATAGAAGGRGKGAYQDRDKPAQIRFSNISAACAVADAIRTSLGPKGMDKMIQDGKGDVTITNDGA
TILKQMQLVHLPAAARMLVELSKAQDIEAGDGTTSVVIIAGSLLDSCTKLLQKGIHPTIISESFQKALEKGIEILTD
MSRPVELSDRETLLNSATTSLNSKVVSQYSSLLSPMSVNAVMMKVIDPATATSVDLRDIKIVKKLGGTIDDCELVE
GLVLTQKVSNSGITRVEKAKIGLIQFCLSAPKTDMDNQIVVSDYAQMMDRVLREERAYILNLVKQIKKTGCNVLLI
QKSILRDALSDLALHFLNKMIMVIKDIEREDIEFICKTIGTKPVAHIDQFTADMLGSAELAEVNLNGSGKLLK
ITGCASPGKTVTIVVRGSNKLVEEAERSIHDALCVIRCLVKKRALIAGGGAPEIELALALTEYSRTLSGMESYC
VRAFADAMEVIPSTLAENAGLNPISTVTELRNRHAQGEKTAGINVRKGGISNILEELVVQPLLVSVSALTTLATET
VRSILKIDDVVNTR

WO 2004/030615

PCT/US2003/028547

817/6881
FIGURE 761A

AGGAAGGAAGGAGCAGTTGGTTCAATCTCTGGTAATCTATGCCAGCAATTATGACAATGTTAGCAGACCATGCAG
CTCGTCAGCTGCTTGATTTTCAGCCAAAACTGGATATCAACTTATTAGATAATGTGGTGAATTGCTTATACCATG
GAGAAGGAGCCAGCAAGAATGGCTCAAGAAGTACTGACACATTTAAAGGAGCATCCTGATGCTTGGACAAGAG
TCGACACAATTTTGGAAATTTTCTCAGAATATGAATACGAAATACTATGGACTACAAATTTTGGAAAATGTGATAA
AAACAAGGTGGAAGATTCTTCCAAGGAACCAGTGCGAAGGAATAAAAAAATACGTTGTTGGCCTCATTATCAAGA
CGTCATCTGACCCAACTTGTGTAGAGAAAAGGAGGTGTATATCGGAAAATTAAATATGATCCTTGTTTCAGATAC
TGAAACAAGAAATGGCCCAACATTGGCCAACTTTTATCAGTGATATTGTTGGAGCAAGTAGGACCAGCGAAAGTC
TCTGTCAAAATAATATGGTGATTCTTAAACTCTTGAGTGAAGAAGTATTTGATTTCTCTAGTGGACAGATAACCC
AAGTCAAATCTAAGCATTTTAAAGACAGCATGTGCAATGAATTCTCACAGATATTTCAACTGTGTGAGTTTGTAA
TGGAAAATTTCTCAAAATGCTCCACTTGTACATGCAACCTTGGAAACATTGCTCAGATTTCTGAACTGGATTCCCC
TGGGATATATTTTTGAGACCAAAATTAATCAGCACATTGATTTATAAGTTCCTGAATGTTCCAATGTTTCGAAATG
TCTCTCTGAAGTGCCCTCACTGAGATTGCTGGTGTGAGTGTAAAGCCAATATGAAGAACAATTTGTAACACTATTTA
CTCTGACAATGATGCAACTAAAGCAGATGCTTCTTTAAATACCAATATTCGACTTGCCTACTCAAATGGAAAAG
ATGATGAACAGAACTTCATTCAAAATCTCAGTTTGTCTCTGCACCTTTCTTAAGGAACATGATCAACTTATAG
AAAAAAGATTAAATCTCAGGGAACTCTTATGGAGGCCCTTCATTATATGTTGTTGGTATCTGAAGTAGAAGAAA
CTGAAATCTTTAAATTTGTCTTGAATACTGGAATCATTTGGCTGCTGAACTCTATAGAGAGAGTCCATTCTCTA
CATCTGCCTCTCCGTTGCTTTCTGGAAGTCAACATTTTGATGTTTCTCCAGGAGACAGCTATATTTGCCCATGT
TATTCAGGTCCGTTTATTAATGGTTAGTCGAATGGCTAAACCAGAGGAAGTATTGGTTGTAGAGAATGATCAAG
GAGAAGTTGTGAGAGAATTCATGAAGGATACAGATTCCATAAATTTGTATAAGAATATGAGGGAAACATTGGTTT
ATCTTACTCATCTGGATTATGTAGATACAGAAAGAATAATGACAGAGAAGCTTCACAATCAAGTGAATGGTACAG
AGTGGTCATGGAAAAATTTGAATACATTGTGTTGGGCAATAGGCTCCATTAGTGGAGCAATGCATGAAGAGGACG
AAAAACGATTTCTTGTTACTGTTATAAAGGATCTATTAGGATTATGTGAACAGAAAAGAGGCAAAGATAATAAAG
CTATTATTGCATCAAATATCATGTACATAGTAGGTCAATACCCACGTTTTTTGAGAGCTCACTGGAATTTCTGA
AGACTGTAGTTAACAAGCTGTTTGAATTCATGCATGAGACCCATGATGGAGTCCAGGATATGGCTTGTGATACTT
TCATTAATAATAGCCCCAAAATGCCGCAGGCATTTTCGTTTCAGGTTTCAGGTTGGAGAAGTGATGCCATTATTGATG
AAATTTTGAACAACATTAACTACTATTATTGTGATCTTCAGCCTCAACAGGTTTCATACGTTTTTATGAAGCTGTGG
GGTACATGATTGGTGCACAAACAGATCAAAACAGTACAAGAGCACTTGTATAGAAAAGTACATGTTTACTCCCTAATC
AAGTGTGGGATAGTATAATCCAGCAGGCAACCAAAATGTGGATATACTGAAAGATCCTGAAACAGTCAAGCAGC
TTGGTAGCATTTTGAACAACATGTGAGAGCTGCAAAAGCTGTTGGACACCCCTTTGTAATTCAGCTTGGAAAGAA
TTTATTTAGATATGCTTAATGTATACAAGTGCCCTCAGTGAAATATTTCTGCAGCTATCCAAGCTAATGGTGAAA
TGTTTACAAGCAACCATTTGATTAGAAGTATGCGAAGCTGTAAGGGAACCTTTAAAGTTAATATCTGGTTGGG
TGAGCCGATCCAATGATCCACAGATGGTCGCTGAAAATTTTGTTCCTCTGTTGGATGCAGTTCTCATTGATT
ATCAGAGAAATGTCCAGCTGCTAGAGAACCAGAAGTGCTTAGTACTATGGCCATAATTGTCAACAAGTTAGGGG
GACATATAACAGCTGAAATACCTCAAATATTTGATGCTGTTTTTGAATGCACATTGAATATGATAAATAAGGACT
TTGAAGAATATCCTGAACATAGAACGAACCTTTTTCTTACTACTTCAGGCTGTCAATTCTCATTGTTTCCAGCAT
TCCTTGCTATTCCACCTACACAGTTTTAACTTGTTTTGGATTCCATCATTGTTGGGCTTTCAAACATACTATGAGGA
ATGTGCGAGATACGGGCTTACAGATACTTTTTACACTCTTACAAAATGTTGCACAAGAAGAAGCTGCAGCTCAGA
GTTTTTATCAAACCTTATTTTTGTGATATTCTCCAGCATATCTTTCTGTTGTGACAGACACTTCACATACTGCTG
GTTTAAACAATGCATGCATCAATTCTTGATATATGTTTAAATTTGGTTGAAGAAGGAAAAATAAGTACATCATTAA
ATCCTGGAAATCCAGTTAACAACCAATCTTTCTTCAGGAATATGTGGCTAATCTCCTTAAGTCGGCCTTCCCTC
ACCTACAAGATGCTCAAGTAAAGCTCTTTGTGACAGGGCTTTTCAGCTTAAATCAAGATATTCCTGCTTTCAAGG
AACATTTAAGAGATTTCTAGTTCAAATAAAGGAATTTGCAGGTGAAGACACTTCTGATTTGTTTTTGGAAAGAGA
GAGAAATAGCCCTACGGCAGGCTGATGAAGAGAAACATAAACGTCAAATGTCTGTCCCTGGCATCTTTAATCCAC
ATGAGATTCCAGAAGAAATGTGTGATTAAATCCAAATTCATGCTGTTTTTTTTCTCTGCAACTCCGTTAGCAGA
GGAAAACAGCATGTGGGTATTTGTGACCAAAATGATGCCAATTTGTAAATTAATAATGTCACCTAGTGGCCCTTT
TTCTTATGTGTTTTTTTTGTATAAGAAATTTCTGTGAAATATCCTTCCATTGTTTAAAGCTTTTGTGTTGGTCATC
TTTATTTAGTTTGCATGAAGTTGAAAATTAAGGCATTTTTTAAAAATTTTACTTCATGCCCATTTTTGTGGCTGGG
CTGGGGGGAGGAGGCAAATTCATTTGAACATATACTTGTAAATCTAATGCAAAATTATACAATTTTTCTGTAA

WO 2004/030615

PCT/US2003/028547

818/6881
FIGURE 761B

ACAATACCAATTTTTAATTAGGGAGCATTTCCTTCTAGTCTATTTTCAGCCTAGAAGAAAAGATAATGAGTAAAA
CAAATTGCGTTGTTTAAAGGATTATAGTGCTGCATTGTCTGAAGTTAGCACCTCTTGGACTGAATCGTTTGTCTA
GACTACATGTATTACAAAGTCTCTTTGGCAAGATTGCAGCAAGATCATGTGCATATCATCCCATTGTAAAGCGAC
TTCAAAAATATGGGAACACAGTTAGTTATTTTTACACAGTTCTTTTTGTTTTTGTGTGTGTGTGCTGTCTGCTTGT
CGACAACAGCTTTTTGTTTTCTCAATGAGGAGTGTTGCTCATTGTGAGCCTTCATTAACTCGAAGTGAAATGG
TTAAAAATATTTATCCTGTTAGAAATAGGCTGCATCTTTTTAACAACCTCATTAAAAAACAAAACAACCTCTGGCTTT
TGAGATGACTTATACTAATTTACATTGTTTACCAAGCTGTAGTGCTTTAAGAACACTACTTAAAAAGCAAATAA
ACTTGTTTTACATTTAAAAAAA

WO 2004/030615

PCT/US2003/028547

819/6881
FIGURE 762

MPAIMTMLADHAARQLLDFSQKLDINLLDNVNVNCLYHGEGAQQORMAQEVLTHLKEHPDAWTRVDTILEFSQNMNT
KYYGLQILENVIKTRWKILPRNQCEGIKKYVVGIIKTSSDPTCVEKEKVYIGKLNMIIVQILKQEWPKHWPTFI
SDIVGASRTSESLCQNNMVILKLLSEEVDFDFSSGQITQVKS KHLKDSMCNEFSQIFQLCQFVMENSQNAPLVHAT
LETLLRFLNWIPLGYIFETKLITLIYKFLNVP MFRNVSLKCLTEIAGVSVSQYEEQFVTLFTLTMMQLKQMLPL
NTNIRLAYSNGKDDEQNFIQNLSLFLCTFLKEHDQLIEKRLNLRETLMEALHYMLLVSEVEETEIFKICLEYWNH
LAAELYRESPFSTASPLLSGSQHFDVPPRRQLYLPMLFKVRLLMVSRMAKPEEVLVVENDQGEVVREFMKDTS
INLYKNMRETLVYLTHLDYVDTERIMTEKLNQVNGTEWSWKNLNTLCWAIGSISGAMHEEDEKRFLVTVIKDLL
GLCEQKRGKDNKAI IASNIMYIVGQYPRFLRAHWKFLKTVVNKLFEFMHETHDGVQDMACDTFIKIAQKCRHFV
QVQVGEVMPFIDEILNNINTIICDLQPQQVHTFYEAVGYMIGAQTQTVQEHLEKYMLLPNQVWDSIIQQATKN
VDILKDPETVKQLGSILKTNVRACKAVGHPFVIQLGRIYLDMLNVYKCLSENISAAIQANGEMVTQPLIRSMRT
VKRETLKLISGWVSRSDNPQMVAENFVPLLDVAVLIDYQRNVPAAREPEVLSTMAIIVNKLGGHITAEIPQIFDA
VFECTLMINKDFEEYPEHRTNFFLLQAVNSHCFAFLAIPPTQFKLVLDSSIWAFKHTMRNVADTGLQILFTL
LQNVAQEEAAQSFYQTYFCDILQHIFS VVTDTSHTAGLTMHASILAYMFNLVEEGKISTSLNPGNPVNNQIFLQ
EYVANLLKSAFPHLQDAQVKLFVTGLFSLNQDIPAFKEHLRDFLVQIKEFAGEDTSDLFLEEREIALRQADEEKH
KRQMSVPGIFNPHEIPEEMCD

WO 2004/030615

PCT/US2003/028547

820/6881
FIGURE 763

GGCGGCGGCAGCAGCTGCTTGGGCGCCGTGCGGTGGTGACTGAGCTACGAGCCTGGCAGCAGGTGTGCGCCGAGC
CCCGGCCTGGCCCGGCCCCGCGTGCCCTCCAGGCTCCGCACCCCTGATGCTGCGCGGGTGCTGAGCCCACTTCG
GCCAGGACGATGGTTAAGTATTTCTGGGCCAGAGCGTGCTCCGGAGTTCCTGGGACCAAGTGTTGCGCGCCTTC
TGGCAGCGGTACCCGAATCCCTATAGCAAACATGTCTTGACGGAAGACATAGTACACCGGGAGGTGACCCCTGAC
CAGAACTGCTGTCCCGGCGACTCCTGACCAAGACCAACAGAATGCCACGCTGGGCAAGCAACTATTTCTGCC
AATGTTGCTCACTCGGTGTACATCCTGGAGGACTCTATTGTGGACCCACAGAATCAGACCATGACTACCTTCACC
TGGAACATCAACCACGCCC GGCTGATGGTGGTGGAGGAACGATGTGTTTACTGTGTGAACTCTGACAACAGCGGC
TGGAAGTAAATCCGCCGGGAAGCCTGGGTCTCCTCTAGCTTATTTGGTGTCTCCAGAGCTGTCCAGGAATTTGGT
CTTGCCCAAGTTCAAAAGCAACGTGACCAAGACTATGAAGGGTTTTGAATATATCTTGACTAAGCTGCAAGGCGAG
GCCCCCTCCAAAACACTTGAGACAGCCAAGGAAGCCAAGGAGAAGGCAGAGGAGACGGCACTGGCAGCTACAGAG
AAGGCCAAGGACCTCGCCAGCAAGGCGGCCACCAAGAAGCAGCAGCAGCAGCAACAGTTTGTGTAGCCAGCCAC
CACCACCACAGCAACCCAGACAGCTAGGCTTAGCCCCCTCTGCCCTCCCTCCATTGTACTTTATCATTAAAAATCA
ACTTCCA

WO 2004/030615

PCT/US2003/028547

821/6881
FIGURE 764

CTGACTCTCTGAGGCTCATTGTCAGTTGTTGAAATTGTCCCCGCAGTTTTCAATCATGTCTGAACCAATCAGAG
TCCTTGTGACTGGAGCAGCTGGTCAAATTGCATATTCAGTGTACAGTATTGGAAATGGATCTGTCTTTGGTA
AAGATCAGCCTATAATTCTTGTGCTGTTGGATATCACCCCATGATGGGTGTCCTGGACGGTGTCTAATGGAAC
TGCAAGACTGTGCCCTTCCCTCCTGAAAGATGTCATCGCAACAGATAAAGAAGACGTTGCCTTCAAAGACCTGG
ATGTGGCCATTCTTGTGGGCTCCATGCCAAGAAGGGAAGGCATGGAGAGAAAAGATTTACTGAAAGCAAATGTGA
AAATCTTCAAATCCCAGGGTGCAGCCTTAGATAAATACGCCAAGAAGTCAGTTAAGGTTATTGTTGTGGGTAATC
CAGCCAATACCAACTGCCTGACTGCTTCCAAGTCAGCTCCATCCATCCCCAAGGAGAAC TTCAGTTGCTTGACTC
GTTTGGATCACAACCGAGCTAAAGCTCAAATTGCTCTTAAACTTGGTGTGACTGCTAATGATGTAAAGAATGTCA
TTATCTGGGGAAACCATTCTCGACTCAGTATCCAGATGTCAACCATGCCAAGGTGAAATTGCAAGGAAAGGAAG
TTGGTGTGTTATGAAGCTCTGAAAGATGACAGCTGGCTCAAGGGAGAATTTGTCACGACTGTGCAGCAGCGTGGCG
CTGCTGTGTCATCAAGGCTCGAAAACCTATCCAGTGCCATGTCTGCTGCAAAAGCCATCTGTGACCACGTCAGGGACA
TCTGGTTTGGAAACCCAGAGGGAGAGTTTGTGTCCATGGGTGTTATCTCTGATGGCAACTCCTATGGTGTTCCTG
ATGATCTGCTCTACTCATTCCCTGTTGTAATCAAGAATAAGACCTGGAAGTTTGTGGAAGGTCTCCCTATTAATG
ATTTCTCACGTGAGAAGATGGATCTTACTGCAAAGGAAGTACAGAGAAGAAAAGAAAGTGCTTTTGAATTTCTTT
CCTCTGCCTGACTAGACAATGATGTTACTAAATGCTTCAAAGCTGAAGAATCTAAATGTCGTCTTTGACTCAAGT
ACCAAATAATAATAATGCTATACTTAAATTACTTGTGAAAAACAACACATTTTAAAGATTACGTGCTTCTTGGTA
CAGGTTTGTGAATGACAGTTTATCGTCATGCTGTTAGTGTGCATTCTAAATAAATATATATTCAAATG

WO 2004/030615

PCT/US2003/028547

822/6881
FIGURE 765

MSEPIRVLVTGAAGQIAYSLLYSIGNGSVFGKDQPIILVLLDITPMMGVLDGVLMELODCALPLLKDVIATDKED
VAFKDLDVAILVGSMFPRREGMERKDLLKANVKIFKSQGAALDKYAKKSVKVIIVGNPANTNCLTASKSAPSIPKE
NFSCLTRLDHNRKAQIALKLGVTANDVKNVIIWGNHSSTQYPDVNHAKVKLQGKEVGVYEALKDDSWLKGEFVT
TVQQRGAAVIKARKLSSAMSAAKAICDHVRDIWFGTPEGEFVSMGVISDGNSYGVPDDLLYSFPVVIKNKTWKFV
EGLPINDFSREKMDLTAKELTEEKESAFEFLSSA

WO 2004/030615

PCT/US2003/028547

823/6881
FIGURE 766

TCTTTTAAGTATACTCTCTACTTATTAAAAAAGTCCTTTCCACGCTACCTGCAGAGGGGTCCATACG
GCGTTGTTCTGGATTCCCATCGTAACCTTAAAGGGAACTTTACAATGTCCGGAGCCCTTGATGTCCTGCAAATG
AAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCTCACTTAGGTGGCACC AATCTTGACTTCCAGATGGAA
CAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTGAAGAGGACCTGGGAGAAGCTTCTGCTG
GCAGCTCGTGCTATTGTTGCCATTGAAAACCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGG
GCCGTGCTAAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTCGCTAAC
CAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCAGGGCTGACCACCAGCCTCTCATG
GAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCACTATGTGGACATTGCC
ATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATG
CGTGGCACCATTTCCTGTGAACACCCATGGGAGGTCATGCCTGATCTGTACTTCTACAGAGATCCTGAAGAGATT
GAAAGAGAAGAGCAGGCTGCTGCTGAAAAGGCAGTGACCAAGGAGGAATTTAGGGTGAATGGACTGCTCCAGCT
CCTGAGTTCACTGTTACTCAGCCTGAGGTTGCAGACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCCC
TACTGAAGACGGGAGCGCTCAGCCTGCCACGGAAGACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGT
AGGAGCAACCACTGACTGGTCTTAAGCTGTTCTTGCATAGGCTCTTAAGCAACATGGAAAAATGGTTGATGGAAA
ATAAACATCAGTTTCT

WO 2004/030615

PCT/US2003/028547

824/6881
FIGURE 767

MSGALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAVLKFAAATGATPIAGRFTPGTFANQIQAAFREPRLLVVTDPRADHQPLMEASYVNLPTIALCNT
DSPLHYVDIAIPCNNKGAHSVGLMWWMLAREVLRMRGTISCEHPWEVMPDLYFYRDPEEIEREEQAAAEKAVTKE
EFQGEWTAPAPEFTVTQPEVADWSEGVQVPSVPIPY

WO 2004/030615

PCT/US2003/028547

825/6881
FIGURE 768

GCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCATCGTAACTTAAAGGGAACTTTACACAATGTCCGGAGCCC
TTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACTCACTTAGGTGGCACCATC
TTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTGAAGAGGACCT
GGGAGAAGCTTCTGGCCGCTTCACTCCTGGAACCTTCGCTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCT
TCTTGTTGGTTACTGACCCAGGGCTGACCACCAGCCTCTCATGGAGGCATCTTATGTTAACCTACCTACCATTGC
GCTGTGTAACACAGATTCTCCTCTGCACTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGT
GGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTGAACACCCATGGGA
GGTCATGCCTGATCTGTACTTCTACAGAGATCCTGAAGAGATTGAAAGAGAAGAGCAGGCTGCTGCTGAAAAGGC
AGTGACCAAGGAGGAATTCAGGGTGAATGGACTGCTCCAGCTCCTGAGTTCAGTGTACTCAGCCTGAGGTTGC
AGACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGC

WO 2004/030615

PCT/US2003/028547

826/6881
FIGURE 769

MSGALDVLQMKEEDVLKFLAAGTHLGSTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLASLLEPSLTRSRQPSG
SHGFLWLLIPGLTTSLSQRHLKLTYPLLCVTQILLCAMWTLP SHATARELTQWV

WO 2004/030615

PCT/US2003/028547

827/6881
FIGURE 770

GGCCCAGCTGCTGAGAGGAGTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGG
ATCAGAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTGTATTGTTAGAA
GATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAATGATCCCGCTGAAAGGGAGCACTCTG
ACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGTTTGTGTTTAAGATCACTACGACCAAACAGCAGGACCACTTC
TTCCAGGCAGCCTTCCTGGAGGAGAGAGATGCCTGGGTTTCGGGATATCAAGAAGGCCATTAAATGCATTGAAGGA
GGCCAGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTTCGACTGCCAGAAACCATTGACTTAGGTGCCTTATAT
TTGTCCATGAAAGACACTGAAAAAGGAATAAAGAAGTGAATCTAGAGAAGGACAAGAAGATTTTTAATCACTGC
TTCACAGGTAACCTGCGTCATTGATTGGCTGGTATCCAACCAGTCTGTTAGGAATCGCCAGGAAGGCCTCATGATT
GCTTCATCGCTGCTCAATGAGGGGTATCTGCAGCCTGCTGGAGACATGTCCAAGAGTGCAGTGGATGGAACCTGCT
GAAAACCCCTTTCCTGGACAACCCCTGATGCCTTCTACTACTTTCCAGACAGTGGGTTCTTCTGTGAAGAGAATTCC
AGTGATGATGATGTGATTCTGAAAGAAGAATTCAGAGGGGTCATTATCAAGCAGGGATGTTTACTGAAGCAGGGG
CATAGAAGGAAAACTGGAAAGTGAGGAAGTTCATCTTGAGAGAAGACCCTGCCTACCTGCACTACTATGACCCCT
GCTGGGGCAGAAGATCCCTGGGAGCAATTCACCTTGAGAGGCTGTGTGGTGACTTCAGTGGAGAGCAACTCAAT
GGCAGGAAGAGTGAGGAAGAGAACCTTTTTGAGATCATCACAGCAGATGAAGTGCATTTCTTGCAAGCAGCC
ACCCCAAGGAGCGCACAGAGTGGATCAGAGCCATCCAGATGGCCTCCCGAAGTAAAGAGACTCCTGC
ATTCTCCTCCCTCCTGAGGGGAAGCCCATGGACAAGCTCAGTCCAGGACCTGTCCACTTCTGTGACAAATCAAC
GGGAAACAGCCAGGGGTGGGAAGTTTTTCAATTTGCAGGGGGTCTGAATGTAACTCACCATGTGGTGTGCAAGGT
TCCCTGCAATTGTATTGCTCACTGCAGCCCTCTGCCCTATCCATGACCCCAAGCAGATATAACAAGCTGTGC
AGCCTCAGTAGGCTGCTTGCCCTCTCCAGGCCTCAGGGCCTCTTCTGGAAAATGAAGAAATTCAACTAGTAGATT
CCTGAGGTCCCCCTAGCTTAAAAAATCTGCCCATGATTCTAACAATCGCAGTAGTGATAGTGATC
TAGTTGTTCTGCTGGTGTCTTTCCTTGCTAAGTCTTGGCCTTCAGTTATCTTCAAATGTACCAGAACCTGAGCC
AACGCCTCCCTGTGAAACTGTTGCTGATCTGTAGTACAGTACCAGGAAGAAACCTCTTTTGTCTCTTTAGACAT
CTTCTACTTGCTCTTGGCCTTGAGATCGTGTAACAAAATGAAGGAGGGCTCTCTTCTTCTTCTCCTCATCCTACTC
AAAACTTCCCCGAGAGCAGTGGTGGTTTTTGAGGGTTTTGACTTCTATTACTTTTGGCAGCCTGGAAAGTTGTGTC
TTCTGGGAAAGAGACCTGGGGAGGCCAGGAGTAGCTGAGGGTCTTTCTGTGCCCTTAAACCGCCAGAGGAGCC
CTATTCCACTCTGGTTTTAGGCTGATCTGAGAGGGTCTCCCTTTGTTCTTTCTGGAGCATTCTCTAACGTTTA
TTACAATTAGGAGGGGGACCCACATCTGTGAGATTCTGTTTCATTTGAGGTTTACAGAAAAAAGTGGCCA
GATGTGTTCCCCCATGGGTGAGAGGCCTGGGCAACTGCCTGGTGAATGTGTCTTGCGGCAGCTGCAGCAAGTGG
AGGGGCTGAACTACTGGCCAGCTCACTGGATGATGGGTAAATACAACAACCTGCACTGTAAGGACTCAGAGCCACA
CAGAACTTCTGAGAGGGGCTGTTAGCATTGCGCAGCATCTTCAGTTCTCCAGTAAATGATATTGCGTTCGTGCCT
CAGCTTTAAGCACAAAGTAGCAGCAGCTCCTGCTTGAGTTCTGAGGGCATCATGGCCCTATGATTAACCAGAGTGA
TCTAACCTAGACTAAAATTGGGAACCTATTTGCAATTTTGAACCTGACCACTAAGTATTCTTCTCCAAA
TTGAGAAAGACAGCACCATTGAAGCAGATATGTGTGTGAAAGTATATTTTCAATTCAGATTTTAAATTTTAA
GGCTCCAGGAAAGAAAGGAGAGTAGAACATTTTCTCATTTTATCAATCCTCTCTTGGCCCTCCCTCAATTCCC
CTGTAAACATTCCTGAAGCTGTTCCCACTCCAGATGGTTTTATCAATAGCCTAGAGGTAAAGAACTGTCTTTTTC
TCTGATTCTTTAATAAATTATCTTTATAGAATATGCACAAGTTTTTCTACACTCAGTGTTAAAGTATTTATTAAT
GGGAAGTCAACTTAATGTTTTGAAATAAATATATGACTCTGTTTAAAT

WO 2004/030615

PCT/US2003/028547

828/6881
FIGURE 771

CTTTCGGGAGACTGGAGTCGAAGGCCGTGAGGTATTTTCTAAGXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXAACCCGGAGGAGGGTGAGGAGCAGAGCTGGCCATAATGGCAGGTGAAGAAATTAATGAAGACTAT
CCAGTAGAAATTCACGAGTATTTGTCAGCGTTTGAGAATTCATTGGTGCTGTGGATGAGATGCTGAAGACCATG
ATGTCGTGTTTCTAGAAATGAGTTGTTGCAGAAGTTGGATCCACTTGAACAAGCAAAAGTGGATTTGGTTTCTGCA
TACACATTAAATTCAATGTTTGGGTTTATTTGGCAACCCAAGGAGTTAATCCTAAGGAACATCCAGTAAACAG
GAATTGGAAAGAATCAGAGTATATATGAACAGAGTCAAGGAAATAACAGACAAGAAAAAGGCTGGCAAGCTGGAC
AGAGGTGCAGCTTCAAGATTTGTAAAAATGCCCTCTGGGAACCAAAATCGAAAAATGCATCAAAAGTTGCCAAT
AAAGGAAAAAGTAAAGTTAACTTTTTGGTTTTGATGTACACATATTCAAAAAGTACATTAATATGTAAATTCAC
AGTAAATATGTAAAGCTAAATACTTTCCTCTCCAAAGATCATTATCTTTATTGATTAGCACTGAGGATTTTAACA
TTGTGATATATTATATATTATAATTTACCATCTCTTGATGAGACTCTTATTTCTTTATATAGGTCAGTCTTGCA
AGTACCATTTTATAAGCAGCTGTGAAATTTAAGTGAAATGTTCTTTGTAAACATTTGTACTATTTTAAATGAATA
ATGACCTTATGAAGTATGCTATCTGTAGGCTGAAATTATAGGTACATCTGTTTTCACTATATGATATTAAGAAAG
CGTGAAATGACTTAAATGTTCATTTTTTCTGTATAGATACTTTATCATGTTTTTCATGATTTTAGGAATTACTGC
TTTGTGATATTCAAAGTGTGAAACTAAAACTTTATGGTTGTACTTTAATTCTTGGCATGTTGCCTCTATGTCCC
ATTTAAATAAAATACATTCTCATTAACTTTAGATGGGAAATAAGGTTGTATGTTGATGGATGAATTTTGGCATG
ATGACTGTACTCTCAATAAAGGCTGAAAAATGTTGT

WO 2004/030615

PCT/US2003/028547

829/6881
FIGURE 772

CCTTCACTTCGCCCTCCAGCTGCTGCAGCTGCAGCCCGACCGCGAGCGTGCCAAGCGGCTTCAGCAGCTAGCGGA
GCGGTGGCGGCGGCCCCGCTCAGGAGACCACCAGATTCCCCTCTTCCCGCGGCCTCGCCATGGCGACCCACGGAC
AGACTTGCGCGCGTCCAATGTGTATTCCCTCCATCATATGCTGACCTTGGCAAAGCTGCCAGAGATATTTTCAACA
AAGGATTGGTTTTGGGTGGTGAAACTGGATGTGAAAACAAAGTCTTGCAGTGGCGTGGAATTTTCAACGTCCG
GTTTCACTAATACAGACACTGGTAAAGTTACTGGGACCTGGAGACCAAATACAAGTGGTGTGAGTATGGTCTGA
CTTTCACAGAAAAGTGAACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTT
TGAAACTGACATTTGATACTACCTTCTCACCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGAC
TGGGGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGA
AGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAGCTAAATA
TCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACCTCTAGCTTAATTGGAGTAGGCTATACTCAGAC
TC

WO 2004/030615

PCT/US2003/028547

830/6881
FIGURE 773

AGCTGCTGCAGCTGCAGCCCGACCGCGAGCGTGCCAAGCGGCTTCAGCAGCTAGCGGAGCGGTGGCGGCGGCCCC
GCTCAGGAGACCACCAGATTCCCCTCTTCCCGCGGCCTCGCCATGGCGACCCACGGACAGACTTGCGCGCGTCCA
ATGTGTATTCCCTCCATCATATGCTGACCTTGGCAAAGCTGCCAGAGATATTTTCAACAAAGGATTTGGTTTTGGG
TTGGTGAAACTGGATGTGAAAACAAAGTCTTGCACTGGCGTGGAATTTTCAACGTCCGGTTCATCTAATACAGAC
ACTGGTAAAGTTACTGGGACCCTGGAGACCAAATACAAGTGGTGTGAGTATGGTCTGACTTTCACAGAAAAGTGG
AACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGAT
ACTACCTTCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTACAAGAGGGAGTGTATAAACCTTGGT
TGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTTCAGCTGTCTTTGGTTATGAGGGCTGGCTTGCT
GGCTACCAGATGACCTTTGACAGTGCCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGG
GACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGAT
CTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAGCTAAATATCAG
TTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACCTCTAGCTTAATTGGAGTAGGCTATACTCAGACTCTG
AGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGGTAGACGGGAAGAGCATTAAATGCTGGAGGCCACAAGGTTGGG
CTCGCCCTGGAGTTGGAGGCTTAATCCAGCTGAAAGAAACCTTTGGGAATGGATATCAGAAGATTTGGCCTTAAT
ATATTTCCATTGTGACCAGCAGCAGGCTTTTTTCCCCAAGAAGATGATCAAAACAAAGGATGATCTCAACAAGA
GCTGTATTTTAAAGTATTTAGACAGTTCTTTGTTAGCTGGTTTCTAGTTGAATTGGTTATCTAGTTACCAATGCTG
CAGTCCTGCAGTCACCTATACATTATTTAAATGTATTTAACTGTAAATGCGCTACCCACCAATAATGAAATAGA
CCTTTATGAAAA

WO 2004/030615

PCT/US2003/028547

831/6881
FIGURE 774

MATHGQTCARPMCIPPSYADLGKAARDIFNKGFGFGLVKLDVKTSCSGVEFSTSGSSNTDTGKVTGTLETKYKW
CEYGLTFTEKWNTDNTLGTEIAIEDQICQGLKLTFTTFSPNTGKKSGKIKSYKRECINLGCDVDFDFAGPAIHG
SAVFGYEGWLAGYQMTFDSA KSKLTRNNFAVG YRTGDFQLHTNVNDGTEFGGSIYQKVCEDLDTSVNLAWTSGTN
CTREFGIAAKYQLDPTASISAKVNNSSLIGVGYTQTLRPGVKLTLSALVDGKSINAGGHKVGLELELEA

WO 2004/030615

PCT/US2003/028547

832/6881
FIGURE 775

ATGGTCTGACTTTCACAGAAAAGTGGAACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATT
GTCAAGGTTTGAAACTGACATTTGATACTACCTTCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTT
ACAAGAGGGAGTGATAAACCTTG GTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG
TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAAAGCTGACAAGGAATA
ACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGAT
CAATTTATCAGAAAGTTTGTGAAGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTC
GTTTTGGCATTGCAGCTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCTGGTGTGAAGCTTACACTCTCTG
CTCTGGTAGACGGGAAGAGCATTAAATGCTGGAGGCCACAAGGTTGGGCTCGCCCTGGAGTTGGAGGCTTAATCCA
GCTGAAAGAAACCTT

WO 2004/030615

PCT/US2003/028547

833/6881
FIGURE 776

GAGAAAACGGCCGGGCGGCGGTGGCTGTAGGTTGTGCGGCTGCAGCGGCTCTTCCCTGGGCGGACGATGGACAGC
CAGGGCAGGAAGGTGGTGGTGTGCGACAACGGCACCGGGTTTGTGAAGTGTGGATATGCAGGCTCTAACTTTCCA
GAACACATCTTCCAGCTTTGGTTGGAAGACCTATTATCAGATCAACCACCAAAGTGGGAAACATTGAAATCAAG
GATCTTATGGTTGGTGTAGGCAAGTGAATTACGATCAATGTTAGAAGTTAACTACCCTATGGAAAATGGCATA
GTACGAAATTGGGATGACATGAAACACCTGTGGGACTACACATTTGGACCAGAGAACTTAATATAGATACCAGA
AATTGTAAATCTTACTCACAGAACCTCCTATGAACCCAACCAAAAACAGAGAGAAGATTGTAGAGGTAATGTTT
GAACTTACCAGTTTTCCGGTGTATATGTAGCCATCCAGGCAGTTCTGACTTTGTACGCTCAAGGTTTATTGACT
GGTGTAGTGGTAGACTCTGGAGATGGTGTGACTCACATTTGCCAGTATATGAAGGCTTTTTCTCTCCCTCATCTT
ACCAGGAGACTGGATATTGCTGGGAGGGATATAACTAGATATCTTATCAAGCTACTTCTGTTGCGAGGATACGCC
TTCAACCACTCTGCTGATTTTGAAACGGTTCGCATGATTAAAGAAAACTGTGTTACGTGGGATATAATATTGAG
CAAGAGCAGAACTGGCCTTAGAAACCACAGTATTAGTTGAATCTTATACACTCCCAGATGGACGTATCATCAA
GTTGGGGGAGAGAGATTTGAAGCACCAGAAGCTTTATTTAGCCTCACTTGATCAATGTTGAAGGAGTTGGTGT
GCTGAATTGCTTTTAAACAATTACAGGCAGCTGACATTGATACCAGATCTGAATTCTACAAACACATTGTGCTT
TCTGGAGGGTCTACTATGTATCCTGGCCTGCCATCACGGTTGGAACGAGAAGCTTAAACAGCTTTAQTAGAACGA
GTTTTGAAGGGTGATGTGAAAAACTTTCTAAATTTAAGATCCGCATTGAAGACCCACCCCGCAGAAAGCACATG
GTATTCCTGGGTGGTGCAGTTCTAGCGGATATCATGAAAGACAAAGACAACTTTTGGATGACCCGACAAGAGTAC
CAAGAAAAGGGTGTCCTGTGCTAGAGAACTTGGTGTGACTGTTGATAAACTCCAAAGCTTGTTCCTGCATA
CCCGTAATGCTTTCTTTTTCTTTATTGCCAATCTTTGAACTCATTCAACTCCAGGACATGGAAGAGGCCTCTC
TCTGCCCTTTGACTGGAAAGGTCAAAGTTTTATTCTGGTGTCTTGGGGAAGCTTTGTAAATTTTTGTAAATGTGG
GTAAATCTGAGTTAATTCAACTGCTTCCCTACATAGACTAGAGGGCTAAGGATTCTGTCTGCTGCTTTGTTTCT
TCTAAGTAGGCATTTAGATCATTCTATAGGCTTCTATTTTCACTTTACTGCTCTAATGCTGCTAGTCGTAGTC
TTTAGCACACTAGGTGGTATGCCTTTATTAGCATAAAAACAAAAAACTTTAACAGGAGCTTTTACATATTACTG
GGATGGGGGGTGGTTCGGGATGGGTGGGCAGCTGCTGAACCTTTAGGGCATTTCCTCTGTAATGTGGCGCTTTC
AACTGTACTGCTGCAGCTTTAAGTACCTTAAAGCTTCTCCTGTGAACCTTCTTAGGGAAATGTTAGGTTTCAAGCT
AAAGTGTTTTGGGTGGGTTTTGTTGCGGGGGGAGGGTAACAATGGGTGGTCTTCTGATTTTTATTTTTGAGGT
TTGTCAACTGGAGTACGTAGAGGAACTTTATTTACAGTACTTTGATTGGCAGGTTTTCTTCTACTTGTGCTCTG
CCTGGAGCTGTTTCCATATGATATAAAAAGCAAGTGTAGTATTCCATTACTATGTGGCTTAGGGATTTATTTGTT
TTTTAAATCAACCATGTTAGCTGGGATTAGACTCCCTACAGTCTTCAATGGAAAAGTAACATTTAAAAATCCT
TTGGGTAAATTCGAATTACAGATTTAAAAGAGCTTAAGATCTGGTGTGTTTTGTTAATGCTTCTGTTTTATTCCAGAAG
CATTAAAGGTAACCCATTGCCAAGTATCATTCTTGCAAATTATCTTTTATATAACTGACCAGTGCTTAATAAAAC
AAGCAGGTACTTACAAATAATTACTGGCAGTAGGTTATAATTGGTGGTTTAAAAATAACATTGGAATACAGGACT
TGTTGCCAATTGGGTAATTTTCATTAGTTGTTTTGTTTGTGTTTGAATTTGAAACCTGGAAATACAGTAAATTTGA
CTGTTTAAATGTTGGCCAAAAAAATCAAGATTTAATTTTTTATTTGTACTGAAAACTAATCATAACTGTTAA
TTCTCAGCCATCTTTGAAGCTTGAAAGAAGAGTCTTGGTATTTGTAAACGTTAGCAGACTTTCCTGCCAGTGT
CAGAAAATCCTATTTATGAATCCTGTGCGGTATTCTTGGTATCTGAAAAAATACCAATAGTACCATACATGAG
TTATTTCTAAGTTTGAAAAATAAAAAGAAATTGCATCACACTAATTACAAAATA

WO 2004/030615

PCT/US2003/028547

834/6881
FIGURE 777

ATGGAGACACTTGTACAAGTGAATCTCTTTAGAAAGAGAGATTTACGCCAGGTACGTGGAACACAGTCTGAGCAG
CACTGCACACCGTATCAAATCAGGTATCCTGTAGGAAGAGTACCTGGGGATGAAATCAACAAGTTCTTAGTGGA
TCTTCTCATTCTTTAGAATGTAATGTGGTTGGATGTTTGAAATTGGTACGAAAGGGGAGAATCCTTTCCCCAA
TTAGGAAAATGGGGAGTGGGGGCAGAGGAAATGAAGCCCAGGTTCTTCATCGGATGGAAGTTCTCTGGTCAGTGT
ACACAGTTTGCTCTTGAGAGGACTGATGGCCTGGGATATGTTATTGATGGTCCTGAAAGGGATCTGCGTTTGAAT
AGGTGAGAGAAGATGTTCTGGAAGTCTGGAGACTGGGATACGCTCCCTTCCCTACAGGCTCATTATCCAGCGTT
CTGGCAGTACCCTCTGGTACCGCACAGACTTCAGGGGACCTTGAACAAGCTCCATTTTGTCTCCTGGAAGCTCAT
TCCACCAGGTTTGAGTATGAGCTTCACCACTGGCTCCACCTTCTCCACCAACTACCAGTCCCTGGGCTCTGTCCA
GGTGCCCAGCTAAGACGCTCGGCCAGTCAGCAGCATGACCAGTATCTCTGCAGGGGCTGGGGGCTCTGGTTCCCA
GATCTCCATGTCCCCCTCCACCAGCTTCTGGGGTGGCATGGGGTCTGGGGCCCTGGCCGTGGGGATGGCCAGGGT
TCTGGCAGGATGGAAGACATCCAGAACAAGAAGGAGACCATGCAAAGCCTGAATGACTGCCTGGCCTCCTACCTG
GACAGAGTGAGGAGACTGGATACCAAGAATCGGAAGCTGGAGAGCAAAATCCGGGAGCACCTGGAGAAGAAGGGA
CCCCAAGTCAGAGACTGGAGCCATTACTTCAAGACCGTGGAGGACCTGAGGGCTCAGATCTTCGCAAATACTGTG
GACAATGCCCGCATCGTTCTGCAAGTCGACAATGCCATCTTGCTGATGACTTTAGAGTCAAGTATGTGACAGAG
CTGGCCATGCGCCAGTCTATGGAGAGCGACATCCATGGGCTCCGCAAGGTCATTGATGACACCAATGTCACTCGG
CTGCAGCTGGAACAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCATGAAGAAGAACGAAGAAGGGGAAATA
AAAGGCCTACAAGCCCAGATTGCCAGCTCTGGGTTGACTGTGGAGGTAGATATCCCCAAATCTCAGGACCTTGCC
AAGCTCATGGCAGACATCTGGGCCCAATATGATGAGCTGGCTCGGAAGAGCCAAGAGGAGCTGGGCAAGTACTGG
TCTCAGCAGATTGAGGAGAGTATCACAGTAGTCACCATGCAGTCCACCGAGATGGAGCAGTTCAACAGGATCCTG
CTGCACCTGGAGTCAGAGCTGGCACAGACCTGGGCAGAGGGACAGTGCCAGGCCAGGAGTACGAGGCCCTGCTG
AGCATCAGGGTCAAGCTGGAGGCTGAGATCGCCACCTACCACCACCTGCTGGAAGATACCACCACCGGCCGGATA
GTGGATGGCAAAGTGGGGTCTGAGACCAACAACACCAAAGTTCTGAGACATTAA

WO 2004/030615

PCT/US2003/028547

835/6881
FIGURE 778

METLVQVNLFRKRDLRQVRGTQSEQHCTPYQIRYPVGRVPGDEINKFLVESSHFLCENVVGCLEIGTKGENPFPQ
LGKVGVGAEEMKPRFFIGWKFSGQCTQFALERTDGLGYVIDGPERDLRLNRSEKMFWKSGDWDTLPSLQAHSSSV
LAVPSGTAQTSGDLEQAPFCLLEAHSTRFEYELHHSLLHQLPVPGLCPGAQLRRSASQQHDQYLCRGWGLWFP
DLHVPLHQLLGWHGVWGPGRGDGQSGRMEDIQNKKETMQSLNDCLASYLDRVRRLDTKNRKLESKIREHLEKKG
PQVRDWSHYFKTVEDLRAQIFANTVDNARIVLQVDNAHLADDFRVKYVTELAMRQSMESDIHGLRKVIDDTNVTR
LQLETEIEALKEELLFMKKNEEGEIKGLQAQIASSGLTVEVDIPKSQDLAKLMADIWAQYDELARKSQEELGKYW
SQQIEESITVVTMQSTEMEQFNRIILLHLESELAQTWAEGQCQAQYEALLSIRVKLEAEIATYHHLEDTTTGRI
VDGKVGSETNNTKVLRH

WO 2004/030615

PCT/US2003/028547

836/6881
FIGURE 779A

CGGTCCCTCGCCGCGCCGCCCGAGGGGCACTTCCGGCGGCGGTTCACTTCCTGGTTGGGTGGATGGAGCCGGGG
GGGAGCGCGCGCGGGGGAGGGGCGGCGGGTCAGTCTCCGCCGCGCTCCCGGGATCAGCTGGCGGGCGGGCGGG
AGCCGAGCGCGGCCCGGCTCTCGCTGCAGCGCCGCTCTTCTCTGCGTCGCAGGCCGCGCGCGGCCGTGACA
ATGTGCGGGGGCTGGTAGCAGGGCGCGCGCGCGAGCCGTCTCAAGTTTAACTTACACGAATCGCTTTCTGGA
GGAGGAGGGGACCCGCTGCGCGATTGACACGCATATTCTTATAGGCATCCTCCCTCAGCCCCACCCCCACGGCC
GGATTGCGGTGGCTCCTCTCCGAGGTGAAATCTGAGAAGAAATCCTTGGATCTCTTTCTTAAAAA
AAAAAATCTAGAAACCATCGGTATTTTGCTTTGCTGCTCCCTATTGCAAGATGAAGAAGTTTTTCGACTC
CCGGCGAGAGCAGGGCGGCTCTGGCCTGGGCTCCGGCTCCAGCGGAGGAGGGGCGAGCACCTCGGGCCTGGGCAG
TGGCTACATCGGAAGAGTCTTCGGCATCGGGCGACAGCAGGTACAGTGGACGAGGTGTTGGCGGAAGGTGGATT
TGCTATTGTATTTCTGGTGAGGACAAGCAATGGGATGAAATGTGCCTTGAAACGCATGTTGTCAACAATGAGCA
TGATCTCCAGGTGTGCAAGAGAGAAATCCAGATAATGAGGGATCTTTCAGGGCACAAGAATATTGTGGGTACAT
TGATTCTAGTATCAACAACGTGAGTAGCGGTGATGTATGGGAAGTGTCTATTCTGATGGACTTTTGTAGAGGTGG
CCAGGTGGTAAACCTGATGAACAGCGCCTGCAACAGGCTTTACAGAGAATGAAGTGCTCCAGATATTTGTGA
TACCTGTGAAGCTGTTGCCCGCTGCATCAGTGCAAACTCCTATTATCCACCGGGACCTGAAGTTGAAAAAT
CCTCTTGATGACCGAGGCCACTATGTCTGTGTGACTTTGGAAGCGCCACCAACAAATTCCAGAATCCACAAAC
TGAGGGAGTCAATGCAGTAGAAGATGAGATTAAGAAATACACAACGCTGTCTATCGAGCACCAGAAATGGTCAA
CCTGTACAGTGGCAAAATCATCACTACGAAGGCAGACATTTGGGCTCTTGGATGTTTGTGTATAAATTATGCTA
CTTCACTTTGCCATTTGGGGAAAGTCAGGTGGCAATTTGTGATGGAACTTCACAATTCCTGATAATTCTCGATA
TTCTCAAGACATGCACTGCCTAATTAGGTATATGTTGGAACAGACCCTGACAAAAGGCCGGATATTTACCAGGT
GTCTACTTCTCATTTAAGCTACTCAAGAAAGAGTGCCCAATTCCAAATGTACAGAACTCTCCCATTCCTGCAAA
GCTTCCTGAACCAAGTGAAGCCAGTGAGGCAGCTGCAAAAAGACCCAGCCAAAGGCCAGACTGACAGATCCCAT
TCCACACAGAGACTTCAATTGCACCCCGCCAGAGGCCATAAGCTGGGCAGACTCAGCCGAACCCAGGAATCCT
TCCCATCCAGCCAGCGCTGACACCCCGGAAGAGGGCCACTGTTAGCCCCACCTCAGGCTGCAGGATCCAGCAA
TCAGCCTGGCCTTTTAGCCAGTGTTCCCAACCAAAACCCCAAGCCCCACCCAGCCAGCCTCTGCCGCAACTCA
GGCCAAGCAGCCACAGGCTCCTCCCACTCCACAGCAGACGCCTTCTACTCAGGCCAGGGTCTGCCGCTCAGGC
CCAGGCCACACCCAGCACCAGCAGCAACTCTTCTCAAGCAGCAACAGCAGCAGCAACAGCCACCGCCAGCACA
GCAGCAGCCGGCAGGCACGTTTTACCAGCAGCAGCAGGCCAGACTCAGCAGTTTCAGGCAGTACATCCAGCAAC
CCAGAAACCAGCAATTGCTCAGTTCCCTGTGGTGTCCCAAGGAGGCTCTCAACAGCAGCTAATGCAGAATTTCTA
CCAGCAGCAGCAGCAGCAGCAACAACAACAGCAACAGCAACAGCTGGCCACAGCCCTGCATCAACAACAGCTGAT
GACTCAGCAGGCTGCCTTGAGCAAAAAGCCCACTATGGCAGCAGGACAGCAGCCCCAGCCACAGCCAGCTGCAGC
CCCACAGCCAGCCCTGCCAGGAGCCAGCGATTCAAGCCCCAGTAAGACAACAGCCAAAGTTTACAGCAACCCC
ACCTCCTGCCGTCCAGGGGCAGAAAGTTGGATCTCTCACTCCACCCTCATCCCCAAAACCCAAAGTTGCTGGGCA
CAGGCGTATTCTCAGTGACGTAACCCACAGTGCAGTCTTTGGGGTCCCTGCCAGCAAATCAACCCAGCTGCTCCA
GGCAGCTGCAGCTGAGGCCAGTCTCAATAAGTCCAAGTCTGCAACCACCACTCCATCAGGCTCTCCTCGGACCTC
TCAACAAAACGTTTATAATCCTTCAGAAGGGTCTACGTGGAATCCCTTTGATGACGATAATTTCTCCAACTCAC
AGCTGAAGAAGTCTAAACAAGGACTTTGCCAAGCTTGGGGAAGGCAACATCCGAGAAGCTTGGAGGCTCAGC
TGAGAGTTTGATCCAGGCTTTCAATCAACCAAGGTGATGCTTTTGCTACGACCTCATTTTCTGCTGGAAGTGC
TGAAAAAAGGAAGGGTGGGCAGACTGTGGACTCTGGCCTCCCGCTTCTAAGCGTGTCTGATCCTTTATTCTCT
TCAAGTACCTGATGCACCAGAAAACTAATTGAGGGACTCAAATCTCCTGACACTTCTCTTCTGCTCCCTGACCT
CTTGCTATGACAGATCCTTTTGGTAGCACTTCTGATGCTGTAATTGGTAAAGTCATCATCTCTGTTTCTTCAGT
CATGCATGATATGTGTGCTGTTTCAAGAATGACAAGTACCTAGTTAACCAATCCCTGGGGAATAGCCCTGCCAC
CCCAGAAGCCAAGGCTATTTAATCTCACTTGATCTCACTCCAAATGAAGTGTTTTCTTGCTTTTGGGGGTACAA
CGTCTATTTTTTGCTTTCTTGATATCTGGAGATTCTAGAGTGGATCTCTTATGAATGAGGAGGAATGTGGAAA
AGCAGATTCTCTTTTTTTTTTTTGGTTGAGACAGAGTTTCACTCTTGTTGCTAGGCTGGAGTGAATGGCA
AGATCTCAGTCACTGCAACCTCCATCTCCCGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGAGA
TTACAGGCATGCACCACTGCCTGGCTAATTTTTATATTTTATAGTAGAGATAGGGTTTCTCCATGTTGGTCAGG
CTGGTCTCGAACTCCTGACCTCAGGTGATCCACCTGCCTTGGCCTCCCAAGTGCTGGGATTACAGGGGTGAGCC

WO 2004/030615

PCT/US2003/028547

837/6881
FIGURE 779B

ACCATGCCCAGCCCAGATTCTTCTTTAGAAAGGCCCATGTACATCCAGCTGCAGTGGGACGAGCCTGGGAAGCATA
GGAAGACCCCATCCCTACAAAAAAATGTTGTTAGTTAGCCAGGTGTGGGGGTGCACACCTGTGCTACCAGCTCT
TTGGGAGGCTGAGACGGAAGATCACTTTGAGCCAGGGGGTTTGAGGCTGCAGTGAGCCCTGATCATGCCACTGCC
CTCCAGCTTAAGTGACAGAGACCCATCTTAAACAAAATTAAAAATTTAAAAAGGTCCATGTATATACCAAGTAT
CAGTAACTGAGAAAACATTTTGGCCACTGGTTAAGCCCCATAAATAGAATCCAGGGCAGGGGCTTGGTCTGCTTC
CTCTCTCACATTTTCTATGTTCCAACAGCAAGGCAGGCAAGATTTGCAAATGTCCAAGGCCCTGTACTCCAG
GAGGGTCCAATCATGAGGCACCTAATAATGCCTTTGGGCAGAAAGTCCTAGAACTCAGAAGTGCCATGACCTTGC
ATAGGGGTAGGCCTGCAGCTGAGGGGTGTCACGTGGTGCAAAGGCCCTCCAGCTACATCCTGGGATGGGGTTTG
AGATGGATTAATGGCCTTTGCATGGCACAGAGGATGTTTGCCCCAGGTTTATCCCTTAATAAAAAGTGAAATTAC
CAGAAAAAATTAAGGTGCCTTTAGCCCATCTCTTCTGACATGGAAGAGGTTTGCTGAGCGGCTTATGTTCTGAA
TTTGTATGAGAACTGATCATTAGTGAGACTGGCCACAGTATTTAACCTTGACATGCATGCTCAGTGAAGCCT
AGACATTCAGAGCAGCAGAAATAAAGTAACCTTATTTTTCTTTCCACCTTGCTGAGACTGGCATTITAGAGACCT
GTTAAAAGAAAGTCTTCACATGGCTGGGTGCAGTGGCTCACACTTGTAACCACAGGACTTTGGGAGGCCAAGGTG
GGATAGATCGCTTGAGCTCAGGAGCAAGACACCATCTCAAAAAATGAGAATT

WO 2004/030615

PCT/US2003/028547

838/6881
FIGURE 780

GCCCCAGGTGCGCTTCCCCTAGAGAGGGATTTTCCGGTCTCGTGGGCAGAGGAACAACCAGGAACCTTGGGCTCAG
TCTCCACCCACAGTGGGGCGGATCCGTCCCGGATAAGACCCGCTGTCTGGCCCTGAGTAGGGTGTGACCTCCGC
AGCCGCAGAGGAGGAGCGCAGCCCGGCTCGAAGAAGCTTCTGCTTGGGTGGCTGAAGTCTGATCTTGACCTAGAG
TCATGGCCATGGCAACCAAAGGAGGTACTGTCAAAGCTGCTTCAGGATTCAATGCCATGGAAGATGCCAGACCC
TGAGGAAGGCCATGAAAGGGCTCGGCACCGATGAAGACGCCATTATTAGCGTCCTTGCCTACCGCAACACCGCCC
AGCGCCAGGAGATCAGGACAGCCTACAAGAGCACCATCGGCAGGGACTTGATAGACGACCTGAAGTCAGAAGTGA
GTGGCAACTTCGAGCAGGTGATTGTGGGGATGATGACGCCACGGTGCTGTATGACGTGCAAGAGCTGCGAAGGG
CCATGAAGGGAGCCGGCACTGATGAGGGCTGCCTAATTGAGATCCTGGCCTCCCGGACCCCTGAGGAGATCCGGC
GCATAAGCCAAACCTACCAGCAGCAATATGGACGGAGCCTTGAAGATGACATTCGCTCTGACACATCGTTTATGT
TCCAGCGAGTGCTGGTGCTCTGTCTGAGCTGGTGGGAGGGATGAAGGAAATTATCTGGACGATGCTCTCGTGAGAC
AGGATGCCAGGACCTGTATGAGGCTGGAGAGAAGAAATGGGGACAGATGAGGTGAAATTTCTAAGTGTCTCT
GTTCCCGGAACCGAAATCACTGTTGCATGTGTTTGTATGAATACAAAAGGATATCACAGAAGGATATTGAACAGA
GTATTAAATCTGAAACATCTGGTAGCTTTGAAGATGCTCTGCTGGCTATAGTAAAGTGCATGAGGAACAAATCTG
CATATTTTGTCTGAAAAGCTCTATAAATCGATGAAGGGCTTGGGCACCGATGATAACACCCTCATCAGAGTGATGG
TTTCTCGAGCAGAAATTGACATGTTGGATATCCGGGCACACTTCAAGAGACTCTATGGAAAGTCTCTGTACTCGT
TCATCAAGGGTGACACATCTGGAGACTACAGGAAAGTACTGCTTGTCTCTGTGGAGGAGATGATTAAAATAAAA
ATCCCAGAAGGACAGGAGGATTCTCAACACTTTGAATTTTTTAACTTCATTTTTCTACACTGCTATTATCATTA
TCTCAGAATGCTTATTTCCAATTAATAACGCCTACAGCTGCCTCCTAGAATATAGACTGTCTGTATTATTATCAC
CTATAATTAGTCATTATGATGCTTTAAAGCTGTACTTGCATTTCAAAGCTTATAAGATATAAATGGAGATTTTAA
AGTAGAAATAAATATGTATTCCATGTTTTTAAAGATTACTTTCTACTTTGTGTTTCACAGACATTGAATATATT
AAATTATTCATATTTTCTTTTCACTGAAAAATTTTTTAAATGGAAGACTGTTCTAAAATCACTTTTTTCCCTAA
TCCAATTTTTAGAGTGGCTAGTAGTTTTCTTCATTTGAAATTGTAAGCATCCGGTCAGTAAGAATGCCCATCCAGT
TTTCTATATTTTATAGTCAAAGCCTTGAAAGCATCTACAAATCTCTTTTTTTAGGTTTTGTCCATAGCATCAGTT
GATCCTTACTAAGTTTTTTCATGGGAGACTTCCTTCATCACATCTTATGTTGAAATCACTTTCTGTAGTCAAAGTA
TACCAAAACCAATTTATCTGAACTAAATTCTAAAGTATGGTTATACAAACCATATACATCTGGTTACCAACATA
AATGCTGAACATTCCATATTATTATAGTTAATGTCTTAATCCAGCTTGCAAGTGAATGGAAAAAAAATAAGCTT
CAAACCTAGGTATTCTGGGAATGATGTAATGCTCTGAATTTAGTATGATATAAAGAAAACCTTTTTGTGCTAAAAA
TACTTTTTAAATCAATTTTGTGATTGTAGTAATTTCTATTTGCACTGTGCCTTTCACTCCAGAAACATTCTG
AAGATGTACTTGGATTTAATTAATAAAGTTCACTTTGT

WO 2004/030615

PCT/US2003/028547

839/6881
FIGURE 781

MAMATKGGTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAQRQEIRTAYKSTIGRDLIDDLKSELS
GNFEQVIVGMMTPTVLYDVQELRRAMKGAGTDEGCLIEILASRTPEEIRRI SQTYQQYGRSLEDDIRSDTSFMF
QRVLVSL SAGGRDEGNYLDDALVRQDAQDLYEAGEKKWGTDEVKFLT V LCSRNRNHLHVFDEYKRISQKDIEQS
IKSETSGSFEDALLAIVKCMRNKSAYFAEKLYKSMKGLGTDDNTLIRVMVSRAEIDMLDIRAHFKRLYGKSLYSF
IKGDTSGDYRKVLLVLCGGDD

WO 2004/030615

PCT/US2003/028547

840/6881
FIGURE 782

CGCCACCGCCGCGCCCTCGCCACCCGCCCGCCCGCCGCTCCCGGGCCCCGCTCGCCCCCTCCGCCGCGCCGCCCC
GCCCCCTGCGACTACGCTGCGGCCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAG
TTTTGGGCTACACCTCCCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAACGAGCCCAACTCCCCCGAAC
GCCGCCCGCCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTGCGCTTCTTA
TGCACGGAAAGGAAGTAGGAAGCATCATTGGGAAGAAAGGGGAGTCGGTTAAGAGGATCCGCGAGGAGAGTGGCG
CGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTA
AGGCTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCA
GGCCCCCGGTCACCTGAGGCTGGTGGTGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGCGGGTGTAAGA
TCAAAGAGATCCGCGAGAGTACGGGGGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCAACTCCACCGAGCGGG
CCATCACCATCGCTGGCGTGCCGCAGTCTGTCAACGAGTGTGTCAAGCAGATTTGCCTGGTCATGCTGGAGACGC
TCTCCAGTCTCCGCAAGGGAGAGTCATGACCATTCCGTACCAGCCCATGCCGGCCAGCTCCCCAGTCATCTGCG
CGGGCGGCCAAGATCGGTGCAGCGACGCTGCGGGCTACCCCCATGCCACCCATGACCTGGAGGGACCACCTCTAG
ATGCCTACTCGATTCAAGGACAACACACCATTTCTCCGCTCGATCTGGCCAAGCTGAACCAGGTGGCAAGACAAC
AGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTGCGCCGAATTGACTCCAGCTCTCCAGAGGTGAAAGGCT
ATTGGGCAAGTTTGATGCATCTACTCAAACCACCCATGAACTCACCATTCCAAATAACTTAATTGGCTGCATAA
TCGGGCGCCAAGGCGCCAACATTAATGAGATCCGCCAGATGTCCGGGGCCCAGATCAAATTGCCAACCCAGTGG
AAGGCTCCTCTGGTAGGCAGGTTACTATCACTGGCTCTGCTGCCAGTATTAGTCTGGCCCAGTATCTAATCAATG
CCAGGCTTTCTCTGAGAAGGGCATGGGGTGCAGCTAGAACAGTGTAGGTTCCCTCAATAACCCCTTTCTGCTGT
TCTCCCATGATCCAACCTGTGTAATTTCTGGTCAGTGATTCCAGGTTTTAAATAATTTGTAAGTGTTCAGTTTCTA
CACAACCTTTATCATCCGCTAAGAATTTAAAAATCACATTCTCTGTTCACTGTTAATGCTGGGATCCATATTTAG
TTTTATAAGCTTTTCCCTGTTTTTAGTTTTGTTTTGGGTTTTTTGGCTCATGAATTTTATTTCTGTTTGTGCGATA
AGAAATGTAAGAGTGGAATGTTAATAAATTTAGTTTAGTTCTGTAATGTCAAGAATTTAAGAATTAATAAACGG
ATTGGTTAAAAAATGCTTCATATTTGAAAAAGCTGGGAATTGCTGTCTT

WO 2004/030615

PCT/US2003/028547

841/6881
FIGURE 783

CCAAGCTGAACCAGGTGGCAAGACAACAGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTGCGCCGGAATTG
ACTCCAGCTCTCCAGAGGTGAAAGGCTATTGGGCAAGTTTGGATGCATCTACTCAAACCACCCATGAATCACC
TTCCAAATAACTTAATTGGCTGCATAATCGGGCGCCAAGGCGCCAACATTAATGAGATCCGCCAGATGTCCGGGG
CCCAGATCAAAATTGCCAACCCAGTGGAAGGCTCCTCTGGTAGGCAGGTTACTATCACTGGCTCTGCTGCCAGTA
TTAGTCTGGCCCAGTATCTAATCAATGCCAGGCTTTCCTCTGAGAAGGGCATGGGGTGCAGCTAGAACAGTGTAG
GTTCCCTCAATAACCCCTTTCTGCTGTTCTCCCATGATCCAACGTGTGAATTTCTGGTCAGTGATTCCAGGTTTT
AAATAATTTGTAAGTGTTCAAGTTTCTACACAACTTTATCATCCGCTAAGAATTTAAGCTTTTCCCTGTTTTAGT
TTTGTTTTGGGTTTTTTGGCTCATGAATTTTA

WO 2004/030615

PCT/US2003/028547

842/6881
FIGURE 784

CGCAGAGCTCGCGCGTCGGTGTGGTTACAGCCGGCAGCCACGGCACCTCCTTCCGGCCGACTAGTCTCCAGGTCC
CGCGGTCTGGCCCTGGTCACCCGGCGCTGTCCCTCGTTCCTTGAAGATCTCCAGTGCTACCTTTTGTTGAACAT
CTCGAATACACCAAACCTTCTAGCTGCTAATACTCAGATTTATGGACAAGAAGTTATCATTGAAATTAAATGGTG
GCAGACATGTCCAAGGAATATTGCGGGGATTTGATCCCTTTATGAACCTTGTGATAGATGAATGTGTGGAGATGG
CGACTAGTGGACAACAGAACAAATATTGGAATGGTGGTAATACGAGGAAATAGTATCATCATGTTAGAAGCCTTGG
AACGAGTATAAATAATGGCTGTTTCAGCAGAGAAACCCATGTCTCTCTCCATAGGGCCTGTTTTACTATGATGTA
AAAATTAGGTCATGTACATTTTCATATTAGACTTTTTGTTAAATAAACTTTTGTAATAGTCAAAAATGCTTTCTC
AGATGTTCTGAATATAGAATATCAGCTCTCATTCCAGTTTTTTCTAACATGAATTTTCTGTTGACATTGATTT
CAAAGGGTTTTATGCATTAAAGTGAAAGAATCTTATTAAATGTGAAACATGGCAAGGATTCCCTTCTGTCCATCAT
CTTCAACACTGAACAGATAAAGAAGTTACAAACATGAGTGAGTTTCTTCTAAACACTAATTTTC

WO 2004/030615

PCT/US2003/028547

843/6881
FIGURE 785

GTACGCCGATTCCATATGGGCGCCGGCGCGGAGCGCCGCGGGGCAGCGCGGGGTGCGCCATGGCTGAGCTGCAGCA
GCTCCGGGTGCAGGAGGCGATGGAGTCCATGGTGAAGAGTCTGGAAAGAGAGAACATCCGGAAGATGCAGGGTCT
CATGTTCCGGTGCAGCGCCAGCTGTTGTGAGGACAGCCAGGCCTCCATGAAGCAGGTGCACCAGTGCATCGAGCG
CTGCCATGTGCCTCTGGCTCAAGCCCAGGCTTTGGTCACCAGTGAGCTGGAGAAGTTCAGGACC GCCTGGCCCCG
GTGCACCATGCATTGCAATGACAAAGCCAAAGATTCAATAGATGCTGGGAGTAAGGAGCTTCAGGTGAAGCAGCA
GCTGGACAGTTGTGTGACCAAGTGTGTGGATGACCACATGCACCTCATCCCAACTATGACCAAGAAGATGAAGGA
GGCTCTCTTATCAATTGGAAAATAAAAGTATTTGCCAGTGGCCATCAGGCTGAGGGCAAGAATATATTTTTTATA
AGGAATTGGGAATTTTAGTCTTTTAAGCAAAGTTTACGAATGAAGAAATGAAGGATGGCCACAAGCGTAAGGCAT
ATGTCACCTGCCTCTGGACACTGGTTATTTTTATGTTTCAGTCCCTAAAAAATGAAATGGAAAAAAGTGGTGCTAA
ATCGAGTCAGAGATATTACAGGAGAGTTTTAGAGCTTATTATTTCTGTGGCCAGTGCTTGTCTGGCAGTAAGG
CTCTCCCCTGTAACAAGCCAGAGCCCTCCAAGGTACCAGACTCTTCTTACTACACAGGTACTAACAGGCTGGCAG
GTTAGAGTTGGTGGAGTCTGAGGAGAGATATTTCTCTTTGTTGCCAACATCCTGTTTACCAAAGTGTCACCCC
ACCATCTTCCATAAGCTGTGAAACAAAATCAATGAGGTCACTAACTTAGAAGGGAAAGAAAGTTTTCTGGGTCTT
TGTTTTCTTGATTTGGGGTAATTTATACAAGGGCATACAAGTTGATTTTAAGATGTGGAACCTGGGAGGTAGACTA
GTTTGGATAAGAACCTTTGAAATGTTCTTGTGGATCCCCATTTCTGGTCATCAAGATGTGGATGTACATTCTTA
AAATTATTACATGCTGCATCTTTAGCCTGGAGACTGTGCAGAAACATGAGAGGTGATGACACACTAATTATGGG
AAGCAGAATTACTGGCTGATGGCCCCCTGAGGCTGTGTGTAACAAAATGACAGGACAATCTTGCAGTAACACTTTC
CCCTTGAAGAGAAGGGGGTTTTGATTGTGATATATACTAGTATCTAGGAATGAACAGTAAAAGAGGAGCAGTTGG
CTACTTGATTACAACAGAGTAAATGAAGTACTGGATTTGGGAAAACCTGGTTTTATTAGAACATATGGAATGAAA
GCCTACACCTAGCATTGCCTACTTAGCCCCCTGAATTAACAGAGCCCAATTGAGACAAACCCCTGGCAACAGGAA
ATTCAAGGGAGAAAAAGTAAGCAACTTGGGCTAGGATGAGCTGACTCCCTTAGAGCAAAGGAGAGACAGCCCCA
TTACCAAATACCATTTTTGCCTGGGGCTTGTGCAGCTGGCAGTGTTCTTGCCCCAGCATGGCACCTTATTGTTTT
GATAGCAACTTCGTTGAATTTTACCAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAG
GCTGTGATATATTTTCTAGTGGTTTGACTTTAAAAATAAATAAGGTTTAATTTTCTCCCC

WO 2004/030615

PCT/US2003/028547

844/6881
FIGURE 786

MAELQQLRVQEAMESMVKSLERENIRKMQGMLFRCSASCCEDSQASMKVHQCIERCHVPLAQAQALVTSELEKF
QDRLARCTMHCNDKAKDSIDAGSKELQVKQQLDSCVTKCVDDHMHLIPTMTKKMKEALLSIGK

WO 2004/030615

PCT/US2003/028547

845/6881
FIGURE 787A

CAGACCCGCCCCGTGGCTGCAGCAGTGGTGTCCCATTTTAAATGACTGCCCAGATTCCCACACTCAGTTCTGCTTCC
ATGGAACCTGCAGGTTTTTGGTGCAGGAGGACAAGCCAGCATGTGTCTGCCATTCTGGGTACGTTGGTGCACGCT
GTGAGCATGCGACCTCCTGGCCGTGGTGGCTGCCAGCCAGAAGAAGCAGGCCATCACCGCCTTGGTGGTGGTCT
CCATCGTGGCCCTGGCTGTCTTATCATCATGTGTGCTGATACACTGCTGCCAGGTCCGAAAACACTGTGAGT
GGTGCCGGGCCCTCATCTGCCGGCACGAGAAGCCAGCGCCCTCCTGAAGGGAAGAACCGCTTGTGCCACTCAG
AAACAGTGGTCTGAAGAGCCCAGAGGAGGAGTTTGGCCAGGTGGACTGTGGCAGATCAATAAAGAAAGGCTTCTT
CAGGACAGCACTGCCAGAGATGCCCTGGGTGTGCCACAGACCTTCTACTTGGCCTGTAATCACCTGTGCAGCCTT
TTGTGGGCCTTCAAACTCTGTCAAGAACTCCGTCTGCTTGGGGTTATTAGTGTGACCTAGAGAAGAAATCAGC
GGACCAGATTTCAAGACTTGTAAAAAAGAACTGCAAAGAGACGGACTCCTGTTTACCTAGGTGAGGTGTGTGC
AGCAGTTGGTGTCTGAGTCCACATGTGTGCAGTTGTCTTCTGCCAGCCATGGATTCCAGGCTATATATTTCTTTT
TAATGGGCCACCTCCCCACAACAGAATTCTGCCCAACACAGGAGATTTCTATAGTTATTGTTTTCTGTCAATTTGC
CTACTGGGGAAGAAAGTGAAGGAGGGGAACTGTTTAAATATCACATGAAGACCCTAGCTTTAAGAGAAGCTGTAT
CCTCTAACCACGAGACCCCTCAACCAGCCCAACATCTTCCATGGACACATGACATTGAAGACCATCCCAAGCTATC
GCCACCCTTGGAGATGATGTCTTATTTATTAGATGGATAATGGTTTTATTTTTAATCTCTTAAGTCAATGTAAAA
AGTATAAAACCCCTTCAGACTTCTACATTAATGATGATGTGTGCTGACTGAAAAGCTATACTGATTAGAAATG
TCTGGCCTCTTCAAGACAGCTAAGGCTTGGGAAAAGTCTTCCAGGGTGCGGAGATGGAACCAGAGGCTGGGTAC
TGGTAGGAATAAAGGTAGGGGTTCAAGAAATGGTGCCATTGAAGCCACAAAGCCGGTAAATGCCTCAATACGTTCT
GGGAGAAAACCTTAGCAATCCATCAGCAGGGATCTGTCCCCTCTGTTGGGGAGAGAGGAAGAGTGTGTGTCTA
CACAGGATAAAACCAATACATATTGTACTGCTCAGTGATTAAATGGGTTCACTTCTCTCGTGAGCCCTCGGTAAGT
ATGTTTAGAAATAGAACATTAGCCACGAGCCATAGGCATTTCAAGGCCAAATCCATGAAAGGGGACCAATCATT
ATTTTCCATTTTGTGCTTGGTTGGTTTGTGCTTTATTTTTAAAGGAGAAGTTTAACTTTGCTATTTATTTTC
GAGCACTAGGAAAACCTATTCCAGTAATTTTTTTTCTCATTTCCATTGAGGATGCCGGCTTTATTAACAAAAAC
TCTAACAAGTCACCTCCACTATGTGGGTCTTCTTTCCCCTCAAGAGAAGGAGCAATTGTTCCCCTGAGCATCTG
GGTCCATCTGACCCATGGGGCTGCCCTGTGAGAAACAGTGGGTCCCCTTCAAATACATAGTGGATAGCTCATCCCT
AGGAATTTTCATTAAAAATTTGGAAACAGAGTAATGAAGAAATAATATATAAACTCCTTATGTGAGGAAATGCTAC
TAATATCTGAAAAGTGAAAGATTTCTATGTATTAATCTTAAAGTGCACCTAGCTTATTACATCGTGAAGGTAACA
TTTAAATATGTTAAATTTGGCTTGAAATTTTCAAGAGAATTTGTCTTCCCCTAATTCTTCTTCTTGGTCTGGAA
GAACAATTTCTATGAATTTTCTCTTTATTTTTTTTATAATTCAGACAATTCTATGACCCGTGCTTCTTCTTTTG
GCACTCTTATTTAACAATGCCACACCTGAAGCACTTGGATCTGTTTCAAGAGCTGACCCCTAGCAACGTAGTTGAC
ACAGCTCCAGGTTTTTAAATTAATAAAGTTCAAGTTTACATCCCTTGGGCCAGATATGTGGGTTGAGGCTT
GACTGTAGCATCCTGCTTAGAGACCAATCAACGGACACTGGTTTTTAGACCTCTATCAATCAGTAGTTAGCATCC
AAGAGACTTTGCAGAGGCGTAGGAATGAGGCTGGACAGATGGCGGAAGCAGAGGTTCCCTGCGAAGACTTGAGAT
TTAGTGTCTGTGAATGTTCTAGTTCCTAGGTCCAGCAAGTCACACCTGCCAGTGCCCTCATCCTTATGCCTGTAA
CACACATGCACTGAGAGGCTCACATATACGCCTCCCCTAGAAGTGCCTTCCAAGTCAGTCCCTTTGGAAACCAGCA
GGTCTGAAAAGAGGCTGCATCAATGCAAGCCTGGTTGGACCATTGTCCATGCCTCAGGATAGAACAGCCTGGCT
TATTTGGGGATTTTTCTTCTAGAAATCAAATGACTGATAAGCATTGGATCCCTCTGCCATTTAATGGCAATGGTA
GTCTTTGGTTAGCTGCAAAAATCTCCATTTCAAGTTAAAAATGCATCTTCTAATCCATCTCTGCAAGCTCCCTG
TGTTTCCCTGCCCTTTAGAAAATGAATTGTTCACTACAATTAGAGAATCATTTAACATCCTGACCTGGTAAGCTG
CCACACACCTGGCAGTGGGGAGCATCGCTGTTTCCAATGGCTCAGGAGACAATGAAAAGCCCCCATTTAAAAAA
TAACAAACATTTTTTAAAGGCTCCAATACTCTTATGGAGCCTGGATTTTTCCCACTGCTCTACAGGCTGTGAC
TTTTTTAAGCATCCTGACAGGAAATGTTTTCTTCTACATGGAAAGATAGACAGCAGCCAACCCTGATCTGGAAG
ACAGGGCCCCGGCTGGACACACGTGGAACCAAGCCAGGGATGGGCTGGCCATTGTGTCCCCGAGGAGAGATGGG
CAGAATGGCCCTAGAGTTCTTTTCCCTGAGAAAAGGAGAAAAAGATGGGATTGCCACTCACCCACCCACACTGGTA
AGGGAGGAGAATTTGTGCTTCTGGAGCTTCTCAAGGGATTGTGTTTTGCAGGTACAGAAAACCTGCCTGTTATCTT
CAAGCCAGGTTTTTCGAGGGCACATGGGTCAACAGTTGCTTTTTTCAAGTCAATTTGGCCGGGATGGACTAATGAGGC
TCTAACACTGCTCAGGAGACCCCTGCCCTCTAGTTGGTTCTGGGCTTTGATCTCTTCCAACCTGCCAGTCACAG
AAGGAGGAATGACTCAATGCCCAAAACCAAGAACACATTGCAGAAGTAAGACAAACATGTATATTTTTTAAATGT
TCTAACATAAGACCTGTTCTCTCTAGCCATTGATTTACCAGGCTTTCTGAAAGATCTAGTGGTTACACAGAGAG

WO 2004/030615

PCT/US2003/028547

846/6881
FIGURE 787B

AGAGAGAGTACTGAAAAAGCAACTCCTCTTCTTAGTCTTAATAATTTACTAAAATGGTCAACTTTTCATTATCTT
TATTATAATAAACCTGATGCTTTTTTTTAGAACTCCTTACTCTGATGTCGTATATGTTGCACTGAAAAGGTTAA
TATTTAATGTTTTAATTTATTTTGTGTGGTAAGTTAATTTTGATTTCGTAAATGTGTTAATGTGATTAGCAGTTA
TTTTCCTTAATATCTGAATTATACTTAAAGAGTAGTGAGCAATATAAGACGCAATTGTGTTTTTCAGTAATGTGC
ATTGTTATTGAGTTGTACTGTACCTTATTTGGAAGGATGAAGGAATGAATCTTTTTTTCCT

PCT/US2003/028547

ATTTCTCTCCACGCTCGTGCGGGAAATGGCTTTAATCTCTACGCGCAGGGCTGTGAGGGACTAGCGGGAACCCGAG
CCTTTTGTCAAGGAACCTGCGGCGCTGGTGGCCAGTCTATCCCCGCCGCCGCGGAGCCGCTGCACTGCTGGGGGATC
TCCCAGCAGCTCTGACGAGCGCGGGCTGCAGCATGGGCAGAAAACGCTGCCCTGCAGATTAGCTGGGTGGATTTT
TTAAGCGCACCCCCACCCCCAAACCATAAAAATAACAAAACCAACCCGACGTGGCCGACCGGAGATAGCTAAGAT
GCCGCGCAGGAGTTTCCACCTGGATGTTTTGAGGTTGTGTAGATGTGGCCGGCACCCCTTGAGAGTGAGAGCTAGGGG
GTGCAGACTGAGCAGTGAACAGAAGGAGCCTTGGACAGGGCTGGGCCAGCCTCCCGAGTTCCAGGAGCGAATTGC
AAACCCACCGGGGAAAATGAGCGAAGAGACGGTCCCCGAGGCTGCCTCGCCGCCGCCCGCAGGGGCAGCCTTAC
TTTGACCGCTTCTCAGAGGACGACCCCCGAGTACATGCGCCTTCGCAACCGGGCGGCGGACCTGCGGCAGGACTTC
AACCTGATGGAGCAGAAGAAGCGCGTCACCATGATCCTGCAGAGTCCCTCTTTCAGGGAGGAGCTGGAAGGCCT
ATCCAGGAGCAGATGAAGAAGGGGAACAACCTCCTCCAACATCTGGGCCCTGCGACAGATCGCGGACTTCATGGCC
AGCACCTCCACGCGAGTCTTCCCACATCTTCCATGAATGTCTCCATGATGACGCCTATCAATGACCTCCACACA
GCTGACTCCCTGAACCTGGCCAAAGGGGAAGCGGCTCATGCGGTGCAAGATCAGCAGTGTCTACCGACTCCTGGAC
CTCTATGGCTGGGCCCAGCTGAGTGACACCTATGTACGTTGAGAGTCAGCAAGGAGCAGGACCACCTCCTGATC
AGCCCTAAGGGAGTTTCTTGACGTGAAGTCACAGCGTCCAGCCTGATCAAGGTGAACATTCTGGGAGAGGTGGTG
GAGAAGGGCAGCAGCTGCTTCCAGTGACACACCAGGCTTCTGTCTGCACTCGGCCATCTATGCAGCGAGGCC
GACGTGCGCTGCATCATCCACCTGCACACACCGGCCACAGCAGCGGTGTGCGCCATGAAGTGGGGCCTCCTGCCT
GTCTCCACAAATGCCCTGCTGGTGGGGGACATGGCCTATTATGACTTCAATGGGGAAATGGAGCAGGAAGCCGAT
CGGATCAACCTGCAGAAGTGCCTTGGACCCACCTGCAAGATCCTGGTGCTAAGAAACCATGGAGTGGTGTGCTCTG
GGTGACACGGTAGAGGAGGCAATTTACAAGATCTTCCACCTGCAGGCTGCATGTGAGATACAGGTGTGCGCTCTG
TCCAGTGCCGGGGGAGTGGAGAACCTCATCCTCCTGGAGCAGGAGAAGCACCGGCCCATGAGGTGGGCTCCGTG
CAGTGGGCGGGGAGCACCTTTGGGCTATGCAGAAGAGTCGGCTGGGGGAGCATGAGTTGAGGCCCTCATGAGG
ATGCTGGACAACCTGGGCTACAGAACAGGTTACACGTATCGCCACCCCTTTGTTCAAGAGAAAACCAACACAAA
AGTGAGGTGGAGATTCCAGCCACGGTCACAGCCTTCGTGTTTGAGGAGGACGGTGCCCCGGTGCCCGCCCTGCGA
CAGCATGCCCAGAAGCAGCAGAAGGAGAAGACCCGCTGGCTCAATACGCCCAACACCTACCTGCGGGTCAATGTG
GCCGATGAGGTCCAGAGGAGCATGGGCAGCCCCGACCCAAGACCACGTGGATGAAGGCTGACGAGGTGGAGAAA
TCCAGCAGTGGCATGCCGATTGCGATCGAAAACCCAAACCAATTTGTGCCTCTCTATACTGACCCCCAGGAAGTA
CTGGAGATGAGGAACAAGATTGAGAACAACCCGACAAGATGTGAAGTCAGCGGGGCCCTCAGTCCCAGCTCCTG
GCGAGCGTCATTGCCGAGAAGAGCCGAAGCCCGTCTACAGAGAGCCAGCTGATGTCCAAGGGAGACGAGGATACC
AAAGACGATTGAGAGGAGACGGTGCCCAACCCCTTCAGCCAACCTCACTGACCAGGAGTTGGAGGAGTACAAGAAA
GAGGTGGAGAGGAAGAACTAGAACTTGATGGAGAGAAAGAACTGCCCCAGAAGAGCCTGGCTCACCTGCAAAG
TCTGCACCTGCTTCTCCAGTGCAGAGCCCAGCGAAGGAGGCAGAGACAAAGAGCCCTTTAGTCTCTCCTTCCAAG
TCTTTAGAGGAAGGTACTAAGAAGACAGAAACAAGCAAGCCGCCACCACAGAGCCCAGAAACAACCCAGCCGGAA
GGGGTGGTGGTCAACGGGAGGGAGGAGGAGCAGACGGCAGAGGAAATCCTCAGCAAAGGCCTGAGCCAGATGACC
ACCAGTGCTGACACGGATGTTGATACCTCTAAGGACAAAACCGAGTCGGTCACCAGCGGCCCATGTCCCCAGAG
GGCTCACCTTCCAAGTCTCCCTCAAAGAAGAAAAAGAAATTCGGAACCCCTCTTCTCTGAAAAGAGCAAAAAG
AAGGAGAAAGTGGAGTCTTGATTGATGACACCTTGGGCTCCCTCCTGCTCCTCTCTCTCCTCCCTTCCCTTC
TCCCATCTCTGTCCCTGCAAGCACAGGGCTAAGGAGGGATAGAGTAGGACCTTGGACCATTCGGAAGGGGAAC
TTAGAGATCACCCGACCAACCCCTTGTTTTACAGTTGCCAAGAGAAATCAGGTGACTTGCCCCAAGGTACACAG
CTAGTTAGCGGCAGAGCCTGCACTCGAATTACAGTCTCCTGACTTCCAGTCCAGTGCTCCTTCTACTACACAACA
CTGCCTAGTTGTGGGCTGCCTTTGTTTGGATGCTGTCCACCAATCTGAGCCTAGGGCAAGAAGGCCAGAAATGGG
CCGTGAGCTCTCAGAGGCTCAGACTAAATCAGAGGTCAAGGCTTCCCCTGAGTAAGGTCCATTCTTCCAGGAA
TCCCAATCTCCTGTGGATGGAGCTATCTCTACATTTAAAAATCTCTTCTCTTTTCCACTTTGGGTCCCTGCCCTGC
TGCTCAAAGTGACTAGCCAAATTGACCCCTCCAACAGAAAGTAATCTTTGTTCCCAAGGGCTGATGGCTTAGCTT
GTACTACCCCAAACATTAAACCTGAGCTTTCTTCATGGAACCTCTTGAATGATGGATGGAAGAGCTATAAGAGGT
GGTAGGCATAGGGGCAAGCCATGTAAGCTGAGGATTGGGGATGGTTTCATCAACATAAGAGGCCAGGAACCTTGAC
CCCTTTGAATTGTGCACTCTCAGGCACCTTCAAACATAAAACCAAAATTTAGCATAGGAAAAAGTTGTTTAAATGCTCA
GGGCAGAAATTTGGGGAAGTTGAAATCCTCTGTTGGCTTTGGGTTGTATAAGGAGGATCAAACAACAGAGGAA
TGCTGACTTTCTAGCTTTGTCATGACACCTGGAGCAATGCACTGTACCTGCCTCACTCCTGTCCAGTGGTCAGGTT

WO 2004/030615

PCT/US2003/028547

848/6881
FIGURE 788B

TCCCCTGACCTTCCCTCACCCCCAGAAACACTTGCTTACAGACCGAAACTGGCATCTTACTCTTGGCACCTTGAC
TTGCACCCTCTGAGGTTCCAACCTCAGTCATTCTTTGTCCAGCAGAGGAGAATCAGAAATGAGCCCTTCAGGATTA
ATCCTCTTGCACCAGCTCTCAGAGAAATGCTGGGTATCCCTGTCCTTGTCCCTATCTGTCCATCCTGGGGCCTGG
TAATGGCCACAGTTATTGTTTTAAATGCCAACACTGCTTCTCATGTTCTTCCGTGGGGCATTGATTAATGAGCA
TTTGTGGCTCCTAAAAATTAGACAATCCATTCTCTTG

WO 2004/030615

PCT/US2003/028547

849/6881
FIGURE 789

GGCACGAGGCGGAGAACAGGAGCATGGAGGGCGGGCTGGGGCGTGCTGTGTGCTTGCTGACCGGGGCCTCCCGCG
GCTTCGGCCGGACGCTGGCCCCGCTCCTGGCCTCGCTGCTGTGCGCCGGCTCCGTGCTTGTCCTTAGCGCCCGCA
ACGACGAGGCACTGCGCCAGCTGGAGGCCGAGCTGGGCGCCGAGCGGTCTGGCCTGCGCGTGGTGCGGGTGCCCG
CCGACCTGGGCGCCGAGGCCGGCTTGACGAGCTGCTCGGCGCCCTGCGCGAGCTCCCCCGGCCCAAGGGGCTGC
AGCGACTGCTGCTTATCAACAACGCGGGCTCTCTTGGGGATGTGTCCAAAGGCTTCGTGGACCTGAGTGACTCCA
CTCAAGTGAACAATACTACTGGGCACTGAACCTTGACCTCCATGCTCTGCCTGACTTCCAGCGTCTCTGAAGGCCTTCC
CGGACAGTCTTGCCCTCAACAGAACCGTGGTTAACATCTCGTCCCTCTGTGCCCTGCAACCTTTCAAAGGCTGGG
CGCTGTACTGTGCAGGAAAGGCTGCTCGTGATATGCTGTTCCAGGTCTTGGCGCTGGAGGAACCTAATGTGAGGG
TGCTGAACTATGCCCCAGGTCTCTGGACACAGACATGCAGCAGTTGGCCCGGGAGACCTCCGTGGACCCAGACA
TGCGAAAAGGGCTGCAGGAGCTGAAGGCAAAGGGGAAGCTGGTGGATTGCAAGGTGTCAGCCCAGAACTGCTGA
GCTTACTGGAAAAGGACGAGTTCAAGTCTGGAGCCACGTGGACTTCTATGACAAATAAGCCCATGTTTTTGGCT
TCCTGAACCTTTTTGCCCCCACTTTTAGACATACCCCAGAGCCCTGTGGCTCCCCACACCCTGCCATAGGGGCAG
TCCTGCCTTACACATAGAAGCATTTCATGCCTGCTGCCCTGCCCTCAGGCACAGCCAGCTGTGAGCTCCCAGGTCA
TTGGCCTTACCAGTTGTCAGGAGTCTGTGCTGTGCACCCTGGGTTATAAGGAGGCTTAGGAGAGAGGTTATGGGT
ATTGGTGTCTCTATCCCCAGGAATAGAACTTAAGGGGTGGGAAGAACAGGAAAAGAAGCTGGAACACAGAAGAGA
GGAGGTGTGTCTCTTGCTCATAGCAAGCCTGTGGGTAGAGGAAAGAGTGATCTGGTGTGCAATAGGAGGACCCA
TGTAGATTTCGAGATGGCCTGGATGGGAGGAAGGGCAGACGGTACATGTCCCAGCCCACATAGATGCCCCTTGCT
GAGGGTAGCAGGACCTTCTGTTGAACTTTGTGTCTCACTCTGATGTCTCTTCTTCAGAACTTACCACCCCTC
CCCCAGGCTGGGAGAAGGGGCTCCTGGGTGTCTGTATACACGCCAAAGGCAGATACAAATAAAATACAGATTGTC
CTTTAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

850/6881
FIGURE 790

MEGGLGRAVCLLTGASRGFGRTLAPLLASLLSPGSVLVLSARNDEALRQLEAELGAERSGLRVVRVPADLGAEAG
LQQLLGALRELPRPKGLQRLLLINNAGSLGDVSKGFVDLSDSTQVNNYWALNLTSMLCLTSSVLKAFDPSGLNR
TVVNISSLCALQPFKGWALYCAGKAARDMLFQVLALEEPNVRVLNYAPGPLD TDMQQLARETSVDPDMRKGLQEL
KAKGKLVDCKVSAQKLLSLLEKDEFKSGAHVDFYDK

WO 2004/030615

PCT/US2003/028547

851/6881
FIGURE 791

GGAGCATGGAGGGCGGGCTGGGGCGTGCTGTGTGCTTGCTGACCGGGGCTCCCGCGGCTTCGGCCGGACGCTGG
CCCCGCTCCTGGCCTCGCTGCTGTGCGCCGGCTCCGTGCTTGCTCCTTAGCGCCCGCAACGACGAGGCACTGCGCC
AGCTGGAGGGCCGAGCTGGGCGCCGAGCGGTCTGGCCTGCGCGTGCTGCGGGTGCCCGCCGACCTGGGCGCCGAGG
CCGGCTTGACAGCAGCTGCTCGGCGCCCTGCGCGAGCTCCCCGGCCCCAAGGGGCTGCAGCGACTGCTGCTTATCA
ACAACGCGGGTAAGACCCCCGGGGCTGGAGCGGACTCCCCATGTGAGCGCCCACTTCCTCCACCGCTGGGGAATTT
AAGGGCTACTCCTAGGGGTGAGATAGGACGCCTAGAAATCTAAAGCCCTAGTTGTTCCAGCTTGAGTAGCAAGTG
GAGGCGAGGTGTACAGGAAGACTCGGTGCCGTGCGGACAACAGTCTGCCCCCACTTCCTGGAAAATTGGCCAGCC
GGGTTTTCCAAAGCGCCTGTAGAACTTTCCCGAGCCCCTTGCTCTGCGCCCTCTGGCGGAGGCCTGAGTCAGGGC
TTGGAGTCTCCAAACAAGTAAACTCTCTGCTTCTCAAAGGACCGCTAGAGCTTTCCTTCAGCCCCACGGCAAGG
GCTCTCTTGGGGATGTGTCAAAGGCTTCGTGGACCTGAGTGACTCCACTCAAGTGAACAACACTACTGGGCACTGA
ACTTGACCTCCATG

WO 2004/030615

PCT/US2003/028547

852/6881
FIGURE 792

GTTCCAAGGTTTGCGGCCCCGGTCTCGGAGAAGAGGGGAGAGTGGAGGGCCGCTGAATAAGCTTCCAAAATGATGC
CCACACCAGTTATCCTATTGAAAGAGGGGACTGATAGCTCCCAAGGCATCCCCAGCTTGTGAGTAACATCAGTG
CCTGCCAGGTGATTGCTGAGGCTGTAAAGAACTACCCTGGGTCCCCGTGGCATGGACAAGCTTATTGTAGATGGCA
GAGGCAAAGCAACAATTTCTAATGATGGGGCCACAATTCTGAAACTTCTTGATGTTGTCCATCCTGCAGCAAAGA
CTTTGGTAGACATTGCCAAATCCCAAGATGCTGAGGTGGGTGATGGCACCACCTCAGTGACCTTGTGGCTGCAG
AGTTTCTGAAGCAGGTGAAACCTATGTGGAGGAAGGTTTACACCCCCAGATCATCATTGAGCTTTCCGCACAG
CCACCCAGCTGGCAGTTAACAAGATCAAAGAGATTGCTGTGACCGTGAAGAAGGCAGATAAAGTGGAGCAGAGGA
AGCTGCTGGAAGTGTGCCATGACCGCTCTGAGCTCCAAGCTGATCTCCAGCAGAAAGCTTTCTTTTGCTAAGA
TGTTGGTGGATGCAGTGATGATGCTCGATGATTTGCTGCAGCTTAAAATGATTGGAATCAAGAAGGTACAGGGTG
GAGCCCTCGAGGATTCTCAGCTGGTAGCTGGTGTTCATTCAAGAAGACTTTCTCTTACGCTGGGTTTGAAATGC
AACCCAAAAAGTACCACAATCCCAAGATTGCCCTTTTGAATGTCGAGCTCGAGTTGAAAGCTGAGAAAGACAATG
CTGAGATAAGAGTCCACACAGTTGAGGATTATCAGGCAATTGTTGATGCTGAGTGGAAACATTCTCTATGACAAGT
TAGAGAAGATCCATCATTCTGGAGCCAAAGTTGTCTTGTCCAAACTCCCCATTGGGGATGTGGCCACCCAGTACT
TTGCTGACAGGGACATGTTCTGTGCTGGCCGAGTACCTGAGGAGGATCTGAAGAGGACAATGATGGCCTGTGGAG
GCTCAATCCAGACCAGTGTGAATGCTCTGTGTCAGCAGATGTGCTGGGTGATGCCAGGTGTTTGAAGAGACCCAGA
TTGGAGGCGAGAGGTACAATTTTTTTACTGGCTGCCCCCAAGGCCAAGACATGCACCTTCATTCTCCGTGGCGGCG
CCGAGCAGTTTATGGAGGAGACAGAGCGGTCCCTGCATGATGCCATCATGATCGTCAGGAGGGCCATCAAGAATG
ATTCAGTGGTGGCTGGTGGCGGGGCCATTGAGATGGAACCTCTCCAAGTACCTGCGGGATTACTCAAGGACTATTC
CAGGAAAACAGCAGCTGTTGATTGGGGCTTATGCCAAGGCCTTGGAGATTATCCCACGCCAGCTGTGTGACAATG
CTGGCTTTGATGCCACAAACATTCTCAACAAGCTGCGGGCTCGGCATGCCAGGGGGGTACATGGTATGGAGTAG
ACATCAACAACGAGGACATTGCTGACAACCTTTGAAGCTTTTCGTGTGGGAGCCAGCTATGGTGCGGATCAATGCGC
TGACAGCAGCCTCTGAGGCTGCGTGCTGATCGTGTCTGTAGATGAAACCATCAAGAACCCCGCTCGACTGTGG
ATGCTCCACAGCAGCAGGCCGGGGCCGTGGTCTGGCCGCCCCCTGAGAGGCACCCACCCATCACATGGCT
GGCTGGCTGCTGGGTGCACTTACCCCTCTTGGCTTGGTTACTTCAATTTTACAAGGAAGGGGTAGTAATTGGCCCA
CTCTCTTCTTACTGGAGGCTATTTAAATAAAATGTAAGACTTCAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

853/6881
FIGURE 793

MMPTPVILLKEGTDSSQGIPQLVSNISACQVIAEAVRTTLGPRGMDKLIVDGRGKATISNDGATILKLLDVVHPA
AKTLVDIAKSQDAEVDGTTSTVLLAAEFLKQVKPYVEEGLHPQIIIRAFRTATQLAVNKIKEIAVTVKKADKVE
QRKLLKCAMTALSSKLISQQAFFAKMVVDVAVMLDDLLQLKMIGIKKVQGGALEDSQLVAGVAFKKTFSYAGF
EMQPKKYHNPKIALLNVELELKAEDNAEIRVHTVEDYQAIVDAEWNILYDKLEKIHHSKAKVVLKLPIGDVAT
QYFADRMFCAGRVPEEDLKRTMMACGGSIQTSVNALSADVLGRCQVFEETQIGGERYNFFTGCPKAKTCTFILR
GGAEQFMEETERSLHDAIMIVRRAIKNDSVVAGGGAIEMELSKYLRDYSRTIPGKQQLLIGAYAKALEIIPRQLC
DNAGFDATNILNKLRRARHAQGGTWYGVDINNEDIADNFEAFVWEPAMVRINALTAASEAACLIVSVDETIKNPRS
TVDAPTAAGRGRGRGRPH

WO 2004/030615

PCT/US2003/028547

854/6881
FIGURE 794

ATATAACCGCGTGGCCCCGCGCGCGCGCTTCCCTCCCGGCGCAGTCACCGGCGCGGTCTATGGCTGCGACTTCTCT
AATGTCTGCTTTGGCTGCCCGGCTGCTGCAGCCCGCGCACAGCTGCTCCCTTCGCCTTCGCCCTTTCCACCTCGC
GGCAGTTCGAAATGAAGCTGTTGTCAATTTCTGGAAGGAACTGGCCCAGCAGATCAAGCAGGAAGTGC GGCAGGA
GGTAGAAGAGTGGGTGGCCTCAGGCAACAAACGGCCACACCTGAGTGTGATCCTGGTTGGCGAGAATCCTGCAAG
TCACTCCTATGTCCTCAACAAAACAGGGCAGCTGCAGTTGTGGGAATCAACAGTGAGACAATTATGAAACCAGC
TTCAATTTTCAGAGGAAGAATTGTTGAATTTAATCAATAAACTGAATAATGATGATAATGTAGATGGCCTCCTTGT
TCAGTTGCCTCTTCCAGAGCATATTGATGAGAGAAGGATCTGCAATGCTGTTTCTCCAGACAAGGATGTTGATGG
CTTTCATGTAATTAATGTAGGACGAATGTGTTTGGATCAGTATTCCATGTTACCGGCTACTCCATGGGGTGTGTG
GGAAATAATCAAGCGAACTGGCATTCCAACCCTAGGGAAGAATGTGGTTGTGGCTGGAAGGTCAAAAAACGTTGG
AATGCCCATTGCAATGTTACTGCACACAGATGGGGCGCATGAACGTCCCGGAGGTGATGCCACTGTTACAATATC
TCATCGATATACTCCCAAAGAGCAGTTGAAGAAACATACAATTCCTGCGATATTGTAATATCTGCTGCAGGTAT
TCCAAATCTGATCACAGCAGATATGATCAAGGAAGGAGCAGCAGTCATTGATGTGGGAATAAATAGAGTTCACGA
TCCTGTAAGTGCCTGAGGTGTTGGCCCCATGACAGTGGCAATGCTAATGAAGAATACCATTATTGCTGCAAAAAAGGT
TCCAGTTCCTGGAGGTGTTGGCCCCATGACAGTGGCAATGCTAATGAAGAATACCATTATTGCTGCAAAAAAGGT
GCTGAGGCTTGAAGAGCGAGAAGTGCTGAAGTCTAAAGAGCTTGGGGTAGCCACTAAT**TAA**CTACTGTGTCTTCT
GTGTACACAAACAGCACTCCAGGCCAGCTCAAGAAGCAAAGCAGGCCAATAGAAATGCAATATTTTTAATTTATTC
TACTGAAATGGTTTAAAATGATGCCTTGTATTTATTGAAAGCTTAAATGGGTGGGTGTTTCTGCACATACCTCTG
CAGTACCTCACCAGGGAGCATTCCAGTATCATGCAGGGTCTGTGATCTAGCCAGGAGCAGCCATTACCTAGTG
ATTAATATGGGAGACATTACCATATGGAGGATGGATGCTTCACTTTGTCAAGCACCTCAGTTACACATTGCGCTT
TTCTAGGATTGCATTTCCCAAGTGCTATTGCAATAACAGTTGATACTCATTTTAGGTACCAGACCTTTTGAGTTC
AACTGATCAAAACCAAAGGAAAAGTGTGCTAGAGAAAATTGGGGAAAAGGTGAAAAAGAAAAAATGGTAGTAATT
GAGCAGAAAAAAATTAATTTATATATGATTGATTGGCAACCAGATTTATCTAAGTAGAACTGAATTGGCTAGGA
AAAAAGAAAAACTGCATGTTAATCATTTTCCTAAGCTGTCCTTTTGAGGCTTAGTCAGTTTATTGGGAAAATGTT
TAGGATTATTCCTTGCTATTAGTACTCATTTTATGTATGTTACCCTTCAGTAAGTTCTCCCCATTTAGTTTTCT
AGGACTGAAAGGATTCTTTTCTACATTATACATGTGTGTTGTCATATTTGGCTTTTGCTATATACTTTAACTTCA
TTGTTAAATTTTTGTATTGTATAGTTTCTTTGGTGTATCTTAAACCTATTTTTGAAAAACAACTTGGCTTGAT
AATCATTTGGGCAGCTTGGGTAAGTACGCAACTTACTTTCCACCAAAGAACTGTCAGCAGCTGCCTGCTTTTCT
GTGATGTATGTATCCTGTTGACTTTTCCAGAAATTTTTAAGAGTTTGAGTTACTATTGAATTTAATCAGACTTT
CTGATTAAAGGGTTTTCTTTCTTTTTTAATAAAACACATCTGTCTGGTATGGTA

WO 2004/030615

PCT/US2003/028547

855/6881
FIGURE 795

MSALAARLLQPAHSCSLRLRPFHLAAVRNEAVVISGRKLAQQIKQEVQRQVEEWWASGNKRPHLSVILVGENPAS
HSYVLNKTRAAAVVGINSETIMKPASISSEELLNLINKLNDDNVDGLLVQLPLPEHIDERRICNAVSPDKDVG
FHVINVGRMCLDQYSMLPATPWGVWEIIKRTGIP TLGKNVVVAGRSKNVGMP IAML LHTDGAHERPGGDATVTIS
HRYTPKEQLKKHTILADIVISAAGIPNLITADMIKEGAVIDVGINRVHDPVTAKPKLVGDVDFEGVRQKAGYIT
PVPGGVGPM TVAMLMKNTIIAAKKVLRLEEREVLKSKELGVATN

WO 2004/030615

PCT/US2003/028547

856/6881
FIGURE 796

GGAAAATTTGTACAGCAGCCAGAGGGGTTTAAACAGGAGTGCAGAGGGATAAGGGCAGCTTCTGCCCTCTGCCCCA
AGAGCTGGCCACCTCTTTAAAGACTGAGGGAACAGTGGGAGGAGGAACCTGTGGGACAGTGTGGTACCTATCTGTC
CCCCCTCTGGAGGGGTTGACAAGGGAAGGGCACCGGGGGGCACAGAGATGCAGGACAGATTGCACATCCTGGAG
GACCTGAATATGCTCTACATTGGCAGATGGCACTCAGCCTGGAGGACACGGAGTTGCAGAGGAAGCTAGACCAT
GAGATCCGGATGAGGGAAGGGGCTGTAAAGCTGCTGGCAGCCTGCTCCCAGCGAGAGCAGGCTCTGGAGGCCACC
AAGAGCCTGCTAGTGTGCAACAGCCGCATCCTCAGCTACATGGGCGAGCTGCAGCGGCGCAAGGAGGCGCAGGTG
CTGGGAAGACAAGCCGGCGGCTTCTGACAGTGGCCCGCCGCTGAGCGCTCCCCCTGCCGCGGCGGGTCTGC
ATCTCTGACCTCCGGATTCCACTCATGTGGAAGGACACAGAATATTTCAAGAACAAAGGTGACTTGCACCGCTGG
GCTGTGTTCTGTGCTGCTGCAGCTGGGGGAACACATCCAGGACACAGAGATGATCCTAGTGGACAGGACCCTCACA
GACATCTCCTTTAGAGCAATGTGCTCTTCGCTGAGGCGGGGCCAGACTTTGAACTGCGGTTAGAGCTGTATGGG
GCCTGTGTGGAAGAAGAGGGGGCCCTGACTGGCGGGCCCCAAGAGGCTTGCCACCAAACCTCAGCAGCTCCCTGGGC
CGCTCCTCAGGGAGGCGTGTCCGGGCATCGCTGGACAGTGTGGGGGTTTCCAGGGAGCAGTCCCATCTTGCTCCCC
ACCCAGTTGTTGGTGGTCCCTCGTTACCACCTCTTGGCTCACACCACACTCACCTGGCAGCAGTGCAAGATGGA
TTCCGCACACATGACCTCACCTTGCCAGTCATGAGGAGAACCCTGCCTGGCTGCCCTTTATGGTAGCGTGTGT
TGCCGTCTGGCAGCTCAGCCTCTCTGCATGACTCAGCCCACTGCAAGTGGTACCCTCAGGGTGCAGCAAGCTGGG
GAGATGCAGAACTGGGCACAAGTGCATGGAGTTCTGAAAGGCACAAACCTCTTCTGTTACCGGCAACCTGAGGAT
GCAGACACTGGGGAAGAGCCGCTGCTTACTATTGCTGTCAACAAGGAGACTCGAGTCCGGGCAGGGGAGCTGGAC
CAGGCTCTAGGACGGCCCTTACCCTAAGCATCAGTAACCAGTATGGGGATGATGAGGTGACACACACCCTTACG
ACAGAAAAGTCGGGAAGCACTGCAGAGCTGGATGGAGGCTCTGTGGCAGCTTTTCTTTGACATGAGCCAATGGAAG
CAGTGCTGTGATGAAATCATGAAAATTGAAACTCCTGCTCCCCGGAAACCACCCCAAGCACTGGCAAAGCAGGGG
TCCTTGTAACCATGAGATGGCTATTGAGCCGCTGGATGACATCGCAGCGGTGACAGACATCCTGACCCAGCGGGAG
GGCGCAAGGCTGGAGACACCCCCACCCTGGCTGGCAATGTTTACAGACCAGCCTGCCCTGCCTAACCCCTGCTCG
CCTGCCTCAGTGGCCCCAGCCCCAGACTGGACCCACCCCTGCCCTGGGGGAGACCCGAACCTTTTCCCTGGAT
GCTGTCCCCCAGACCACTCCCCTAGGGCTCGCTCGGTTGCCCCCTCCCACCTCAGCGATCCCCACGGACCAGA
GGCCTCTGCAGCAAAGGCCAACCTCGCACTTGGCTCCAGTCACCAAGTGTGAGAGAGAAAGGTGCTGGCATAGGAT
CTGCCCAGAAGAGAAAATGACCCATGCGCAGTTGGGCTCTGGATACGGCGCTGTCTATAGCAAGTTGGCCAGTCT
GGCTCCTGTTCTCTGCTGGACCTGGGGTAGGCTGCAGGGGTGGGCAGAAGCCCTCTTAAATTGTGGTTGCCA
TGGTACCGAGGGACTCATTCCTGGGGCTCGCTGGGACCTCCCTAAACCCTTCTTGAAGAAAACCTGGAACCACT
CTGCCCTACCTCCCTGCACTAACCAGCTTTGAGGATGGCACTGAAGAACCCTTGAGCAACATACCTCCCTGT
GACTCCACATCAACCATTAAGTTATTTAACAGCAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

857/6881
FIGURE 797

MQDRLHILEDLNMLYIROMALSLEDTELQRKLDHEIRMREGACKLLAACSQREQALEATKSLVCNSRIILSYMGE
LQRRKEAQVLGKTSRRPSDSGPPAERSPCRGVCISDLRIPLMWKDTEYFKNKGDHLRWAVFLLLQLGEHIQDTE
MILVDRTLTDISFQSNVLF AEAGPDFELRLELYGACVEEEGALTGGPKRLATKLSSSLGRSSGRRVRASLDSAGG
SGSSPILLPTPVVGGPRYHLLAHTTLTAAVQDGFRTDHLTLASHEENPAWLPLYGSVCCRLAAQPLCMTQPTAS
GTLRVQQAGEMONWAQVHGVLKGTNLCYRQPEDADTGEEPLLTIAVNKETRV RAGELDQALGRPFTLSISNQYG
DDEVTHLTQTESREALQSWMEALWQLFFDMSQWKQCCDEIMKIETPAPRKPPQALAKQGSLYHEMAIEPLDDIAA
VTDILTQREGARLETPPPWLAMFTDQPALPNPCSPASVAPAPDWTPLPWGRPRTFSLDAVPPDHSPRARSVAPL
PPQRSRPRTRGLCSKGQPRTWLQSPV

WO 2004/030615

PCT/US2003/028547

858/6881
FIGURE 798

GACTACGTGGGTCTGGAGCTGACTGCCGTCTTGACACGTCTAGAGCTGCAAGTCCTGCCAGAGAGCCACCATGA
CCTCTCAGCCTCTCAGGCTAGCAGAAGAGTATGGCCCAAGTCCTGGGGAGTCTGAACTGGCTGTGAACCCCTTTG
ATGGGCTTCCCTTCTCTTCCCGCTACTATGAGCTGCTGAAGCAGCGCCAAGCCTTGCCCATCTGGGCTGCTCGCT
TTACCTTCTTGGAGCAGTTGGAGAGTAACCCCACTGGAGTGGTGTCTGGTGTCTGGGGAGCCTGGTTCTGGCAAGA
GCACCCAGATCCCTCAGTGGTGTGCAGAGTTTGCCTGGCCAGAGGGTTCCAGAAAGGACAGGTTACTGTTACTC
AGCCCTACCTCTTGCAGCCCCGGGAGCCTGGCTCTGCGGGTTGCTGATGAGATGGACCTGACCCCTGGGTCATGAG
GTTGGATCCAGCATCCCCAGGAGGACTGCACGGGGGCCAACACCCTGCTCAGGTTCTGCTGGGACAGGCTGCTT
CTGCAGGAGGTGGCTCGACCCGAGGCACTGGAGCCTGGGGCGTGCTGGTACTAGATGAGGCTCAGGAGCGGTCTG
GTGGCATCAGATTCACTCCAGGGGCTACTGCAAGATGCCAGGCTGGAAAACTTCCGGGGGACCTCAGAGTGGTT
GTGGTTACTGACCCAGCCCTTGAACCTAAGCTCCGAGCTTTCTGGGGCAATCCTCCTATTGTGCATATACCCAGA
GAGCCTGGTGAGAGACCTTCCCCCATCTACTGGGACACCATCCACCTGATCGGGTGGAAGCTGCCTGCCAAGCA
GTGCTTGAATTGTGTGCGGAAGGAGCTTCCAGGAGATGTGCTAGTGTTCCTGCCCAGTGAGGAGGAAATTTCCCTG
TGCTGTGAATCCTTGTCCAGGGAGGTAGAGTCCTTGCTTCTCCAAGGGCTTCCACCACGAGTACTGCCCTTCAC
CCAGACTGTGGACGAGCCGTTCAAGGCTGTGTATGAGGACATGGATGCCCGAAAGGTTGTGGTCACTCACTGGCTG
GCTGACTTCTCCTTCTCCCTCCCTTCCATCCAACATGTCATCGACTCAGGACTGGAGCTCCGAAGTGTTTACAAT
CCTAGGATCCGAGCAGAATTCCAAGTGTGAGGCCAATCAGCAAGTGTGAGGACAGAGGCAAGACGATTGCGAGCA
AGAGGGTTCCCAACAGGATCCTGCCTCTGCCTGTATCCTAAGTCCTTCTTAGAACTAGAAGCTCCACCATTGCCA
CAACCCAGGGTGTGTGAGGAGAATCTGAGCTCCCTGGTGTACTACTAAAAAGGAGACAGATTGCAGAGCCAGGG
GAGTGTCACTTCTTGACCAGCCTGCTCCAGAAGCACTGATGCAAGCCCTGGAAGATTTAGACTATCTGGCAGCC
CTGGATGATGATGGGGACCTGTGAGATCTGGGTGTCTACTATCAGAAATCCCTCTGGCCCTGAGCTGGCCAAA
GCCCTGCTGGCCTCATGCGAGTTTACTGTGTGGACGAGATGCTCACCTGGCTGCCATGCTCACAGCTGCCCT
GGGTTTACCCGTCTTCACTCAGTGCAGAAGAAGCTGCCCTGCGTCGGGCCCTGGAACACACGGATGGTGACCAC
AGTTCTCTGATCCAGGTGTATGAAGCCTTTATACAAAGTGGAGCAGATGAGGCTTGGTGCCAGGCTCGAGGTCTG
AATTGGGCAGCATTGTGCCAAGCCCATAACTTCCGGGAGAACTCCTAGAACTCATGCAACGAATTGAACTTCCC
TTGTCCCTACCAGCCTTTGGCTCTGAGCAGAATCGCAGAGACCTTCAGAAAGCACTGGTGTGAGAATACTTTCTC
AAGGTGGCCAGAGACACAGACGGGACTGGAAATTACCTTCTCTAACCATAAGCATGTGGCCAGCTCTCCTCA
TACTGCTGCTACCGAAGCCGACAGAGCTCCTGCCAGACCCCAACCATGGGTGCTCTACCACAATTTACCATATCC
AAAGACAACTGCCTCTCCATTGTTTCTGAGATTCAACCACAGATGCTGGTGGAATTGGCCCTCCATACTTCTG
AGTAACTTGCTCCAGTGAGAGCAGAGACCTTCTGAACCACTAAGGGAAGGAATGGCAGATTCTACAGCAGGG
AGCAAATCATCCTCAGCCCAGGAGTTCAGAGATCCCTGTGTCTGCTGAGTGAACCTGCCTGCCTATGGAATGGAGCT
GGGTTCACTCATCACATTAGATTATCCCTCAGGGTGACACCAAGCACCCAGACAGATTTAGAAGCCCAAGTT
TAGGGTCAAATGTAAACCCTGGAACCTGAGTCCCAAGAAATGGTAGACTGGGAATGGAAGAATGGGGTAAACCA
CAGTCTACATAGGGAAGGACTCTTTCCTTAGCCTTCTCTTATTGATTGGAGAGGGACTGACATGCTCCTCATTCT
CTTAACCTTTGCCAAACCCATTCTTGTACTCCCTTGTGATCTATAAAAGATTTTTCTATGATGCCAAAAAAAAA
AAAAAAAAA

WO 2004/030615

PCT/US2003/028547

859/6881
FIGURE 799

MDLTGHEVGSSIPQEDCTGPNLTLLRFCWDRLLLQEVASTRGTGAWGVLVLDEAQERSVASD\$SLQGLLQDARLEK
LPGDLRVVVVTDPALEPKLRAFWGNPPIVHIPREPGERPSPIIYWDTIPPDRVEAACQAVLELCRKELPGDVLVFL
PSEEEISLCCESLSREVESLLLQGLPPRVLP LHPDCGRAVQAVYEDMDARKVVVTHWLADFSFSLPSIQHVIDSG
LELRSVYNPRIAEFQVLRPISKQAEARRLRARGFPPGSCCLCLYPKSFLELEAPPLPQPRVCEENLSSLVLLLK
RRQIAEPGECHFLDQPAPEALMQALEDLDYLAALDDDGDLSDLGVILSEFPLAPELAKALLASCEFDCVDEMLTL
AAMLTAAPGFTRPPLSAEEAALRRALEHTDGDHSSLIQVYEAFIQSGADEAWCQARGLNWAALCQAHKLRGELLE
LMQRIELPLSLPAFGSEQNRDLQKALVSEYFLKVARDTDGTGNYYYYLTHKHVAQLSSYCCYRSRRAPARPPPWW
LYHNFTISKDNCLSIIVSEIQPQMLVELAPPYFLSNLPPSESRLNQLREGMADSTAGSKSSSAQEFRDPCVLQ

WO 2004/030615

PCT/US2003/028547

860/6881
FIGURE 800

CGAAAAATGGCGGCGGCGGCGACGGCCGGGCGCTCCTGAAGCAGCAGTTATGGAGCTTCCCTCAGGGCCGGGGCCG
GAGCGGCTCTTTGACTCGCACCGGCTTCCGGGTGACTGCTTCCTACTGCTCGTGCTGCTGCTCTACGCGCCAGTC
GGGTTCGCTCCTCGTCTGCGCTCTTTCTCGGGATCCACGTCTTCCTGGTCAGCTGCGCGCTGCCAGACAGC
GTCTTCGCAGATTGCTAGTGCGGACCATGTGTGCGGTGCTAGGGCTCGTGGCCCGGCAGGAGGACTCCGGACTC
CGGGATCACAGTGTGAGGGTCTCATTTCCAACCATGTGACACCTTTGACCACAACATAGTCAATTTGCTTACC
ACCTGTAGCACCCCTCTACTCAATAGTCCCCCAGCTTTGTGTGCTGGTCTCGGGGCTTCATGGAGATGAATGGG
CGGGGGGAGTTGGTGGAGTCACTCAAGAGATTCTGTGCTTCCACGAGGCTTCCCCCACTCCTCTGCTGCTATT
CCTGAGGAAGAGGCCACCAATGGCCGGGAGGGGCTCCTGCGCTTCAGTTCTGGCCATTTTCTATCCAAGATGTG
GTACAACCTCTTACCCTGCAAGTTCAGAGACCCCTGGTCTCTGTGACGGTGTGAGATGCCTCCTGGGTCTCAGAA
CTGCTGTGGTCACTTTTCGTCCCTTTACGGTGTATCAAGTAAGGTGGCTTCGTCTGTTCATCGCCAAGTGGG
GAAGCGAATGAGGAGTTTGCCTCCGTGTACAACAGCTGGTGGCCAAGGAATTGGGCCAGACAGGGACACGGCTC
ACTCCAGCTGACAAAGCAGAGCACATGAAGCGACAAAGACACCCAGATTGCGCCCCAGTCAGCCCAGTCTTCT
TTCCCTCCCTCCCTGGTCTCTCTCTGATGTGCAACTGGCAACTCTGGCTCAGAGAGTCAAGGAAGTTTGGCC
CATGTGCCATTGGGTGTGATCCAGAGAGACCTGGCCAAGACTGGCTGTGTAGACTTGACTATCACTAATCTGCTT
GAGGGGGCCGTAGCTTTTCATGCCTGAAGACATCACCAAGGGAAGTCCCTACCCACAGCCTCTGCCTCCAAG
TTTCCCAGCTCTGGCCCGGTGACCCCTCAGCCAACAGCCCTAACATTTGCCAAGTCTTCTGGGCCCGGCAGGAG
AGCCTGCAGGAGCGCAAGCAAGCACTATATGAATACGCAAGAAGGAGATTACAGAGAGACGAGCCCAGGAGGCT
GACTGAGCTCAAAGGAACAGGATGGCACCCAGAGCCGAGGACGGAGACTGGGGGCAGCCCTCACCCAACTCACA
ACAGGCTGGATGGGTGGGTGGTAAAAAGGGAAGGATGAGGCTCCCCCAATGTACATTAAATTCATGGTTTTTCAT
TC

WO 2004/030615

PCT/US2003/028547

861/6881
FIGURE 801

CGTGGATCCCGAGAAAGAGGCGCAGGACGAGGAGGCAGAACCCGACTGGCGCGTAGAGCAGCAGCACGAGCAGTA
GGAAGCAGTCACCCGGAAGCCTGGGGGCGAGAGGCGAAGTGGTCAGGCGCCGAAGGCCGAGAGCACGCGGGGATC
GGTCTCTTCCCGCCGGGTCTCTTACCGGTGCGAGTCAAAGAGCCGCTCCGGCCCCGGCCCTGAGGGAAGCTCCAT
AACTGCTGCTTCAGGAGCGCCCGGCGTCCCGCCGCCGCCATTTTCGCGCCCGGCCGCGAGGGGCTCTTGGGAAG
GCGGAGTCTTTGGGCATCCGCCCGGGGTGAGGGGACCCGAAGTCTGAGGCGCGCCGGAAGGGCTAGCGGTCCCA
GCATACCCCGCGGCCCTTGGGCCGTCTCACAACCTCGCGTCCGGCGGAGACCACAATTCCCGGCATTCTGTGGGGC
AGGGAGGAGTCGGCTCCCGGAATCCTGGTCCCGGCGTGCACTTCTGAAGGACTTCAGGTACCGGCGTGCCCCGC
GTCCTACTGTCCGCTGCTCGCGTCTTGGGTGCCGCTCTGAGTAGGGCGGGCGAGGAGGCAGCCAAGGCGGAGC
TGATGGCTGCGCCGAGGGCGGGGCGGGGTGCAAGGCTGGAGCCTTCGGGCATGGCGGGCTTTGGGGGGCATTCTGCT
GGGGGAGGAGACCCGTTTGACCCCTGACCTCCGGGCCCTGCTGACGTCAGGAACCTTCTGACCCCGGGCCCGAG
TGACTTATGGGACCCCAAGTCTCTGGGCCCGGTTGTCTGTTGGGGTCACTGAACCCCGAGCATGCCTGACGTCTG
GGACCCCGGGTCCCCGGGCACAACCTGACTGCGGTGACCCAGATACCAGGACCCGGGAGGCCTCAGAGAACCTCTG
GAACCCGTTTCGCGCGCTGGCTGGCGGTGGCGCTGGGCGCTGGGGGGGCAAGTGTCTGTTGTTGTTGTTGGGGCGGGG
GTCGGGGTCTCCGGCCGTCTCGCGCCGTCCTAGCCCGCCGCCGCTTCTCCCGGAGTCAGTACAACCTTCA
TCGCAGATGTGGTGAGAGAAGACAGCACCTGCCGTGGTCTATATCGAGATCCTGGACCGGCACCCCTTCTTGGGCC
GCGAGGTCCCTATCTCGAACGGCTCAGGATTCTGTGGTGGCTGCCGATGGGCTCATTGTACCAACGCCCATGTGG
TGGCTGATCGGCGCAGAGTCCGTGTGAGACTGCTAAGCGGCGACACGTATGAGGCGGTGGTCACAGCTGTGGATC
CCGTGGCAGACATCGCAACGCTGAGGATTGAGACTAAGGAGCCTCTCCCCACGCTGCCTCTGGGACGCTCAGCTG
ATGTCCGGCAAGGGGAGTTTGTGTTGCCATGGGAAGTCCCTTTGCACTGCAGAACACGATCACATCCGGCATTG
TTAGCTCTGCTCAGCGTCCAGCCAGAGACCTGGGACTCCCCAAACCAATGTGGAATACATTCAAACCTGATGCAG
CTATTGATTTTGGAACTCTGGAGGTCCCCTGGTTAACCTGGATGGGGAGGTGATTGGAGTGAACACCATGAAGG
TCACAGCTGGAATCTCCTTTGCCATCCCTTCTGATCGTCTTCGAGAGTTTCTGCATCGTGGGGAAAAGAAGAATT
CCTCCTCCGGAATCAGTGGGTCCCAGCGGCGCTACATTGGGGTGATGATGCTGACCCTGAGTCCCAGCATCCTTG
CTGAACTACAGCTTCGAGAACCAAGCTTTCCCGATGTTTACGATGGTGTACTCATCCATAAAGTCATCCTGGGCT
CCCCTGACACCCGGGCTGGTCTGCGGCCTGGTGATGTGATTTTGGCCATTGGGGAGCAGATGGTACAAAATGCTG
AAGATGTTTATGAAGCTGTTTGAACCAATCCAGTTGGCAGTGCAGATCCGGCGGGGACGAGAAACACTGACCT
TATATGTGACCCCTGAGGTCACAGAAATGAATAGATCACCAAGAGTATGAGGCTCCTGCTCTGATTTCTCCTTGC
CTTCTGGCTGAGGTTCTGAGGGCACCGAGACAGAGGGTTAAATGAACAGTGGGGGAGGTCCCTCCAACCACC
AGCACTGACTCCTGGGCTCTGAAGAATCACAGAAACACTTTTATATAAAATAAAATTATACCTAGCAACATATT
ATAGTAAAAAATGAGGTGGGAGGGCTGGATCTTTTCCCCCACCAAAAGGCTAGAGGTAAAGCTGTATCCCCCTAA
ACTTAGGGGAGATACTGGAGCTGACCATCCTGACCTCCTATTAAAGAAAATGAGCTGCTGAAAAA

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WO 2004/030615

PCT/US2003/028547

862/6881
FIGURE 802

MAAPRAGRAGWSLRAWRALGGIRWGRRPRLTPDLRALLTSGTSDPRARVTYGTPSLWARLSVGVTEPRACLTSG
TPGPRAQLTAVTPDTRTREASENSGTRSRRAWLAVALGAGGAVLLLLWGGRGPPAVLAAVPSPPPASPRSQYNFI
ADVVEKTAPAVVYIEILDRHPFLGREVPISNGSGFVVAADGLIVTNAHVVADRRRVVRLLSGDTYEAVVTAVDP
VADIATLRIQTKEPLPTLPLGRSADVQGEFVVAMGSPFALQNTITSGIVSSAQRPARDLGLPQTNVEYIQTDA
IDFGNSGGPLVNLGDEVIGVNTMKVTAGISFAIPSDRLREFLHRGEKKNSSSGISGSQRRYIGVMMLTLSPSILA
ELQLREPSFPDVQHGVLIHKVILGSPAHRAGLRPGDVILAIGEOMVQNAEDVYEAVRTQSQLAVQIRRGRETTL
YVTPEVTE

WO 2004/030615

PCT/US2003/028547

863/6881
FIGURE 803

GCAACGCGAGTGGGAGCACCAGGATCTCGGGCTCGGAACGAGACTGCACGGATTGTTTTAAGAAAATGGCAGACA
AACCAGACATGGGGGAAATCGCCAGCTTCGATAAGGCCAAGCTGAAGAAAACGGAGACGCAGGAGAAGAACACCC
TGCCGACCAAAGAGACCATTGAGCAGGAGAAGCGGAGTGAAATTTCTTAAGATCCTGGAGGATTCCTACCCCCG
TCCTCTTCGAGACCCCAGTCGTGATGTGGAGGAAGAGCCACCTGCAAGATGGACACGAGCCACAAGCTGCACTGT
GAACCTGGGCACTCCGCGCCGATGCCACCGGCCTGTGGGTCTCTGAAGGGACCCCCCCCCAATCGGACTGCCAAA
TTCTCCGGTTTGGCCCGGGATATTATAGAAAATTATTTGTATGAATAATGAAAATAAAACACACCTCGTGGCATG
GCA

WO 2004/030615

PCT/US2003/028547

864/6881
FIGURE 804

MADKPDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSEIS

WO 2004/030615

PCT/US2003/028547

865/6881
FIGURE 805

CACCAAATGGCGGATGACGCCGGTGCAGCGGGGGGGCCAGAGCCCTGGTGGCCATGGGATAGGGAACCGCGGTG
GCTTCCACGGAGGTTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGGAGTGGACGGGGCCGTGCCGAGGCCGCGG
AGCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCTGTCACCAAGCTGGGCCGCTTGGTCAAGGACATGAA
GATCAAGTCCCTGGAGGAGATCTATCTTCTCCCTGCCATTAAAGGAATCTGAGATCATTGATTTCTTCCTGGG
GGACTCTCTCAAGGATGAGGTTTTGAAGATTATGCCGGTGCAGAAGCAGACCCGTGCCGGCCAGCGCACCAGGTT
CAAGGTGACAGGCCGCTGCGGCTCTGTGCTGGTGCGCCTCATCCCTGCACCCAGGGGCACTGGCATCGTCTCCGC
ACCTGTGCCCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTACACCTCAGCCCCGGGGCTGCACTGCCAC
CCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATCTCTAAGACCTACAGCTACCTGACCCCCGACCTCTGGAA
GGAGACTGTATTTACCAAGTCTCCCTATCAGGAATTCAGTACCACCTCGTCAAGACCCACACCAGAGTCTCGGT
GCAGCGGACCCAGGCTTCAGATGTGGCTACAACATAGGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCCTG

WO 2004/030615

PCT/US2003/028547

866/6881
FIGURE 806

CGCAGGCTGGAAGGAAGACGAACCTACGAAGCAGAGATCTGAAGACAGCATGTACACAGCCATTCCCCAGAGTGG
CTCTCCATTCCCAGGCTCAGTGCAGGATCCAGGCCTGCATGTGTGGCGGGTGGAGAAGCTGAAGCCGGTGCCTGT
GGCGCAAGAGAACCAGGGCGTCTTCTTCTCGGGGGACTCCTACCTAGTGTGCTGCACAATGGCCCAGAAGAGGTTTC
CCATCTGCACCTGTGGATAGGCCAGCAGTCATCCCGGGATGAGCAGGGGGCCTGTGCCGTGCTGGCTGTGCACCT
CAACACGCTGCTGGGAGAGCGGCCTGTGCAGCACCGCGAGGTGCAGGGCAATGAGTCTGACCTCTTCATGAGCTA
CTTCCCACGGGGCCTCAAGTACCAGGAAGGTGGTGTGGAGTCAGCATTTTACAAGACCTCCACAGGAGCCCCAGC
TGCCATCAAGAACTCTACCAGGTGAAGGGGAAGAAGAACATCCGTGCCACCGAGCGGGCACTGAACTGGGACAG
CTTCAACACTGGGGACTGCTTCATCCTGGACCTGGGCCAGAACATCTTCGCCTGGTGTGGTGGAAAGTCCAACAT
CCTGGAACGCAACAAGGCGAGGGACCTGGCCCTGGCCATCCGGGACAGTGAGCGACAGGGCAAGGCCCAGGTGGA
GATTGTCACTGATGGGGAGGAGCCTGCTGAGATGATCCAGGTCCTGGGCCCCAAGCCTGCTCTGAAGGAGGGCAA
CCCTGAGGAAGACCTCACAGCTGACAAGGCAATGCCCAGGCCGAGCTCTGTATAAGGTCTCTGATGCCACTGG
ACAGATGAACCTGACCAAGGTGGCTGACTCCAGCCCCTTTGCCCTTGAAGTCTGATATCTGATGACTGCTTTGT
GCTGGACAACGGGCTCTGTGGCAAGATCTATATCTGGAAGGGGCGAAAAGCGAATGAGAAGGAGCGGCAGGCAGC
CCTGCAGGTGGCCGAGGGCTTCATCTCGCGCATGCAGTACGCCCCGAACACTCAGGTGGAGATTCTGCCTCAGGG
CCGTGAGAGTCCCATCTTCAAGCAATTTTCAAGGACTGGAAATTGAGGGGTGGGCGTCTTCCTGCCCCATGCTCCC
CTGCCCCCACCACCTGCCTGCTTGCTTCTCTGGCTGCCTGGTCAGTGCAGAGGTGCCCCCTGCAGATGTTCAAT
AAAGGAGACAAGTGCTTTCCC

WO 2004/030615

PCT/US2003/028547

867/6881
FIGURE 807

MYTAIPQSGSPFFPGSVQDPGLHVWRVEKLKPVVPAQENQGVFFSGDSYLVLHNGPEEVSHLHLWIGQQSSRDEQG
ACAVLAVHLNLTLLGERPVQHREVQGNESDLFMSYFPRGLKYQEGGVESAFHKTSTGAPAAIKKLYQVKGKKNIRA
TERALNWD SFNTGDCFILDLGQNI FAWCGGKSNI LERNKARDLALAIRDSERQGKAQVEIVTDGEEPAEMIQVLG
PKPALKEGNPEEDLTADKANAAALYKVSDATGQMNLT KVADSSPFALELLISDDCFVLDNGLCGKIYIWKGRK
ANEKERQAALQVAEGFISRMQYAPNTQVEILPQGRESPIFKQFFKDWK

WO 2004/030615

PCT/US2003/028547

868/6881
FIGURE 808

GGCACGAGGCGCCCGCCTGCTACGAGTAGAACGCTGTCCGCAGCTTGCGCATTTTCGCAGCCGCTGCCGCCTCGCC
GCTGCTCCTTCGTAAGGCCACTTCCGCACACCGACACCAACATGAACGGACAGCTCAACGGCTTCCACGAGGCGT
TCATCGAGGAGGGGCACATTCCCTTTTACCTCAGAGTCGGTTCGGGAAGGCCACCCAGATAAGATTTGTGACCAAA
TCAGTGATGCTGTCCTTGATGCCACCTTCAGCAGGATCCTGATGCCAAAGTAGCTTGTGAAACTGTTGCTAAAA
CTGGAATGATCCTTCTTGCTGGGAAAATTACATCCAGAGCTGCTGTTGACTACCAGAAAGTGGTTCTGTGAAGCTG
TTAAACACATTGGATATGATGATTCTTCCAAAGGTTTTGACTACAAGACTTGTAACGTGCTGGTAGCCTTGGAGC
AACAGTCACCAGATATTGCTCAAGGTGTTTCATCTTGACAGAAATGAAGAAGACATTGGTGTGGAGACCAGGGCT
TAATGTTTGGCTATGCCACTGATGAACTGAGGAGTGATGCCCTTTAACCATTGTCTTGGCACACAAGCTAAATG
CCAACTGGCAGAACTACGCCGTAATGGCACTTTGCCCTTGGTTACGCCCTGATTCTAAACTCAAGTTACTGTGC
AGTATATGCAGGATCGAGGTGCTGTGCTTCCCATCAGAGTCCACACAATTGTTATATCTGTTTACAGCATGATGAAG
AGGTTTGTCTTGATGAAATGAGGGATGCCCTAAAGGAGAAAGTCATCAAAGCAGTTGTGCCTGCGAAATACCTTG
ATGAGGATACAATCTACCACCTACAGCCAAGTGGCAGATTTGTTATTGGTGGGCTCAGGGTGATGCTGGTTTGA
CTGGACGCAAAATCATTGTGGACACTTATGGCGTTGGGGTGCTCATGGAGGAGGTGCCCTTTTCAGGAAAGGATT
ATACCAAGGTCGACCGTTCAGCTGCTTATGCTGCTCGTTGGGTGGCAAAATCCCTTGTTAAAGGAGGTCTGTGCC
GGAGGGTCTTGTTCAGGTCTCTTATGCTATTGGAGTTTCTCATCCATTATCTATCTCCATTTTCCATTATGGTA
CCTCTCAGAAGAGTGAGAGAGAGCTATTAGAGATTGTGAAGAAGAATTTGATCTCCGCCCTGGGGTCATTGTCA
GGGATCTGGATCTGAAGAAGCCAATTTATCAGAGGACTGCAGCCTATGGCCACTTTGGTAGGGACAGCTTCCCAT
GGGAAGTGCCCAAAAGCTTAAATATTGAAGTGTAGCCTTTTTTCCCCAGACTTGTGGCGTAGGCTACAGAG
AAGCCTTCAAGCTCTGAGGGAAGGGCCCTCTTCCCTAAATTTTCTGTCTCTTTCAGCTCCTGACCAGTTGCA
GTCACCTCTAGTCAATGACATGAATTTTAGCTTTTGTGGGGGACTGTAAGTTGGGCTTGCTATTCTGTCCCTAGGT
GTTTTGTTACCAATTATAATGAATTTAGTGAGCATAGGTGATCCATGTAAGTGCCTAGAAACAACACTGTAGTAA
ATAATGCTTTGAAATTGAACCTTTGTGCCCTATCACCAACGCTCCAAAGTCATAATTGCATTGACTTTCCCCAC
CAGATGCTGAAAATGTCCTTGATGTGCACGTAAAGTACTTGTAGTTCCACTTATAGCCTCTGTCTGGCAATGC
CACAGCCCTGTCAGCATGAATTTGTAATGCTTGAGCTCTATTATGAATGTGAAGCCTTCCCCCTTATCCTCCCTG
TAACTTGATCCATTTCTAATTATGTAGCTCTTTGTGAGGAGTGTCCCTATCCAATCAATCTTGCATGTAACGC
AAGTTCCCAGTTGGAGCTCCAGCCTGACATCAAAAAGGCAGTTACCATTAAACCATCTCCCTGGTGCTTATGCT
CTTAATTGCCACCTCTAACAGCACCAATCAAATCTCTCCACTTTCAGCTGTCTTTTGGAGGACGTACGTAATA
AGGTTTTAATTTAGTAAACCAATCCTATGCATGGTTTCAGCACTAGCCAAACCTCACCAACTCCTAGTTCTAGAA
AAACAGGCACTTGGCAGCCTTGATGTGCATACAGAGAAAGTCACAGGGCAGTACCTGAGGGTCTGTAGGTTGCAC
ACTTTGGTACCAGATAACTTTTTTTTTTCTTTATAAGAAAGCCTGAGTACTCCACACTGCACAATAACTCCTCCC
AGGGTTTTAACTTTGTTTTATTTTCAAACCAGGTCCAATGAGCTTTCTGAACAGCTGGTGTAGCTACAGAGAAA
CCAGCTTCTTCAGAGAGCAGTGCTTTTGGCGGGGAGGAGGAAATCCCTTCATACTTGAACGTTTTTCTAATTGCT
TTTTTTCTCTCAACACCATGATTCTTTTAAACAACATGTTTCCAGCATTTCCAGGTAGGCCAAGGTGTCTTACAG
AAAACTTGGGTAGACCTACAGGGGGTCTGGCTGGTGTAAACAGAAGGGAGGGCAGAGCTGGTGCGGCTGGCC
ATGGAGAAAGCTGACTTGGCTGGTGTGGTACAGAGAAGCCAGCTTGTTTACATGCTTATTCCATGACTGCTTGCC
CTAAGCAGAAAGTGCCCTTTCAGGATCTATTTTTGGAGGTTTATTACGTATGTCTGGTTCTCAATTCCAACAGTTT
AATGAAGATCTAAATAAAATGCTAGGTTCTACCTTAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

869/6881
FIGURE 809

MNGQLNGFHEAFIEEGTFLFTSESVGEGHPDKICDQISDAVLDAHLQQDPDAKVACETVAKTGMILLAGEITSRA
AVDYQKVVREAVKHIGYDDSSKGFYKTCNVLVALEQQSPDIAQGVHLDRNEEDIGAGDQGLMFGYATDETEECM
PLTIVLAHKLNAKLAE LRRNGTLPWLRPDSKTQVTVQYMQDRGAVLP IRVHTIVISVQHDEEVCLDEMRDALKEK
VIKAVVPAKYLDED TIYHLQPSGRFVIGGPQGDAGLTGRKIIVD TYGGWGAHGGGAFSGKDYTKVDRSAAYAARW
VAKSLVKGGLCRRVLVQVSYAIGVSHPLSISIFHYGTSQKSERELLEIVKKNFDLRPGVIVRDLDLKKPIYQRTA
AYGHFGRDSFPWEVPKKLKY

WO 2004/030615

PCT/US2003/028547

870/6881
FIGURE 810

ATGACACTCTGAGCGCTCCGGGAACGGACAGCCCGGCGGCTTCCCGAAGCCGGCGGCGCAGCTGCCCGGGGGCGAG
GGGGAGAAAGGGAGAGAGGGGAGGGGGAGGGCGGGCGAAGCGGGAGAGCCAGAGACTCCTCGGCGCTGAGCGCGGC
GGCGGGCCCGGGCAGCCCCACGCCCTGCCTCGCGCGCCGCGCCGCGCCATGAAGCACATCCCGGTCTCGAGGACG
GGCCGTGGAAGACCGTGTGCGTGAAGGAGCTGAACGGCCTTAAGAAGCTCAAGCGGAAAGGCAAGGAGCCGGCGC
GGCGCGCAACGGCTATAAACTTTCCGACTGGACTTGAAGCGCCCGAGCCCCGCGCCGTAGCCACCAACGGGC
TGCGGGACAGGACCCATCGGCTGCAGCCGGTCCCGGTACCGGTGCCGGTGCCAGTCCCAGTGGCGCCGGCCGTTT
CCCCAAGAGGGGGCACGGACACAGCCGGGGAGCGCGGGGGCTCTCGGGCGCCCGAGGTCTCCGACGCGCGGAAAC
GCTGCTTCGCCCTAGGCGCAGTGGGGCCAGGACTCCCCACGCCCGCCGCGCCGCGCCCTCTGCGCCCCAGAGCC
AGGCACCTGGGGGGCCAGAGGCACAGCCTTTCCGGGAGCCGGGTCCGCGTCTCGCATCTTGCTGTGCGCACCGC
CCGCGCGCCCCGCGCCGTGACACCCCCAGCAGCGCCCCCGGAGTCCACTGTGCGCCCTGCGCCCCCGA
CGCGCCCCGGGGAAAGTTCTACTCGTCAATTTACACGTAATTTACAATAACCACCAGGATTCTCCGCGTCGC
CTAGGAAACGACCGGGCGAAGCGACTGCCGCTCTCCGAGATCAAAGCCCTGCAGCAGACCCGGAGGCTCTTG
CGAACGCCAGGGAGCGGACGCGGGTGACACCATCAGCGCAGCCTTCGAGGCGCTCAGGAAGCAGTGCCGTGCT
ACTCATATGGGCAGAAGCTGTCCAACTGGCCATCCTGAGGATCGCCTGTAACTACATCCTGTCCCTGGCGGGC
TGGCTGACCTTGACTACAGTGCCGACCACAGCAACCTCAGCTTCTCCGAGTGTGTGCAGCGCTGCACCCGACCC
TGCAGGCCGAGGGACGTGCCAAGAAGCGCAAGGAGTGAAGTGGCTGCAGGCAAGACCAAGGCCACCACTGTGGGC
CTCCTTCCAGTCAGGCTGAGGACAAGGTGAGCTCGCTGAGTCCAGCCTCGTGGTCTTCTCCAAGATGCCGCCAG
ATGCCAGCCTACAGCCTCTCAGGGTCGGATCGGAGCACGCCTGCCTCCCTCTCCCTCCGCGCTCAGCCCCGACTCACTCAGACCCC
ATCCGAGGCTGCTTCGCACTTTGCCCTCTGCCTGGTGGGGAGGGGAGAGCTCAGCCCCGACTCACTCAGACCCC
AAGGCCCACTGTCCAGCTGCAGAAATTCGTTGCCAAAGATTGGACAGAGACACCGAAGGAAATGGGGTGGTGA
CCCCACAGCGAAAAGCCACACCGTTGCTCTGTGACTTTTGCTCCTCCTGTTGCCTGAGCCCCATCTCAAGCCAAA
GATGAGTCAGTGGTTCTGCTAGGAACTCATGGAATGGATGGGCATTTGATGACCCCTGGGGGTCTCTTGCCCT
CTGACCTGGTGCTCTCTCTCCACTGGGCCTTGCTGCTGGCTGAGTGCAAGACAAGCCTTAGGGGCTGTGAGAGGGA
GGCTGGGGTGCTGGGGCGGGCTGGGAGTGGGACCTGAGATCCCTGCCCCACTCTCTCCCTTCACTGGCTGCCA
GGCCACTGGCCCCAGTTCTCAGTGTCCCTTGGGTCCAGGCTCCTTGGGCCCTAAGCATCACCAGAAGGGAGTAAG
CAGGGAGAGAAGCAATATTACTCCCTCCCTACACCAGGACTTGCCCCAGGGCAGCTACCTATGGGTCTTTGCT
TCCCCAGCCAGCCTCTCCTCACTGTGACCCACCCCCATGGGCCCCCGTCCCAGGCAGCCAGCACCATGGGCAGGC
CCTGCCATGGGCAGAAAAAGAGTTTTTCTTTGTTTTCAGCCTGCACGTGGCCTGAGGAAGGAGTAGAGGCTGGGT
GGCTGGAGCCGCTCTACTGGGCAAGATGGCGCCCCACTTGAGGGCGGTGGTCTGTTACAGGGTGTGCAGGGGCA
GAGAAGGAAGGGACAGGGGACTGGGCCAGTATGTGGAGGATGGGGCCTGCGTGTTCAAAGCCAAGGCCCGCCCC
TTCCTTGTGCTCAAATGGCCAAAGCTGTTACGTCTGTGCTCAACCATCTGCTTCAAATTGAAGTAAAGCCCCA
AAATGTCAAGAAAAA
AAAAG

WO 2004/030615

PCT/US2003/028547

871/6881
FIGURE 811

MKHIPVLEDGPWKTVCVKELNGLKKLKRKGKEPARRANGYKTFRLDLEAPEPRAVATNGLRDRTHRLQPVFVPVP
VPVPVAPAVPPRGGTDTAGERGGSRAPVSDARKRCFALGAVGPGGLTPPPPPPPAPQSQAPEGGEAQPFREPGP
RPRILLCAPPARPAPSAPPAPPAPPESTVRPAPPTRPGESSYSSISHVIYNNHQDSSASPRKRPGEATAASSEIK
ALQQTRRLLANARERTRVHTISAAFEALRKQVPCYSYGQKLSKLAILRIACNYILSLARLADLDYSADHSNLSFS
ECVQRCTRTLQAEGRAKKRKE

WO 2004/030615

PCT/US2003/028547

872/6881
FIGURE 812

GGCACGAGGGATGGCGGTTGTATCTGCTGTTTCGCTGGCTGGGCCTCCGCAGCAGGCTTGGCCAGCCGCTGACGGG
TCGGCGGGCGGGTTTGTGTGAACAGGCACGCAGCTGCAGATTTTATTCTGGTAGTGCAACCCTCTCAAAGGTTGA
AGGAACTGATGTAACAGGGATTGAAGAAGTAGTAATTCCAAAAAGAAAACCTGGGATAAAGTAGCCGTTCTTCA
GGCACTTGCAATCCACAGTAAACAGGGATACACAGCTGTGCCTTATGTGTTTCAAGATGATCCTTACCTTATGCC
AGCATCATCTTTGGAATCTCGTTCAATTTTACTGGCAAAGAAATCCGGGGAGAATGTGGCCAAGTTTATTATTAA
TTCATACCCCAAATATTTTCAGAAGGACATAGCTGAACCTCATATACCGTGTTTAAATGCCTGAGTACTTTGAACC
TCAGATCAAAGACATAAGTGAAGCCGCCCTGAAGGAACGAATTGAGCTCAGAAAAGTCAAAGCCTCTGTGGACAT
GTTTGATCAGCTTTTGCAAGCAGGAACCACTGTGTCTCTTGAAACAACAAATAGTCTCTTGGATTTATTGTGTTA
CTATGGTGACCAGGAGCCCTCAACTGATTACCATTTTCAACAACTGGACAGTCAGAAGCATTGGAAGAGGAAAA
TGATGAGACATCTAGGAGGAAAGCTGGTCATCAGTTTGGAGTTACATGGCGAGCAAAAAACAACGCTGAGAGAAT
CTTTTCTCTAATGCCAGAGAAAAATGAACATTCTTATGCACAATGATCCGAGGAATGGTGAAGCACCAGCTTA
TGAGCAGGCATTAACTTGTACACTGAGTTACTAAACAACAGACTCCATGCTGATGTATACACATTTAATGCATT
GATTGAAGCAACAGTATGTGCGATAAATGAGAAATTTGAGGAAAAATGGAGTAAATACTGGAGCTGCTAAGACA
CATGGTTGCACAGAAGGTGAACCAAATCTTCAGACTTTTAAATACCATTCTGAAATGTCTCCGAAGATTTTCATGT
GTTTGCAAGATCGCCAGCCTTACAGGTTTACGTGAAATGAAAGCCATTGGAATAGAACCCTCGCTTGCAACATA
TCACCATATTATTGCGCTGTTTGATCAACCTGGAGACCCTTTAAAGAGATCATCCTTCATCATTTTATGATATAAT
GAATGAATTAATGGGAAAGAGATTTTCTCCAAAGGACCCGGATGATGATAAGTTTTTTCAGTCAGCCATGAGCAT
ATGCTCATCTCTCAGAGATCTAGAACTTGCCACCAAGTACATGGCCTTTTAAAAACCGGAGACAACCTGAAAT
CATTGGACCTGATCAACATCGTAATTTCTATTATTCCAAGTTCTTCGATTGATTGTCTAATGGAACAAATGA
TGTTACCTTGAAGTGGTATGAGGACCTGATACCTTCAGCCTACTTTCCCACTCCCAACAATGATACATCTTCT
CCAAGCATTGGATGTGGCCAATCGGCTAGAAGTGATTCTTAAATTTGGAAGATAGTAAAGAATATGGTCATAC
TTTCCGCAGTGACCTGAGAGAAGAGATCCTGATGCTCATGGCAAGGGACAAGCACCACAGAGCTTCAGGTGGC
ATTTGCTGACTGTGCTGCTGATATCAAATCTGCGTATGAAAGCCAACCCATCAGACAGACTGCTCAGGATTGGCC
AGCCACCTCTCTCAACTGTATAGCTATCCTCTTTTAAAGGGCTGGGAGAACTCAGGAAGCCTGGAAAATGTTGGG
GCTTTTCAGGAAGCATAATAAGATTCCTAGAAGTGAGTTGCTGAATGAGCTTATGGACAGTGCAAAAGTGTCTAA
CAGCCCTTCCCAGGCCATTGAAGTAGTAGAGCTGGCAAGTGCCTTCAGCTTACCTATTTGTGAGGGCCTCACCCA
GAGAGTAATGAGTGATTTTGCAATCAACCAGGAACAAAAGGAAGCCCTAAGTAATCTAACTGCATTGACCAGTGA
CAGTGATACTGACAGCAGCAGTGACAGCGACAGTGACACCAGTGAAGGCAAATGAAAGTGGAGATTGAGGAGCAG
CAATGGTCTCACCATAGCTGCTGGAATCACACCTGAGAACTGAGATATACCAATATTTAACATTGTTACAAAGAA
GAAAAGATACAGATTTGGTGAATTTGTTACTGTGAGGTACAGTCAGTACACAGCTGACTTATGTAGATTTAAGCT
GCTAATATGCTACTTAACCATCTATTAATGCACCATTAAAGGCTTAGCATTTAAGTAGCAACATTGCGGTTTTCA
GACACATGGTGAGGTCCATGGCTCTTGTCTATCAGGATAAGCCTGCACACCTAGAGTGTCGGTGAGCTGACCTCAC
GATGCTGCTCCTCGTGCGATTGCCCTCTCCTGCTGCTGGACTTCTGCCTTTGTTGGCCTGATGTGCTGCTGTGATG
CTGGTCCCTTCATTTAGGTGTTTCATGCAGTTCTAACACAGTTGGGGTTGGGTCAATAGTTTCCCAATTTTCAGGAT
ATTTGATGTATGAGAAATAACGCATCTTAGGAATGACTAAACAAGATAATGGCAGTTTAGGCTGCACAACCTGGTAA
AATGACTGTAGATAAATGTTGTAATTAGTGACACGTTTGTATTTTGTAAATATAGCCGCTGCCATAGTTTCT
AACTTGAACAGCCAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

873/6881
FIGURE 813

MVAQKVKPNLQTFNTILKCLRRFHV FARSPALQVLRMKAIGIEPSLATYHHIIRLFDQPGDPLKRSSFIIYDIM
NELMGKRFSPKDPDDDKFFQSAMSISSLRDLELAYQVHGLLKTGDNWKFIGPDQHRNFYYSKFFDLICLMEQID
VTLKWYEDLIPSAYFPHSQTMIHLLQALDVANRLEVIPKIWKDSKEYGHTFRSDLREEILMLMARDKHPPQLQA
FADCAADIKSAYESQPIRQTAQDWPATSLNCIAILFLRAGRTQEAWKMLGLFRKHNKIPRSELLNELMDSAKVSN
SPSQAIEVVELASAFSLPICEGLTQRVMSDFAINQEQKEALSNLTALTSDSDTDSSSDSDSDTSEK

WO 2004/030615

PCT/US2003/028547

874/6881
FIGURE 814

ACGCGGGCACGCACACACGGAAGCACGCCTCCACTTAACTCGCGCCGCCGCGGCAGCTCGAGTCCACCAGCAGCG
CCGTCCGCTTGACCGAGATGCTGCGGGCCTGTCACTTATCGGGTGTGACCGCCGCCCGCCAGAGTTGTCTCTGTG
GGAAGTTTGTCTCCGTCCATTGCGACCATGCCGCAGATACTCTACTTCAGGCAGCTCTGGGTTGACTACTGGCA
AAATTGCTGGAGCTGGCCTTTTGTGTTGGTGGAGGTATTGGTGGCACTATCCTATATGCCAAATGGGATTCCC
ATTTCCGGGAAAGTGTAGAGAAAACCATACCTTACTCAGACAACTCTTCGAGATGGTTCTTGGTCCTGCAGCTT
ATAATGTTCCATTGCCAAAGAAATCGATTCACTCGGGTCCACTAAAAATCTCTAGTGTATCAGAAGTAATGAAAG
AATCTAAACAGTCTGCCTCACAACCTCCAAAAACAAAGGGAGATACTCCAGCTTCAGCAACAGCACCTACAGAAG
CGGCTCAAAATTATTTCTGCAGCAGGTGATACCCTGTGCGGTCCCAGCCCCCTGCAGTTCAGCCTGAGGAATCTTTAA
AAACTGATCACCTGAAATTGGTGAAGGAAAACCCACACCTGCACCTTTCAGAAGAAGCATCCTCATCTTCTATAA
GGGAGCGACCACTGAAGAAGTTGCAGCTCGCCTTGACACAACAGGAAAAACAAGAACAAGTTAAAATTGAGTCTC
TAGCCAAGAGCTTAGAAGATGCTCTGAGGCAACTGCAAGTGTCACTCTGCAGGCTATTGCAGCTCAGAATGCTG
CGGTCCAGGCTGTCAATGCACACTCCAACATATTGAAAGCCGCCATGGACAATTCTGAGATTGCAGGCGAGAAGA
AATCTGCTCAGTGGCGCACAGTGGAGGGTGCATTGAAGGAACGCAGAAAGGCAGTAGATGAAGCTGCCGATGCC
TTCTCAAAGCCAAAGAAGAGTTAGAGAAGATGAAAAGTGTGATTGAAAATGCAAAGAAAAAGAGGTTGCTGGGG
CCAAGCCTCATATACTGTGTCAGAGGGTAACTTCACAACATGATAGTTGATCTGGATAATGTGGTCAAAAAGG
TCCAAGCAGCTCAGTCTGAGGCTAAGGTTGTATCTCAGTATCATGAGCTGGTGGTCCAAGCTCGGGATGACTTTA
AACGAGAGCTGGACAGTATTACTCCAGAAGTCCTTCCTGGATGGAAGGAATGAGTGTTCAGACTTAGCTGACA
AGCTCTCTACTGATGATCTGAACTCCCTCATTGCTCATGCACATCGTCGTATTGATCAGCTGAACAGAGAGCTGG
CAGAACAGAAGGCCACCGAAAAGCAGCACATCACGTTAGCCTTGGAGAAACAAAAGCTGGAAGAAAAGCGGGCAT
TTGACTCTGCAGTAGCAAAAGCATTAGAACATCACAGAAGTGAATACAGGCTGAACAGGACAGAAAGATAGAAG
AAGTCAGAGATGCCATGGAATGAAATGAGAAGCCAGCTTCGCCGACAGGCAGCTGCCCACACTGATCACTTGC
GAGATGTCCTTAGGGTACAAGAACAGGAATTGAAGTCTGAATTTGAGCAGAACCTGTCTGAGAACTCTCTGAAC
AAGAATTACAATTTGCTCGTCTCAGTCAAGAGCAAGTTGACAACCTTTACTCTGGATATAAATACTGCCTATGCCA
GACTCAGAGGAATCGAACAGGCTGTTTCAGAGCCATGCAGTTGCTGAAGAGGAAGCCAGAAAAGCCACCAACTCT
GGCTTTCAGTGGAGGCATTAAAGTACAGCATGAAGACCTCATCTGCAGAAACACCTACTATCCCGCTGGGTAGTG
CAGTTGAGGCCATCAAAGCCAACTGTTCTGATAATGAATTCACCCAAGCTTTAACCAGCTATCCCTCCAGAGT
CCCTGACCCGTGGGGTGTACAGTGAAGAGACCTTAGAGCCCGTTTCTATGCTGTTCAAAAAGTGGCCCGAAGGG
TAGCAATGATTGATGAAACCAGAAATAGCTTGTACAGTACTTCTCTCTACCTACAGTCCCTGCTCCTATTCC
CACCTCAGCAACTGAAGCCGCCCCCAGAGCTCTGCCCTGAGGATATAAACACATTTAAATTACTGTATATGCTT
CTATTGCAATTGAGCATGGTGATCTGGAGCTAGCAGCAAAAGTTTGTCAATCAGCTGAAGGGGGAATCCAGACGAG
TGGCACAGGACTGGCTGAAGGAAGCCCCGAATGACCCTAGAAACGAAACAGATAGTGGAAATCCTGACAGCATATG
CCAGCGCCGTAGGAATAGGAACCACTCAGGTGCAGCCAGAGTGAAGGTTTAGGAAGATTTTCATAAAGTCATATTT
CATGTCAAAGGAAATCAGCAGTGATAGATGAAGGGTTCGCAGCGAGAGTCCCGGACTTGTCTAGAAATGAGCAGG
TTTACAAGTACTGTTCTAAATGTTAACACCTGTTGCATTTATATTCTTTCCATTTGCTATCATGTCACTGAACGC
CAGGAGTGCTTTCTTTGCAACTTGTGTAACATTTTCTGTTTTTTCAGGTTTTACTGATGAGGCTTGTGAGGCCAA
TCAAAATAATGTTTGTGATCTCTACTACTGTTGATTTTGCCCTCGGAGCAAACCTGAATAAAGCAACAAGATG

WO 2004/030615

PCT/US2003/028547

875/6881
FIGURE 815

MLRACQLSGVTAAAQSCLCGKFVLRPLRPCRRYSTSGSSGLTTGKIAGAGLLFVGGGIGGTILYAKWDSHFRESV
EKTIPYSDKLFEMVLGPAAYNVPLPKKSIQSGPLKISSVSEVMKESKQSASQLQKQKGDTPASATAPTEAAQIIS
AAGDTLSVPAPAVQPEESLKTDPHPEIGEGKPTPALSEEASSSSIRERPPEEVAARLAQKEKQEQVKIESLAKSLE
DALRQTASVTLQAIAAQNAAVQAVNAHSNILKAAMDNSEIAGEKKSAQWRTVEGALKERRKAVDEAADALLKAKE
ELEKMKSVIENAKKKEVAGAKPHITAAEGKLHNMIVDLDNVVKVQAAQSEAKVVSQYHELVVQARDDFKRELD
ITPEVLPGWKGMSVSDLADKLSTDDLNLSIAHAHRRIDQLNRELAEQKATEKQHI TLALEKQKLEEKRAFD
KALEHHRSEIQAEQDRKIEEVRDAMENEMRTQLRRQAAAHTDHLRDVLRVQEQELKSEFEQNLSEKLSEQELQFR
RLSQEQVDNFTLDINTAYARLRGIEQAVQSHAVAEERKAKHQLWLSVEALKYSMTSSAETPTIPLGSAVEAIK
ANCSDNEFTQALTAIIPPESLTRGVYSEETLRARFYAVQKLARRVAMIDETRNSLYQYFLSYLQSLLLFPPQQLK
PPPELCPEDINTFKLLSYASYCIEHGDLELAAKFVNQLKGESRRVAQDWLKEARMTLETQKIVEILTAYASAVGI
GTTQVQPE

WO 2004/030615

PCT/US2003/028547

876/6881
FIGURE 816

TAGTGCCGCCGCTCCCTACTCTGGGGGTGGGACTACCTCCTTTTCCGCGGGCCCCGCCAGGCGGCTGCCCCGTG
ACCTGCCTGGGCGCGGGGAAGTGAAGCCGGAAGGGGCAAGACGGGTTCAGTTCGTATGGGGCTGTTTGAAAG
ACCCAGGAGAAGCCGCCCAAAGAACTGGTCAATGAGTGGTCATTGAAGATAAGAAAGGAAATGAGAGTTGTTGAC
AGGCAAATAAGGGATATCCAAAGAGAAGAAAGAAAGTGAACGATCTGTGAAAGATGCTGCCAAGAAGGGCCAG
AAGGATGTCTGCATAGTTCTGGCCAAGGAGATGATCAGGTCAAGGAAGGCTGTGAGCAAGCTGTATGCATCCAAA
GCACACATGAACTCAGTGCTCATGGGGATGAAGAACCAGCTCGCGGTCTTGCGAGTGGCTGGTTCCCTGCAGAAG
AGCACAGAAGTGATGAAGGCCATGCAAAGTCTTGTGAAGATTCCAGAGATTCAGGCCACCATGAGGGAGTTGTCC
AAAGAAATGATGAAGGCTGGGATCATAGAGGAGATGTTAGAGGACACTTTTGAAAGCATGGACGATCAGGAAGAA
ATGGAGGAAGAAGCAGAAATGGAAATTGACAGAATTCTCTTTGAAATTACAGCAGGGGCCTTGGGCAAAGCACCC
AGTAAAGTGACTGATGCCCTTCCAGAGCCAGAACCTCCAGGAGCGATGGCTGCCTCAGAGGATGAGGAGGAGGAG
GAAGAGGCTCTGGAGGCCATGCAGTCCCGGCTGGCCACACTCCGCAGCTAGGGGCTGCCTACCCCGCTGGGTGTG
CACACACTCCTCTCAAGAGCTGCCATTTTATGTGTCTCTTGCACTACACCTCTGTTGTGAGGACTACCATTTTGG
AGAAGGTTCTGTTGTCTCTTTTCACTCTCTGCCCAGGTTTTGGGATCGCAAAGGGATTGTTCTTATAAAAGTGG
CATAAATAAATGCATCATTTTTAGGAGTATAGACAGATATATCTTATTGTGGGAGGGGAAAGAAATCCATCTGC
TCATGAAGCACTTCTGAAAATATAGGTGATTGCCTGAATGTGCAAGACTCTACTTTTGTCTATAAAACATATAT
AAATGAATTTTAAATAAATTTTTGCTTTAGCACTTGGCCCCATTGTAGATTGCCCTGTGCAGTAAACTTTCAAGGT
GTCGGCTGCCCCAGATTGCTTCATTTGCTGGGTGTGGAAAGAGTTGCTATGGCCAGGCATATGGGATTTGGAAGC
TCAGCAGAAGTGACTTCTGCTCTGTGGTTGCTGCTCCCCGGCTTTACAGACATGGTATGGCAGCCATTCTTTTA
TCTATTTAACCAGAGGATGCTGGGGAAATTGTGCTGCTTGTCTGTTGGCTGGTGGCTGCATTATGCTCTGGGGT
GTGCATGTGGGTCTATTTAGAGCTTCTGTCCCTTCCTTCCCATTGCAAGTTGCACCCAGATGAGACAGCTGTAGT
ACTAGGTCTCTTTACCTCTCATTGCCTGTCCCTGCTTCGAGCTGGTTGTCTTGTGCGTGGGACATGGGCCTTCC
TATCTGTGTTTTCTCAAAGTCAGGAGCTGACCAGGAGCACACTAAGGTGTGGTCATGCATCATAACCAACATTCA
CTCATCTGGGACATTCTTAAGATACATTTATAAATCATTTACAGCACTAGTACTTTGTATGTGTTGAGAGTTTACA
GAGCTCTTTGACATACGCGATCTTAGTCTTTACAAATAAGGAAACAGCTCAGTTTGGGAAGTATCAGAGATGGG
ATTCAAACCCAGATCCTCTGCTCCAAGTTGTATGTGCACTGAACATAATCAGGCAGGAAAAAGCCAGCCACTGT
CTCACAGATTGTTTTTGTATATTGTAGCAAAATCCTGAAACAATGGGGTCTTCCAGTCTCATCATACAAATG
GCAATCTTGGCTGGGTGCGGTGTTTCATGCCTATAATCCCAGTGCTTTACAAGGCTGAGGCAGGAGGCTCTCTTG
AGAATAGGAGTTCAAGACCAGCCTGGGCAACATAGCAAGATCCTGTCTCTCCAAAAAAGGAAATTTCTCATATATCCC
AAAATTTCATTTTTGTAGTCCAGAGGACCCTCCTATTACTCTTGATTTTCTCAGAGTGTAGTTAAAAAATTAT
TTTAAATAATTATTTTTTAAATCAGTTGTAGGTTACAGCAAAAGTGGACAAAAAGAAATTTCTCATATATCCC
CTGCCCTCACACATGCATAGCCTCCCACCCTATCAGTATCCCACACCAGAGTGGTACATTTGTTACAATCAATA
AACCTCCATTGACACATCATTATCACCCAAAGTCCATAGTTTACATGAAGATTCACTCTGGTGTGTACATTGTA
TGGGCTTAGACAAATGTATGATGATATCTACAATTATAGAATCATAACAGAAATGTTTCACTGCCCTAAAATTCT
CTATGCTTCACCTGTTTCATCCCTTTCTTCCCTAATCCCTGGCAACCACTTTAAAAAAGGAAATTTAGGTTTCAAGG
GTACATGTGCAGGTAAACTCGTGACAAGGGGTTTGTATACAGATTATTTAGTGACCCAGGTACTAAGCCTAGT
ACCAATAGTTTACTTTTTCTGGTCTGTCCCTTTTCCACCCTCCACCCTCAGGTAGGCCCCAGTATGTTATTCT
TTGTGTCCATGTTATTTCACTCCCCTTGTGAGAACATGGAATATTTGGTTTCTGTTCTATGTTAGTTTGTTA
AGGATAATGGCCTCCAGCCCCATCCATGTTCTTGCAAGGACATGATCTTCTTTGGCAACCACTTTTACTGTC
GCCATAGTTCTTCTTTTCTAGAATGTCATATTGGAATCATATAGTATGTAGCCTTTTCACTGGCTTCTTTCA
CTTAATAATATGCAATTAAGGTTCTCCATGTCATTTTCATGGCTTAATAGTGCATTTATTTTACTGACTGAATAA
TACTCCATTGTCTAGATGAATAGTTTATCCATTACCTATTGAAAGACTTCTTGGTGGTTTCCAAGTTTTGGCAA
TTATGAATAAAGCTGTTGTAAACATCTTGTGCAGGTTTTTCTATGGGCATGTTTTTAATTCATTTGAATAAATA
CCAAGAGCTTCAGTGCTGGATCATA

WO 2004/030615

PCT/US2003/028547

877/6881
FIGURE 817

CAGGACACAGCATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCAAAT
GTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGG
CCAGTCAGAGTATTAGTAGCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATA
AGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCCTCTCACCA
TCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTCCACATGGACGT
TCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGT
GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCTTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGGCCCCACCTGC
TCCTCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCC

WO 2004/030615

PCT/US2003/028547

878/6881
FIGURE 818

GCGGCCGTTACGGCGCTCAGGCGTCTCGACGCGCGGATTAAAAACAGCTCAGGAGACGCCAAGGAAAGATGGG
ACCTCCCGGGCCAGCACTGCCAGCCACAATGAATAACTCTTCTTCAGAGACGCGAGGACACCCCCACAGTGCCCTC
CTCTCCTTCAGAGCGTGTGTTCCCGATGCCCCCTGCCAGGAAGGCGCCTCTCAATATTCCTGGCACCCCAGTCTCT
CGAAGACTTTCCTCAGAATGACGATGAGAAAGGAGCGGCTGCAGCGGAGGCGCTCGAGGGTCTTTGATCTGCAGTT
CAGCACTGACTCACCCTCGCTTATTGGCCTCCCCCTCCAGCAGGAGTATTGACATTTAGCTACTATCCCCAAGTT
TACAAACACGCAGATTACGGAACATTACTCCACCTGTATCAAATGTCCACTGAAAATAAAATCACTACCAAGAA
TGCTTTTGGTTTGCACTTGATTGATTTTATGTACAGAGATTCTTAAACAGAAAGACACCGAACCAACCAACTTTAA
AGTGGCTGCGGGTACTCTGGATGCCAGCACCAAGATCTATGCTGTGCGCGTGGATGCCGTCCATGCCGATGTATA
CAGAGTCCTTGGGGGGCTGGGGCAAAGATGCACCGTCTTTGGAAGAAGTAGAAGGCCATGTTGCTGATGGAAGTGC
TACTGAAATGGGAACAACCAAAAAGGCTGTAAAGCCAAAGAAGAAGCACTTACACAGAATATTGAGCAGAACAT
AAACAACCTCAATGTCTCCGAAGCAGATCGGAAGTGTGAGATTGATCCCATGTTTCAGAAGACAGCAGCCTCATT
TGATGAGTGCAGCACAGCAGGGGTGTTTCTGTCCACTCTCCACTGCCAGGACTACAGAAGTGAAGTGTGTTTCC
CTCTGATGTCCAGACTCTCTCCACGGGAGAACCTCTCGAGTTGCCAGAGTTAGGTTGTGTAGAAATGACAGATT
AAAAGCGCCCTTGCAAGTGTGCAGAAGATCGCCAGATCTGCCCTTCCCTGGCCGGGTTCAGTTTACACAGTG
GGACAGTGAAACACATAATGAGTCTGTGTGCGCCCTGGTAGACAAGTTTAAAGAAGATGACCAGGTATTTGACAT
CAATGCTGAAGTTGACGAGAGTGACTGTGGAGACTTCCCCGATGGGTCCCTGGGGGATGACTTTGATGCCAACGA
TGAACCTGACCACACCGCAGTTGGGGATCATGAAGAGTTTCAAGAGCTGGAAGGAGCCCTGCCAGGTTTCAAGCTG
CCAGGAAGAAATGATTTCCCTTGGGGATGGAGACATCAGGACCATGTGCCCCCTTCTGTCTATGAAACCTGGAGA
ATATTCTTATTTAGTCTCGGACCATGTGATGTGGGTGGCCCGGATCACTGGCGCTTTAGGCCTCGACGCAA
ACAAGATGCTCCTTCCCAATCAGAAAACAAAAGAAGAGTACAAAAAAGATTTTGAATTGACTTTGAAGATGA
TATTGACTTTGATGTATATTTTAGAAAAACAAAGGCTGCTACTATTCTGACCAAGTCCACTTTGGAGAACCAGAA
TTGGAGAGCTACCACCTTCTACAGATTTCACTACAATGTTGACACTCTGGTCCAGCTTCACCTCAAACCAGG
CACCAGGTTACTTAAGATGGCCCAGGGCCATAGGGTAGAGACTGAGCATTATGAAGAAATTGAAGACTATGATTA
CAACAACCTTAACGACACCTCCAACCTTTTGGCCCTGGATTACAGGCTGCTGACAGTGATGATGAAGATTTGGATGA
CTTATTTGTGGGACCTGTTGGGAACTCTGACCTCTCACCTTATCCTTGCCATCCACCTAAGACAGCACAAACAGAA
TGGTGACACTCCAGAAGCCCCAAGGATTAGACATCACAACATATGGGGAGTCAAACCTTGGTAGCTGAGCCTCAGAA
GGTAAATAAAATTGAAATTCATATGCCAAGACTGCCAAAAGATGGACATGAAGAACTGAAGCAGAGCATGTG
GAGTCTGCTGACAGCGCTCTCCGGAAGGAGGCAGATGCAGAGGCAAACCACAGGGAAGCTGGAAAAGAAGCGGC
CCTGGCAGAAGTGGCTGACGAGAAGATGCTTAGCGGGCTCACGAAGGACCTGCAGAGGAGCCTGCCCCCTGTCTAT
GGCTCAGAACCTCTCCATACCTCTGGCTTTTGCCTGTCTCTACATTTAGCCAATGAAAAGAATCTAAAACCTGGA
AGGAACAGAGGACCTCTCTGATGTTCTTGTGAGGCAAGGAGATTGAGTTCACTATGGAGAAGTCAGCAGCAGGAG
GCCCATCCCTTACTCAGTTGCCGGGACATCCCCAGTCTCGGGGGAAGAAGATGCCATGGGCTTATACCCAGGCTG
TAGCCAACCTACCAACGTGCCTGTTTGTGTTGTTGCTCTTCTCTCTCCATCATAGTCTGGGTGCCAGCGCCCTG
AAGCTCCGTGCTCAACTGATTAACTTTTACTGCCCTATGGTGACCATCTAGGAGAGGGGAGGGCAGAGGGGGTGA
GGGTACTATTCTGGATTGAGAAAACCTATATCCATTCTTTATATCAATGTATAGTTTTAGTCTCCTAAATTGATC
TGTTATTTTCCAACTATTCTCTTGTAGAAAATTTCCAGTGGGCACCTTAATGGTGCCCTTGAAGAACTTCCTAA
TCCATGTACATAAAATACATCATATGTACACTTATAAATGTATATAGAATGCTCAAAAATAAAATTCTTAATAAT
AGAACTGGCAAAATA

WO 2004/030615

PCT/US2003/028547

879/6881
FIGURE 819

MGPPGPALPATMNNSSSETRGHPHSASSPSERVFPMPLPRKAPLNIPGTPVLEDFPQNDDEKERLQRRRSRVFDL
QFSTDSPRLLASPSSRSIDISATIPKFTNTQITEHYSTCIKLSTENKITTNAFGLHLIDFMSEILKQKDTEPTN
FKVAAGTLDASTKIYAVRVDADVIRVLGGLGKDAPSLEEVEGHVADGSATEMGTTKAVKPKKKHLHRTIEQ
NINNLNVSEADRKCEIDPMFQKTAASFDECSTAGVFLSTLHCQDYRSELLFPQSDVQTLSTGEPLLELPELGCVEMT
DLKAPLQQCAEDRQICPSLAGFQFTQWQDSETHNESVSALVDKFKKNDQVFDINAEVDESDCGDFPDGSLGDDFDA
NDEPDHTAVGDHEEFRSWKEPCQVQSCQEEMISLGDGDIRTMCPLLSMKPGEYSYFSPRTMSMWAGPDHWRFRPR
RKQDAPSQSENKKKSTKKDFEIDFEDDIDFDVYFRKTKAATILTKSTLENQNWRTTLPTDFNYNVDTLVQLHLK
PGTRLLKMAQGHRVETEHYEEIEDYDYNPNPNDTSNFCPLQAADSDDDLDDLFVGPVGNLSPYPCHPPKTAQ
QNGDTPEAQGLDITTYGESNLVAEPQKVNKIEIHYAKTAKKMDMKKLKQSMWSLLTALSGKEADAEANHREAGKE
AALAEVADEKMLSGLTQDLQRSPLPPVMAQNLSIPLAFACLLHLANEKNLKLKLEGTEDLSDVLRQGD

WO 2004/030615

PCT/US2003/028547

880/6881
FIGURE 820A

TTCCAAGAAGAAGGATTTCACCCCTCGGGATATTGATGCATTTTGGCTGCAGCGGCAGCTCAGTCGTTTCTATGA
TGATGCCATCGTGTCTCGAGAAGAAGGCAGATGAAGTATTGGAGATTTTGAAGACGGCCAGTGATGATCGGGAATG
TGAAAATCAGCTGGTTCTGCTGCTTGGTTTCAACACCTTTGATTTTCATTAAAGTGTTGCGGCAGCACAGGATGAT
GATTTTATACTGTACCTTGCTGGCCAGTGACAAAGTGAAGCTGAAAAGGAAAGGATTATGGGAAAGATGGAAGC
TGACCCAGAGCTATCCAAGTTCCTCTACCAGCTTCATGAAACCGAGAAGGAGGATCTGATCCGAGAGGAAAGGTC
CCGGAGAGAGCGAGTGCGTCACTCTCGAATGGACACAGATCTGGAAACCATGGATCTCGACCAGGGTGGAGAGGC
ACTGGCTCCACGGCAGGTTCTGGACTTGGAGGACCTGGTTTTTACCCAAGGGAGCCACTTTATGGCCAATAAACG
CTGTACAGCTTCCTGATGGATCCTTCCGTCGCCAGCGTAAGGGCTATGAAGAGGTGCATGTGCCTGCTCTGAAGCC
CAAGCCCTTTGGCTCAGAAGAACAACCTGCTTCCAGTGGAAGCTGCCAAAGTATGCCAGGCTGGGTTTGAGGG
CTTCAAAACACTGAATCGGATCCAGAGTAAGCTCTACCGTGCTGCCCTTGAGACGGATGAGAATCTGCTGCTGTG
TGCTCCTACTGGTGCTGGGAAGACCAACGTGGCCCTGATGTGCATGCTCCGAGAGATTGGGAAACACATAAACAT
GGACGGCACCATCAATGTGGATGACTTCAAGATTATCTACATTGCCCCCATGCGCTCCTTGGTGCAGGAGATGGT
GGGCAGCTTTGGAAAGCGCCTGGCCACTTATGGCATCACTGTTGCTGAACTGACTGGGGACCACCAGCTGTGCAA
AGAAGAGATCAGTGCCACTCAGATCATCGTCTGACCCCCGAGAAGTGGGACATCATCCCCGAAGGGTGGTGGA
GCGCACCTACACCCAGCTGGTGCGGCTCATATTCTGGATGAGATTTCATCTTCTCCACGATGACAGAGGTCTGT
CTTAGAAGCTTTAGTGGCCAGGGCCATCCGAAACATTGAGATGACCCAAGAGGATGTCCGACTCATTGGTCTCAG
TGCCACCCTACCCAACCTATGAAGATGTAGCCACCTTTCTACGTGTTGACCCTGCCAAGGGTCTCTTTTACTTTGA
CAACAGCTTCCGTCCAGTGCCCTCTGGAACAGACATATGTGGGTATCACAGAGAAAAAGCTATCAAGCGTTTCCA
GATCATGAATGAAATCGTCTATGAAAAATCATGGAACATGCTGGAAAAATCAGGTGCTGGTGGTTTGTCCACTC
CCGGAAGGAGACTGGAAAGACAGCCAGGGCCATCCGGGACATGTGCCTAGAAAAGGACACTCTGGGTCTGTTTCT
GAGGGAGGGCTCAGCCTCCACAGAAGTCTGCGAACAGAAGCTGAGCAGTGCAAGAACCTAGAGCTGAAGGATCT
TCTGCCTTATGGCTTTGCTATTTCATCAGCAGGCATGACCAGGGTTGACCGAACACTCGTGGAGGATCTTTTTCG
TGATAACATATTCAAGTTTATGTTTCCACAGCAACTCTAGCTTGGGGTGTGAATCTCCCTGCACATACAGTCAT
CATCAAAGGCACCCAGGTGTACAGTCCAGAGAAGGGCGTTGGACAGAAGTGGAGCACTGGACATTCTGCAGAT
GCTGGGACGTGCCGGAAGACCCAGTATGACACCAAGGGTGAAGGCATACTCATCACATCTCATGGGGAGCTACA
GTACTACCTGTCCCTCTCAATCAACAACCTTCTATTGAAAGCCAGATGGTTTTCAAAGCTTCTGACATGCTCAA
TGCAGAAATCGTGCTAGGAAATGTCCAGAATGCCAAGGATGCGGTGAAGTGGCTGGGCTATGCCTACCTCTATAT
CCGAATGCTGCGATCCCCAACCTCTATGGCATCTCTCATGATGACCTCAAGGGAGATCCCCTGCTGGACCAGCG
CCGACTAGATCTGGTTCATACAGCTGCCCTGATGCTGGACAAGAACAATCTGGTCAAGTACGACAAGAAGACGGG
CAACTTCCAGGTGACAGAAGTGGGCCGTATAGCCAGCCACTACTACATCACCAATGATACAGTGCAGACTTACAA
CCAGCTGCTGAAGCCACCTGAGTGAGATTGAGCTTTTTCAGGGTCTTCTCATTGTCTCTGAGTTCAAGAACAT
CACAGTGAGAGAGGAGAGAAGCTGGAGCTGCAGAAGTTGCTGGAGAGGGTGCCTATCCCTGTAAAGGAGAGCAT
TGAGGAACCCAGTGCTAAGATCAACGTTCTTCTGCAAGCCTTCATCTCACAGCTGAAATTGGAGGGCTTTGCACT
GATGGCTGACATGGTGTATGTACACAGTCGGCTGGCCGGTTGATGCGAGCGATATTTGAAATTGTCTGAACCG
AGGTTGGGCACAGCTTACAGACAAGACCCTGAACCTCTGCAAGATGATCGACAAACGCATGTGGCAGTCCATGTG
TCCTCTGCGCCAGTTCCGGAAACTCCCTGAGGAAGTAGTGAAGAAGATTGAGAAGAAGAATTTCCCTTTTGAGCG
TCTGTACGACCTGAATCATAATGAGATTGGGGAGCTTATCCGCATGCCAAAGATGGGGAAGACCATCCACAAATA
TGTCCATCTGTTTCCCAAGTTGGAGTTGTCACTGCACCTGCAGCCTATCACACGCTCCACCCTGAAGGTGGAGCT
GACCATCACGCCAGACTTCCAGTGGGATGAAAAGGTGCATGGTTTCATCCGAGGCTTTTTGGATTCTGGTGGAGGA
TGTGGACAGCGAGGTGATTCTGCACCATGAGTATTTTCTCTCAAGGCCAAGTACGCCAGGACGAGCACCTCAT
TACATTCTTCGTGCTGTCTTTGAACCGCTGCCCCCTCAGTACTTCATCCGAGTGGTGTCTGACCGCTGGCTCTC
TTGTGAGACCCAGCTGCCTGTCTCTTCCGGCACCTGATCTTGCCGGAGAAGTACCCCTCCAACCGAACTTTT
GGACCTGCAGCCCTTGCCCGTGTCTGCTCTGAGAAACAGTGCCTTTGAGAGTCTTTACCAAGATAAATTTCTTTT
CTTCAATCCCATCCAGACCCAGGTGTTTAACACTGTATAACAACAGTGACGACAACGTGTTTGTGGGGGCCCCAC
GGGCAGCGGGAAGACTATTTGTGCAGAGTTTGGCATCTGCGAATGCTGCTGCAGAGCTCGGAGGGGCGCTGTGT
GTACATCACCCCATGGAGGCCCTGGCAGAGCAGGTATACATGGACTGGTACGAGAAGTTCCAGGACAGGCTCAA
CAAGAAGGTGGTACTCTGACAGGCGAGACCAGCACAGACCTGAAGCTGCTGGGCAAAGGGAACATTATCATCAG
CACCCCTGAGAAGTGGGACATACTTTCCCGGCGATGGAAGCAGCGCAAGAACGTGCAGAACATCAACCTCTTCGT

WO 2004/030615

PCT/US2003/028547

881/6881
FIGURE 820B

GGTGGATGAGGTCCACCTTATCGGGGGCGAGAATGGGCCTGTCTTAGAAGTGATCTGCTCCCGAATGCGCTACAT
CTCCTCCCAGATTGAGCGGGCCATTTCGATTGTGGCACTCAGCTCTTCGCTCTCCAATGCCAAGGATGTGGCCCA
CTGGCTGGGCTGCAGTGCCACCTCCACCTTCAACTTCCATCCCAATGTGCGTCCCGTCCCCTTGGAGCTGCACAT
CCAGGGCTTCAACATCAGCCATACACAAACCCGCCTGCTCTCCATGGCCAAGCCTGTGTACCATGCTATCACCAA
GCACTCGCCCAAGAAGCCTGTCTATTGTCTTTGTGCCGTCTCGCAAGCAGACCCGCCTCACTGCCATTGACATCCT
CACCACCTGTGCAGCAGACATCCAACGGCAGAGGTTCTTGCCTGCACCGAGAAGGATCTGATTCCGTACCTGGA
GAAGCTAAGTGACAGCACGCTCAAGGAAACGCTGCTAAATGGGGTGGGCTACCTGCATGAGGGGCTCAGCCCCAT
GGAGCGACGCTGGTGGAGCAGCTCTTCAGCTCAGGGGCTATCCAGGTGGTGGTGGCTTCTCGAGTCTCTGCTG
GGGCATGAACGTGGCTGCCCACCTGGTAATCATCATGGATACCCAGTACTACAATGGCAAGATCCACGCCTATGT
GGATTACCCCATCTATGACGTGCTTCAGATGGTGGGCCACGCCAACCGCCCTTTGCAGGACGATGAGGGGCGCTG
TGTCATCATGTGTGTCAGGGCTCCAAGAAGGATTTCTTCAAGAAGTTCTTATATGAGCCATTGCCAGTAGAATCTCA
CCTGGACCACTGTATGCATGACCACTTCAATGCTGAGATCGTCACCAAGACCATTGAGAACAAGCAGGATGCTGT
GGACTACCTCACCTGGACCTTTCTGTACCGCCGCATGACACAGAACCCCAATTACTACAACCTGCAGGGCATCTC
CCATCGTCACTTGTGCGGACCACTTGTGAGAGCTGGTGGAGCAGACCCTGAGTGACCTGGAGCAGTCCAAGTGCAT
CAGCATCGAGGACGAGATGGACGTGGCGCCTCTGAACCTAGGCATGATCGCCGCCTACTATTACATCAACTACAC
CACCATTGAGCTCTTCAGCATGTCCCTCAATGCCAAGACCAAGGTGCGAGGGCTTATCGAGATCATCTCCAATGC
AGCAGAGTATGAGAACATTCCTCATCCGGCACCATGAAGACAATCTCCTGAGGCAGTTGGCTCAGAAGGTCCCCCA
CAAGCTGAATAACCTAAGTTCAATGATCCGCACGTCAAGACCAACCTGCTCCTGCAGGCTCACTTGTCTCGCAT
GCAGCTGAGTGCTGAGTTGCAGTCAGATACGGAGGAAATCCTTAGTAAGGCAATCCGGCTCATCCAGGCCTGCGT
GGATGTCTTTCCAGCAATGGGTGGCTCAGCCCTGCTCTGGCAGCTATGGAATGGCCAGATGGTCACCCAAGC
CATGTGGTCCAAGGACTCATACCTGAAGCAGCTGCCACACTTCACCTCTGAGCATATCAAACGTTGCACAGACAA
GGGAGTGGAGAGTGTTCGACATCATGGAGATGGAGGATGAAGAACGGAACGCGTTGCTTCAGCTGACTGACAG
CCAGATTGCAGATGTGGCTCGCTTTTGTAAACCGCTACCTAATATCGAACTATCTTATGAGGTGGTAGATAAGGA
CAGCATCCGCAGTGGCGSGCCAGTTGTGGTGTGCTGGTGCAGCTGGAGCGAGAGGAGGAAGTCACAGGCCCTGTCTAT
TGCGCTCTCTTCCCGCAGAAACGTGAAGAGGGCTGGTGGGTGGTGAATGGAGATGCCAAGTCCAATAGCCTCAT
CTCCATCAAGAGGCTGACCTTGACGACAGAGGCCAAGGTGAAGTTGGACTTTGTGGCCCCAGCCACTGGTGCCCA
CAACTACACTCTGTACTTCATGAGTGACGCTTACATGGGATGTGACCAGGAGTACAAATTCAGCGTGGATGTGAA
AGAAGCTGAGACAGACAGTGATTGAGATTGAGTCTGAGGCATTTACTTTTGGGTAAAGGAGAGTTGAGCCTGAA
TTAGGAATGTGTACATTGTAGGAATCCTGGTTGTGGGGACCAGGTCTGTGGGCCTCAGGTCTGGCCAGCCAGGGC
TGGTGTCTGTCCCGCTACCTCCACTTCCCTTTCCCTTGCTCACTCTGGATCCAGTGACAGCAGGTGTCTATGGGTC
AAGCATAAATCATATATAGCATTTCAGGCATGTTCTGGTAGTTCTTTTGTAGTCTGACATTCTAATAAAATAAT
TTGTAGAAACC

WO 2004/030615

PCT/US2003/028547

882/6881
FIGURE 821

MADV TARS LQY EY KANS NLVL QADR SLIDR TRRDEPTGEVLSLVGKLEGRMGDKAQRTKPQM QEERRAKRRKRD
EDRHDINKMKG Y TLLSEGI DEMVG I IYKPKTKETRETYEVLLSFIQAALGDQPRDILCGAADEVLA VLKNEKLRD
KERRKEID LLLGQTD DTRYHVLVNLGKKITDYGGDKEIQNMDDNIDETYG VNVQFESDEEEGEDDVYGEVREEAS
DDDMEGDEAVVRCTLSANLVASGELMSSKKKDLHPRDIDAFWLQRQLSRFYDDAIVSQKKADEVLEILKTASDDR
ECENQLV LLLGFNTFD FIKVLRQH RMILYCTLLASAQSEAEKERIMGKMEADPELSKFLYQLHETEKEDLIREE
RSRRERVRQSRMDTDLETMDLDQGGEALAPRQVLDLEDLVFTQGS HFMANKRCQLPDG SFRRQRKGYEEVHV PAL
KPKPFGSEEQLLPVEKLPKYAQAGFEGFKTLNRIQSKLYRAALETDENLLLCAPTGAGKTNVALMCM LREIGKHI
NMDGTINVD DFKI IYIAPMRSLVQEMVGSFGKRLATYGITVAELTGDHQLCKEEISATQIIVCTPEKWDIITRKG
GERTYTQLVRLIILDEIHLHDDRGPVLEALVARAIRNIEMTQEDVRLIGLSATLPNYEDVATFLRVDPAGLIFY
FDNSFRPVPLEQTYVGITEKKAIRKFQIMNEIVYEKIMEHAGKNQVLVVFVHSRKETGKTARAI RDMCLEKDTLGL
FLREGSASTEVLRTEAEQCKNLELKDLLPYGFAIHHAGMTRVDR TLVEDLFADKHIQVLVSTATLAWGVNLP AHT
V I I KGTQVYSPEKGRWTELGALDILQMLGRAGRPQYDTKGEGILITSHGELQYYLSLLNQQLPIESQMVSKLPDM
LNAEIVLGNVQNAKDAVNWLGYAYLYIRMLRSP TLYGISHDDLKGDPLLDQRRDLVHTAALMLDKNNLVKYDKK
TGNFQVTELGRIASHYYITNDTVQTYNQ LKPTLSEIELFRVFSLSSEFKNITVREEEKLELQKLLERVPIPVKE
SIEEPSAKINVLQAFISQLKLEGFALMADMVYVTSAGRLMRAIFEIVLNRGWAQLTDKTLNLCKMIDKRMWQS
MCPLRQFRKLPEEVVKKIEKKNFPPERLYDLNHNEIGELIRMPKMGKTIHKYVHLFPKLELSVHLQPI TRSTLKV
ELTITPDFQWDEKVGHSSEAFWILVEDVDSEVILHHEYFLKAKYAQDEHLITFFVPVFEP LPPQYFIRVVS DRW
LSCETQLPVSFRHLILPEKYPPPTELLDLQPLVSALRNSAFESLYQDKFPFFNP IQTQVFNTVYNSDDNVFVGA
PTGSGKTICAEFAILRMLLQSSEGRVCYITPMEALAEQVYMDWYEKFQDR LNKKVLLTGETSTDLKLLGKGNII
ISTPEKWDILSRRWKQRKNVQNINLFVVEVHLIGGENGPVLEVICS RMRYISSQIERPIRIVALSSSL SNAKDV
AHLWGCSATSTFNHFNVRPVPLELHIQGFNISH TQIRLLSMAKPVYHAITKHSPKKPVIVFVPSRKQTR LTAID
ILTTCAADIQRQRF LHCTEKDLIPYLEKLSDSLKETLLNGVGYLHEGLSPMERRLVEQLFSSGAIQVVVASRSL
CWGMNVA AHLVIIMDTQYYNGKIHAYVDYPIYDVLQMVGHANRPLQDDEGR CVIMCQGSKKDFFKKFLYEPLPVE
SHLDHCMHDHFN AEIVTKTIENKQDAVDYLTWTFLYRRMTQNP NYNLQGISHRHLS DHLSSELVEQTLSDLEQSK
CISIEDEMDVAPLNLGMIAAYYYINYTTIELFSMSLNAKTKVRGLIEIISNAAEYENIPIRHHEDNLLRQLAQKV
PHKLNNPKFNDPHVKTNLLLQAHL SRMQLSAELQSDTEEILSKAIRLIQACVDVLSSNGWLSPALAAMELAQMVT
QAMWSKDSY LKQLPHFTSEHIKRC TDKGVESVFDIMEMEDEERNALLQLTDSQIADVARFCNRYPNIELSYEVVD
KDSIRSGGPVVVLVQLEREEV TGPVIAPLFPQKREEGWV VIGDAKSNLSISIKRLTLQQKAKVKLDFVAPATG
AHNYTLYFMSDAYMGCDQEYKFSVDVKEAETDSDSD

WO 2004/030615

PCT/US2003/028547

883/6881
FIGURE 822

GTTTCCATCCCTCCTCTGGAGGCTTTTGAAGTCACCGGGAGACAGATGTGCTCTGTGGCAGGCAGGGGAGTGGGG
GTGCTCAGGCACCTTGGGAGGTCTGGGAGCTCCTCAGTGTGACCGCTGGGACCCACCAGGACTTTTTCTTTGTCA
GAAGCCTTTGGTTGCTTTGCTGCTCTGCATGTGTCACTGTGGAGGGGCAATAGAGCAAGGCCTTACATGGCATGG
TCATTTCTCGGGCCCAGGAGGCTTAGAGGCCTGCCCTGGCGCTCAAGTATTGAACCAGAACCATGGGGTGGCAC
TGAAGCCTCCTCACCACATCATGATAAATAACGGGGACATTACAGAGCAGGCACTGTTTCTCAGTCCATGGCT
GAGTACATCACCGGTGTTTTCTCTCTTATTCCTCCCATCAAGCCTAAAAGGAATCTCTATTGGAGATACTGCCAT
TAGTGTTCCTTTTATAGGTGAGGAACTGAGGCATAGAGGGTTCCCCAGTTGAACCAACTGATAAATAGTAGAACT
TGGATTTTAATTCAGTCTTGATGCCAGGGATAAGGCTCTTACTTTCTACCTTAGGCTATTTCTAGGAAACGCAGG
AGAGTGTTGAAGGGGCAGAGAAAGGGATCCAGTTCCTTTCTGTCCCGCATCCTAGTCCCTGAGAAGCAAAGAAGA
ATGTGTGGCTTCTTTTGCTTTGCTTTGTGTGTCATCCACACATCTCCAGGGGACCTGGGCTCTTGATCTTGCC
TCTTCCCCTTTAACTGTTAAGTGGGAGCAGGTAAGGGGGTACAGTAGGGCTGGCCTGGAGTTAGAGGCTTGGATG
CCTTAGCTCCTCTGTCTGCACTCCAGAACTGCCTGACTTCATTTTCGTATGTTGTCTTTGTTTTGACAATTGATC
CATGTCCCAGTCCGTCTCTTCTTCTTCTTGATACTTACACTGCTTCTTTCTGTTGGTTTCCAGTGTTTAACACT
GTATACAACAGTGACGACAACGTGTTTGTGGGGGCCCCACGGGCAGCGGGAAGACTATTTGTGCAGAGTTTGCC
ATCCTGCGAATGCTGCTGCAGAGCTCGGAGGGGCGCTGTGTGTACATCACCCCATGGAGGCCCTGGCAGAGCAG
GTATGACGTGGCGCTGTGTGTCATGTGAATTTCCCAAGAAGCATTTCATCTGTGATTCCGTATGAAGGCTTTCTAAG
CCCTGAAATTTGCAGGGTCATTTCCCTCAGTTTGTGTATTAAAGAAAAGCTGCCCCAGCCAAGCGTGGTGGCTCAC
GCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCAGATCTCCGAGATCAGGAGTTTCGAGACCAGCCTGGCC
AACATGGTGAAACCCTGTCTCTACTAAAAATACAGAAATTAGCTGGGCGTGGTGGTGTGCGCCTGTAATCCCAGC
TACTTGGAAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGTTTCGCACCACT
GCACTCCAGCCTGGGCAACAAGAGCGAGACTTCATCTCA

WO 2004/030615

PCT/US2003/028547

884/6881
FIGURE 823

GCGGAAGGCGCGGGAGCTTGCGTGCTGCTGGGCCTGAGCTGTCTGTCTCGTTTCTGTCCGCGCGCCCTGCATCCC
GGCCCCGGGCGCCCCGCTGGAGGTCGCCGAGGAGCCACAGGGCTGACTGGTCTGCTGCCCGGGGCCAGGAGTGCCT
GGTGTAGCAGTCGCGGAGCCATCCCGGCGTCTGCTGCCATGACCGACTCTCCCCTCAGAGGAGACTCTTCCTCAG
CGGTGGCTGCAGAGACAGATGAGCGCGCGCTCCTGGCCGCGGGACCGTGAGACGGGTTCTGTGGCCGGCCATTTAG
GGGGACGCTGCGACCACCGCTGCGCCCCCTCCGGAAGCTCGCGGGCGGGGCCCTGCTGGCGCTT
GGAGGCGGCATGCTCCCGCGGAGGCTGCTGGCCGCGCTGGCTGGCGGGGACGCGGGGCGGGGGCCTGCTGGCGCTT
CTGGCCAATCAGTGCCGCTTCGTCACGGGCGCTGCGCGTGCGGCGCGCGCAGCAGATCGCGCAGCTCTACGGCCGC
CTCTACTCCGAGAGCTACGCCGCGTTCCTCCTCGGCCGCTCTGGCGCCGGCTGCACGGCCGCTCTGGCCATGCC
TCTGCCTTGATGGCGCGCTTAGCCGGCGTCTTCGTTTGGGACGAGGAGAGGATCCAGGAGGAGGAGTTGCAGAGA
TCTATTAATGAGATGAAGCGGTTGGAAGAAATGTCAAATATGTTTTCAGAGCTCTGGAGTCCAGCACCACCCTCCA
GAACCAAAAGCCCAACAGAAGGGAATGAAGATTCAGAGGGCAAAGAGCAACGTTGGGAAATGGTGATGGATAAG
AAACACTTTAAGCTGTGGCGCGCCCAATTACAGGCACCCACCTTTACCAGTACCGAGTTTTTGGAACTACACA
GATGTGACACCTCGGCGAGTTCTTCAATGTTTCAGCTGGACACAGAGTATAGAAAAAATGGGATGCCCTGGTAATC
AAGCTGGAGGTGATTGAGAGGGATGTGGTTAGTGGTTCGAGGTTCTTCACTGGGTAAACCCATTTTCCTTATCCA
ATGTACTACGGGATTATGTTTATGTTTCGGCGGTATAGTGTGGATCAGGAAAACAACATGATGGTGTGGTGTCG
CGTGCTGTGGAGCATCCGAGTGTGCCAGAGTCTCCAGAATTCGTCAGGGTCAGATCATATGAATCCCAAATGGTT
ATCCGTCACCAAGTCAATTTGATGAGAATGGCTTTGACTACTTACTAACATACAGTGACAATCCCCAAACGGTG
TTTCCTCGCTACTGTGTTAGTTGGATGGTTTCCAGTGGCATGCCAGATTTCTTGAGAAGCTGCACATGGCCACT
CTGAAAGCCAAGAATATGGAGATTAAAGTAAAGGACTACATCTCAGCTAAGCCTCTGGAAATGAGTAGTGAAGCC
AAGGCCACCAGCCAGTCCCTCTGAGCGAAAGAACGAGGGCAGCTGTGGCCCTGCTCGGATTGAGTATGCTTGACAG
GCTTTGGGATAAGAAGGGACAAGGTGCTTCTAGCCCTGTCTCAGTCCGTTATCACTCTGCTGTAGAAGGGGGACA
TGCCACATGTATTAGAAGGCATCTGCTGTAACTTCCAGTGCAAGATAATTCAATAACTGATGTCCCATTTTCATT
AGAGCCCTTATTGCTCTTATCAAAACAGAAGAGGCTACATTTGTGGGAGTGTGTGCATATTCTCAGGCCAATG
TTTTGAAATTCGGTATCTCACTGAGCTAATCTGGAACAAACCTCTCACCTCAGGCCAGAAGGGGATGATCCAT
TTGCTTCTCTGAGTAGTTTCTCTGCTGACATTCCAAATCCCAACATCGATTGTGCAGCGCTTTGGATTTCCTTC
AGTTCTCCAGGTCCACCTGGAAAGTATAGTTGGCCAGTTGAGTCTCTCAAATGAGGGGCTACTGGGAGTGCTCTT
GGTAACAATCATGATGTGAATGGGTGTGAACGATACTTGCTATGTAAAGTGCTTGTCCGCACCTTGCTTTTAT
CTCTAGAGACATGAAGTTATTATTAATTTTTTTTTTTTAAAGTAGAGATGGAGTTTCACTCTGTTTCCAGGCT
GGTCTTGAACCTCTGGGCCATGCCTGGCCAGGGACATGAATTTGTACAAAGAAATTTCCCTCCCTGCCTGCACAA
TATCACCATTGACTCACCTTATCCAAAGCAAGTTTCTGTGAATCGGCCAGTTCTTCTATATTTCATTGGATCAT
TGCCCTCCTTCTAACCTTCCCATTTACCAAGAACACTGGGAGACTAATCCTTTTAGATAGTAGCTTTTTTGATGC
TCAAAACATCACATTTAAATTTAGTTTAAAAATTTTTTAACTTTTGTGTCAAATAGGAGTTGAGGAATTGAGCAG
GATTCATCCCTAGTCCGATTGTATAGAAAACACCATTTTGATTACAGGTATTATTTTTTCATATTTTCAGGTTTACT
TGTTCTTTTTCAGAAGGCTAAAGTCAGAGGAATGGGGCTGGGCCACTCCCTTGGAGCTCTCAGATCTACAGACAA
GCTGTGTGAATGCATAGATGTAATCTTGTCTCAAATACTAATACAGTGGAGATTTGGTTTATGTTACCATTAAGT
TCCTCTAAAAAGTTTTTCTCCTCTCTTCAGAGCCAAAATAAAAGTGAACACTACACTGTTTCAGATAAGGTACAAT
CTGATGCTGTGAGTTTGACCGAGCTGGTTTTGCTTATGGTCATGCTGCAATTTGTTAGAATAATAGGGATCAAGT
TTTAAATCCTCCTCCTTCCCTTTTTTCTGGAGTCTTGAGGGCCAGAGTTTTTGTTTTTGTTTTGTTTTGTTTT
CCTGCTTGCTACTGTTTTGTGGTGTGAAAAGTGGTTTAAACCTGAGACTAACTTAAACACTTCTTGACCTTCT
TGTTGCCGTGTTTCAATTTTTGTGCCAAGGAAGTAGCTGCCCCAGTGATGTCTTGCCCTCTCCGCGTCATTGTTGGA
AGAGGAGAGATGCATCGAGCAGTCCAGCTGCTTTTCATTTATTACTTCTTCTTCCAGGACCTGACAGAAGTCA
GGGAAGAGTCCCTGGGTTATGTCCAACTTAGCACCTGCAATTGTTGGGATGTGGATGGATGTGTGCATAAGAGA
GAGAGAGAATATGTGTGTGTGTGTGTGCGCTGCGAGCGCACACACATGCACAAGTGCAGAGGAGTTGCGGTTGC
TCCATGTTCTGACTTAGGGCAATTTGATTCTGCACTTGGGGTCTGTCTGTACAGTTACTCATGTCAATTGTAATGA
TTTCACTCCTAACTGTGACATTTTTATCAAATGTGTGAATAAATACATAAAGATTGGTAC

WO 2004/030615

PCT/US2003/028547

885/6881
FIGURE 824A

CGCGCTTAGGGATCCGGCCGTGGCCGAGCGCGCGGCCGTAAGACCGCGGGTGACTAGCATGCAGATACCCATGCT
CTGACTTTCTGCCCCCTCCACTGACATGGCCACCGGGGTGGGGAGAGGGACTTCCAGACTTCAGCTCGACGCATG
GGCACCCTCGCTGCTCTTCCAGCTTTCAGTGCATGAACGGGAGCTGGACCTGGTTTTTCTGGATCATAGCTATGCC
AAGCCTTGAGTGCCACCCAGATGCCAGTAGTGGCCGCCCCACCCGCATGCTCTTTGTCACTCCCCGGCGGCAG
CACGAAAGTACCATTGAATCAGACGTCCCAATAGATGTGGAGACGGTCACATCAACGCCTATGCCACTCTATGAC
AATCAGAAGGCACGCAGCGTGATGAATGAGTGTGAACGGCATGTATCTTTGCCAGGACTGATGCAGATGCCCCCT
CCTCCACCAGAGGACTGGGAGGAGCATGTCAACAGGACTGGCTGGACAATGGCCCAGAACAAGCTATTCAACAAG
ATCCTCAAAGCCCTGCAGTCTGACCGGCTTGCCCGCTTGCCCAACGAAGGGGCTTGTAATGAGCCAGTGTGCGC
CGTGTGTCTGTGGACAAGTGTGCAAGGAGAGTGGGCGAGGCTCTGGCAAGTGTGAGCTGGGATAGCTGTATC
CAGTGGCTGCACACCACCTTGTGGAGACCTTGAGTCTGCCCATGCTGGCAGCCTACCTGGATGCTTTGCAGACG
CTGAAGGGGAAGATCCCAACCTTGATTGACCGGATGCTTGTGTATCCAACACAAAGACTGGGGCTGCAGGAGCT
GAGGCCTTGTCTCTCTACTGAAGAGGCCCTGGGACCCTGTGTGGGTGTGCTTTCTCATAACAAACCAAGCAAA
CTCCCTGGCTCTCCGCTGATTCTCATCGCTCCTCTGGTCCCTCCAGCTCTGTGTTTCCCACTTACGCCGCCAC
CGCTTCTGGCAATCTCAGCTGTCTGCTTGGGCAAGGTATCCCTGTAGCCACCCATCTGCTGAACAATGGCAGT
GGGGTAGGAGTTCTACAGTGTCTCGAGCATATGATTGGGGCAGTGAGAAGCAAAGTGTGGAGATTACAGCCAT
TTCCACACAAACCCATTATCTTGATTGGCTGGAACACAGGAGCTTTGGTGGCCTGTCTGTGTGAGTAATGGAG
TATGTCACTGCAGTTGTCTGCCTTGGGTTTCCCTCTGCTTACTGTGGATGGCCCCAGAGGGGATGTAGATGATCCC
CTCTTGGATATGAAGACTCCAGTCTCTTGTCTATTGGTTCAGAATTCCTTCAATGTACCCCTGAAGCCATGGAG
GACTTCCGGGAGAAGATTTCAGAGCTGAGAACAGCTTGGTGGTGGTGGGGGAGCTGATGACAATCTCAGAATAAGC
AAAGCAAAGAAGAAATCAGAAGGGTTGACTCAGAGCATGGTGGACAGATGTATTAGGATGAGATTGTGGACTTT
CTGACTGGAGTGTCTACTCGTGCTGAGGGTCACATGGGCTCTGAACCTCGGGATCAGGATGCTGAGAAGAAGAAG
AAGCCCCGCGATGTGGCCCGCAGAGACTTGGCCTTTGAAGTCCCTGAGCGGGGCGAGTCGACCTGCCTCCCCAGCT
GCCAAGCTGCCCGCTCACCCCTCAGGCTCAGAGGATCTCTCCAGTGTGTCCAGCAGCCCCACCTCCAGTCCCAAG
ACCAAAGTGACCACAGTGACCTCTGCCCAGAAGTCCAGTCAGATTGGAAGTTCTCAGCTGTGTAAGAGACATGTG
CAGCGGACAGAAGCTGTGCTGACCCACAAACAAGCTCAAGCACAGTTTGTGCTTTTCTGAAACAAAATATGCTG
GTGAGGAAAGCTCTTCCCTCCGGCACCTCCTCCTGTCTCTTTGTTCCCATTTTCATCAGAACCACAGAGGAAGGA
GAGAAAGAGGATCTTAGGGTTAGCTGAAGCGACACCATCCCTCGAGTCCCCTTCTGGCAGTAAGACCTCCAAA
CGACCGAAGATCAAGGTGTCCCTTATCTCCCAAGGGGACACAGCTGGAGGGCCTTGTGCTCCTTCCCAAGGAAGT
GCTCCAGAAGCTGCAGGTGGGAAGCCATCACCATGACACTGGGGCAGGCTTCAGCAGGGGCCAAGGAGCTCACA
GGACTTCTCACCACAGCCAAGTCCAGTTCTTCTGAAGGTGGAGTCTCAGCCAGCCAGTCCCTTCACTGGTCTCC
AGCAGCACTGCACCCAGTGCCTTGCACACACTGCAGAGCCGCTGGTGGCCACATCTCCTGGCAGCTCCCTCCCA
GGGGCCACATCAGCCAGCAGCTTCTTCAAGGCCCTCAGCTTCACTTGCAGGATATCAGCAGCAAGACCTCTGGC
CTTCCAGCAAATCCCTCCCCAGGACCAGCCCCACAGGCTTGAAGGTCCCCACCACCTTACTCTGACACTTCGTG
GCCAGCCGAGCAGGATCACTACACTGAGCCCTATGGGCTCAGGAGCAGCCCCATCCGAGGAGTCTCTTCCAGG
TGCTGCCCTCCAGCTCACAGCGCTGCCTCCAGCACCCTGAAGATGCTGTGTGATATGTCTCTCTTACCAAGTTG
GTGATGGCTGCCTCATGGTGGGCCCCTGGACAGGTGTGTGGTCTGCTGAGCTGTCCACGTGTCCGAAGACCTGTT
TAAGACAGTCATTTTTGCCTCTCCGCCAACTGTCTTCAGAGAAACCATTAGGTTAGGTGATACGGTGCCAGCAAG
GGAAGCACCATCGTCCAGGATCTGCAATCTGGTTCTTGGGAACCCAGACTCCTCAGCAGATCTGGCTGTACAT
GGATCAGAACCCTTCTTCCCCCGCTTAAGCTGTGGTTTGACCAAGGGTCAGCATATAGGACTGCCTGCTGCAT
TTAATGAAGGTGTTTTCTTTTGGAAAGTCTGTGCTACCCTCTGCGCTAGTTGGGAGGAGACATCCATCTGGTCTG
GGATTTCCGGAGTTAGAATGGAAAGCTCTTTGCTAAAGACTGGAGTCATCTGGCCTGCCAACTGGTGGTTTCAGA
GCCGGACGGGCTTGTGTTTGGACATCACTGTTGCCTTCACTCAGCAGCCACGGGAGAGTGTCTCCCCATGCAACTCC
ACCTTAGAAACCACGTGAGATACTGAGTAGCTTGTGACTCTTGGAACTTCTGGTTTTTGTAGTATCATAATG
AAGGCAAAGAGAACTAGGCTGTCTATCTTTCAGCCTCTTGTACTTACTCTAGATGTTGGGAGCAGTGGTTGCCAGG
TGAAACCTGGGCCCTTTGTCTTTTTACCATGCTTTGGGCGAGTTCTGTATCCAGAGAGTCCGAGGTTTCAGATA
AGCTGAAGAAGAGTAATAGAACAGCAAAGGAAGTGGCTTGAAGGATGTGCTAGTAAGCCCTGTGGTTTGTGCTTA
GGTCTCTGCTCTGCTACCCAAGGAAGTGGTGGTTTCAGCTGGAGATAAAAAAGAAATTTGCCAAGTCAGAGAAGA
AACCCCAACCCCGGAAAATCCTCTGTCTCCAGTCTCTGGAGGTGAAGCAGGGACAATAAGCTAAGGTAGTATCTT

WO 2004/030615

PCT/US2003/028547

886/6881

FIGURE 824B

GGCCATCCCAGGAACTTGTGGCATTAGGACGATGAAGGCCATGCTTCAGTGTTTTCGTTTTCTATTTTCATGAGAC
TTTTTGTCTTCCTGCTTACAAGTGGGAAGATGATTGACAGTGACTCTACTATGCAGGGCTGTTGGTACCAACCTG
AGCCCTATAGGTGGCAGTCCCTGGAGAAGTGGTCACAGAAGATGGAGCTCTGATCCCCTGCTTACCTCTTCACAA
CACTTGTGTGCAAAGATAGTTTTAGATTTGGTTTAGAAGCTATCCTCCAGAACAGGCTCCCATACTTAGAATGTT
TCTAGTTAAGGTAATAAATTAGGCAACCCAAGTGTGACTCCACTCAAGTGTCCTTTTTCTGTAGGCAGGAAGGGCC
CACAACATGGCTTAAATGTAGTCCATGGTTCTGGCCACAGTACAGTGTGTATCTATACCAGGTCACCTGTGTT
CAATCTGGGAGCCTTCCTGGCCAGTCTGAGTGGCAGCCAGAAGGGAGCTCATAGTGTCTAGGAGTCTCAGGCAAG
GTAGGTGAGGGTACTGTGGGCAGGGGGGATGTGTGTGATAGGAGAGGGTACCCTAAACCCCATACCTTCCCTCCC
TGACCTGAAAAGCTGATCTCAACAGGGATTACACAGAAATTAGGCTGTGTTTTTGCATTAGCTGGTAGGTGACTT
TCTCAAAATTCTTAAATTCAGAAAGTATTTAGTAAACTTGAGGAAGGTATGAAATCTGGAGGAGGCATCCAGGAC
CCAGGGGTTTGATAGCTTTACAGGTAGGATCATAACCACACCAAAAGAGCAGTGGACAATAAGACTATATGAGCTA
TATGAAGCTTTTAGGAATCATTTAGGACAGACAGAGCCCTAAACAACCCATTTCATGACTTAAGTTGTTGGCTCAG
TGTATGCTGGGGACAAAGAAAACTAACAAGCCGACCTGCCTTTATGATAAATTCTAGTGTGCTTACAAGGGATG
ACTTCCTGAGGTGTGATCTGTCCACCTTGAAGAACTCCACAAGTGAAGAAGGGGAGCTGTGAGAACGTGGATTGT
TCTACAACCTTGACAGGGTAACAGAGGAAGTGGCTGAGGCCTAGAGTCACGTTTTCCAGTTCCTTCGCAAACTA
TATTTCTTGGAACGCGAAAGGAAGCTTTACCTATTTTCATAGAAGACCTGGAATCCATAACCTCAGAAGGCAATAT
TATTGATAGAAAATGTGGAAGGATCAGGAAGTTCTTAGATTCTTGGATGACAGATGCATGTTGATGCCCTATGGA
GATGTCCTTGTGTTTTGAGGTCACTGAGGTAGGAAGACCTGTCTACTCTTGGTTTACCAGTACAGTCTTGG
GCTGGATGGGTTATAGAGCTGAGCGGCTGTGATGGTTCTGTTTTTACATTAACAAAAACAATTAAAAACACCAA
AAC

WO 2004/030615

PCT/US2003/028547

887/6881
FIGURE 825

CACACCCTGCAGGACACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAGTGGGGTGACATGTAC
CTGTCGGCCATCTGTGAGTACCAGTTGGAAGAGATCCAGCGGGTGTTTGAAGGGCCCTATAAGGAGTACCATGAG
GAAGCCCAGAAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCTCGGCCTGGCTCGTGCAATTAACAACCTGGCAT
CGGCGCCACGGCTACACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAGAAGCACCCGCTGATG
GAGGAGCAGGTGGGGCCTCGGTGGAGCCGCCCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC
GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTTATTGACACAGGAGACGGCTGGCTGCTCAAG
GCTGTGAGCCTGGGGCCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGAACAGGAGCCCATGAGAAGCCTG
GTGCTATCTCAGAGCAAGAAGCTGCTCTTTGCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC
ATGAAGTATCGCTCCTGTGCAGACTGTGTCTCGCCCCGGGACCCCTATTGCGCCTGGAGCGTCAACACCAGCCGC
TGTGTGGCCGTGGGTGGCCACTCTGGATCTCTACTGATCCAGCATGTGATGACCTCGGACACTTCAGGCATCTGC
AACCTCCGTGGCAGTAAGAAAGTCAGGCCCACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGTCTG
CCCTGCCACCTCTCCTCCAACCTGGCCCATGCCCGCTGGACCTTTGGGGGCCGGGACCTGCCTGCGGAACAGCCC
GGGTCTCTCCTCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGCTGCCAGCCCCGCCATGCCGGGGCCTAC
CACTGCTTTTCAGAGGAGCAGGGGGCGCGCTGGCTGCTGAAGGCTACCTTGTGGCTGTCTGTGGCAGGCCGCTCG
GTGACCTTGGAGGCCCGGGCCCCCTGGAAAACCTGGGGCTGGTGTGGCTGGCGGTGGTGGCCCTGGGGGCTGTG
TGCCTGGTGTCTGTCTGTCTGGTGTCTGTCATTGCGCCGGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAGGCT
ACTGAGAGGACCTTGGTGTACCCCCTGGAGCTGCCCAAGGAGCCCCACAGTCCCCCTTCCGGCCCTGTCTGAA
CCAGATGAGAACTTTGGGATCCTGTCTGGTTACTACTATTAGATGGCTCCCTTAAGATAGTACCTGGGCATGCC
CGGTGCCAGCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCCAGGCCAGCCTCTGCCTTCTCCAACCTCGG
CTTACCTGGGGGGTGGGCGGAACCTCAAATGCCAATGGTTACGTGCGCTTACAACCTAGGAGGGGAGGACCGGGGA
GGGCTCGGGACCCCCCTGCCGTAGCTCGCGGATGAACTGAGACGCAAACTGCAGCAACGCCAGCCACTGCCCGAC
TCCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGCTCGGCGGGAAGCGTGGGAGGTGTAGCTCCTA
CTTTTGACAGGCACCAGCTACCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGGGACAGATACTGCCAGCA
CCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACTGCCACTTGGTGTGGCTCACCAGGGCACCAGCCT
CGCAGAAGGCATCTTCTCTCTCTGTGAATCACAGACACGCGGGACCCAGCCGCCAAAACCTTTTCAAGGCAGA
AGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTGTGTATGTGTGTGTGCACGCGCTGC
GCGCTTGTGGCATAGCCTTCTGTTTCTGTCAAGTCTTCCCTTGGCCTGGGTCTCTCTGGTGAGTCAATTGGAGCT
ATGAAGGGGAAGGGTTCGTATCACTTTGTCTCTCTACCCCCACTGCCCCGAGTGTGCGGCAGCGATGTACATAT
GGAGGTGGGGTGGACAGGGTGTGTGCCCCCTCAGAGGGAGTGCAGGGCTTGGGGTGGGCTAGTCTCTGCTCCTA
GGGCTGTGAATGTTTTAGGGTGGGGGGAGGGAGATGGAGCCTCCTGTGTGTTTGGGGGGAAGGGTGGGTGGGGC
CTCCCACTTGGCCCCGGGGTTCAGTGGTATTTTATACTTGCCTTCTTCTCTGTACAGGGCTGGGAAAGGCTGTGTG
AGGGGAGAGAAGGGAGAGGGTGGGCCTGCTGTGACAATGGCATACTCTTCCAGCCCTAGGAGGAGGGCTCCT
AACAGTGAACCTATTGTGTCCCCGCTATTTATTGTTGTAAATATTTGAGTATTTTTATATTGACAATAAAAT
GGAGAAAATGAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

888/6881
FIGURE 826

MYLSAICEYQLEEIQRVFEGPYKEYHEEAQKWDRYTDPVPSRPGSCINNWHRRHGYTSSLELPDNIILNFVKKHP
LMEEQVGPRWSRPLLKKGTFNTHLVADRVTGLDGATYTVLFIDTGDGWLLKAVSLGPWVHLIEELQLFDQEPMR
SLVLSQSKKLLFAGSRSQVLVQLPVADCMKYRSCADCVLARDPYCAWSVNTSRCVAVGGHSGSLLIQHVMTSDTSG
ICNLRGSKKVRPTPKNITVVAGTDLVLPCHLSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMQAQPRHAG
AYHCFSEEQGARLAAEGYLVAVVAGPSVTLEARAPLENLGLVWLAVVALGAVCLVLLLLLVLSLRRRLREELEKGA
KATERTLVYPLELPKEPTSPFPRCPEPDEKLWDPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLPSP
TRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELADELRRKLQQRQPLPDSNPEESSV

WO 2004/030615

PCT/US2003/028547

889/6881
FIGURE 827

CGGAAGTTTTGCTGCTAGTCGCGGACGCAATGCTTCAAGGTTACTTCGCGGAGCTGGAACGCTGGCCGCGCAGG
CCCTGAGGGCTCGCGGCCCCAGTGGCGCGGCCGCGATGCGCTCCATGGCATCTGGAGGTGGTGTTCCTACTGATG
AAGAGCAGGCGACTGGGTTGGAGAGGGAGATCATGCTGGCTGCAAAGAAGGGACTGGACCCATACAATGTACTGG
CCCCAAAGGGAGCTTCAGGCACCAGGGAAGACCCTAATTTAGTCCCCTCCATCTCCAACAAGAGAATAGTAGGCT
GCATCTGTGAAGAGGACAATACCAGCGTCGTCTGGTTTTGGCTGCACAAAGGCGAGGCCAGCGATGCCCCGCT
GTGGAGCCCATTAAGCTGGTGCCCCAGCAGCTGGCACACTGAGCACCTGCACTAAATTACTCAAATGTGCTG
TAAAGTTTCTTCTTTCCAGTAAAGACTAGCCATTGCATTGGCTCCTTCTCCATAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

890/6881
FIGURE 828

MASRLLRGAGTLAAQALRARGPSGAAAMRSMASGGGVPTDEEQATGLEREIMLAACKGLDPYNVLAPKGASGTRE
DPNLVPSISNKRIVGCICEEDNTSVVFWLHKGEAQRCPRCGAHYKLVPQQLAH

WO 2004/030615

PCT/US2003/028547

891/6881
FIGURE 829

TTGCAGCCGCCGGCAGCTACTGCAAGGCAAAAGCCGGAGTGGACGTGTCTTTTGAAACTGCTGCTCTTTCACTTC
TCAGGCGTCACCGAGAGCTCAGCACCCAGGCTGAACTCTGTACCATTTGGAAGAAATGGAAGCTGATGCATCTGTT
GACATGTTTTCCAAAGTCCTGGAGCATCAGCTGCTTCAGACTACCAAAGTGGTGGAAAGAACATTTGGATTCTGAA
ATTCAAAAAGTGGATCAGATGGATGAGGATGAATTGGAACGCCCTTAAAGAAAAGAGACTCCAGGCACTAAGGAAA
GCTCAACAGCAGAAACAAGAAATGGCTTTCTAAAGGACATGGGGAATACAGAGAAATCCCTAGTGAAAGAGACTTT
TTTCAAGAAGTCAAGGAGAGTGAAAATGTGGTTTGCCATTTCTACAGAGACTCCACATTCAGGTGTAAAATACTA
GACAGACATCTGGCAATATTGTCCAAGAAACACCTCGAGACCAAATTTTTGAAGCTGAATGTGGAAAAAGCACCT
TTCCTTTGTGAGAGACTGCATATCAAAGTCATTCCACACTAGCACTGCTAAAAGATGGGAAAACACAAGATTAT
GTTGTTGGGTTTACTGACCTAGGAAATACAGATGACTTCACCACAGAACTTTAGAATGGAGGCTCGGTTCTTCT
GACATTCTTAATTACAGTGGAAATTTAATGGAGCCACCATTTCAGAACCAAAGAAATTTGGAACAACTTCACA
AAGCTGGAAAAGAAAAGTATCCGAGGAAAAGAAATATGATTACAGACTCTGATGATGATTAGAGCTCAATAATTCTT
TGTAATTGTCTTTTTTTTTCTGCTTCAGATTTAAATGTGTTTTTAAATTTCTATTAATGTCTATACATTGGTCA
CCTAAATACTCATATTTCTCGAGTTTATACAGTTGTATCACATCGAAAAGTGTCTTTACTGTTTTCTGTGTGGCC
ATCATGTTTAAGTTGAGGAAAAGTCAAGTTCTTAAATTTATCTGGGAAGGGTCTGGATTCTCTATTTTTGAGATTGA
CTTTATCACAATATGATTCTTACATCTTTATACCATTTACAATTGTGTTTTAGATCTACAGAGTTAGAAATTCGA
AACTATTCCAGGACTAATTCTTAATCGGCATTATTTATACAAGAGGTCAAGTAACATTTACTAGCGCAATACTG
CACTTGTAATGAATTATAAACGCTCTTCTGGAATATATTTAAATAACCATTAAAGAACTGCTTATTCATTCTGG
ACACTGCATGTTGATGTTGAATCACTGATGCCAGCAGAAAGCTATTTTGATTTGTGAACATACTGCCTTATTTA
AAGGGTCCTGATTGCTTGATTTTAAAGACATTCATTAATAAGAAACCAGGAAACACTTTTGAAATAACAGCATAA
GGAACCTCACTGTCTCTGCTCAATAAAATACCTGTAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

892/6881
FIGURE 830

MEADASVDMFSKVLEHQLLQTTKLVEEHL DSEIQKLDQMD EDELERLKEKRLQALRKAQQQKQEWLSKGHGEYRE
IPSERDFFQEVKESENVVCHF YRDSTFRCKILDRHLAILSKKHLET KFLKLNVEKAPFLCERLHIKVIPTLALLK
DGKTQDYVVGFTDLGNTDDFTTETLEWRLGSSD ILNYSGNLMEPPFQNKFGTNFTKLEKKTIRGKKYDSDD
D

WO 2004/030615

PCT/US2003/028547

893/6881
FIGURE 831A

CGCGGGTCTGTGGAGAGCCGGGTGCGAGCGGCGGCAGCACGAGGGGAAAAAGAGCTGAGCGGAGACCAAAGTCAGC
CGGGAGACAGTGGGTCTGTGAGAGACCGAATAGAGGGGCTGGGGCCACGAGCGCCATTGACAAGCAATGGGGAAG
AAACAGAAAAACAAGAGCGAAGACAGCACCAAGGATGACATTGATCTTGATGCCTTGGCTGCAGAAATAGAAGGA
GCTGGTGTGCCAAAGAACAGGAGCCTCAAAAGTCAAAAGGGAAAAAGAAAAAAGAGAAAAAAGCAGGACTTT
GATGAAGATGATATCCTGAAAGAACTGGAAGAATTGTCTTTGGAAGCTCAAGGCATCAAAGCTGACAGAGAACT
GTTGCAGTGAAGCCAACAGAAAAAATGAAGAGGAATTCACCTCAAAAGATAAAAAAAGAAAGGACAGAAGGGC
AAAAACAGAGTTTTGATGATAATGATAGCGAAGAATTGGAAGATAAAGATTCAAATCAAAAAAGACTGCAAAA
CCGAAAGTGGAAATGTACTCTGGGAGTGATGATGATGATTTTTAACAACTTCTTAAAAAGCTAAAGGGAAA
GCTCAAAATCAAATAAGAAAGTGGGATGGGTGAGAGGAGGATGAGGATAACAGTAAAAAAATTAAAGAGCGTTCA
AGAATAAATCTTCTGGTGAAAGTGGTGATGAATCAGATGAATTTTTGCAATCTAGAAAAGGACAGAAAAAAAT
CAGAAAAACAAGCCAGGTCTTAACATAGAAAGTGGGAATGAAGATGATGACGCTCTTCAAAATTAAGACAGTG
GCCCAAAAGAAGGCAGAAAAGAAAGGAGCGCGAGAGAAAAAGCGAGATGAAGAAAAAGCGAAACTGCGGAAGCTG
AAAGAAAAAGAAGAGTTAGAAACAGGTAAAAAGGATCAGAGTAAACAAAAGGAATCTCAAAGGAAATTTGAAGAA
GAACTGTAAATCCAAAGTGACTGTTGATACTGGAGTAATTCCTGCCTCTGAAGAGAAAGCAGAGACTCCACA
GCTGCAGAAGATGACAATGAAGGAGACAAAAAGAAAGATAAGAAGAAAAAGAAAGGAGAAAAAGGAAGAAAA
GAGAAAGAGAAGAAAAAGGACCTAGCAAAGCCACTGTTAAAGCTATGCAAGAAGCTCTGGCTAAGCTTAAAGAG
GAAGAAGAAAGACAGAAGAGAGAAGAGGAAGAACGTATAAAACGGCTTGAAGAATTAGAAGCCAAGCGTAAAGAA
GAGGAACGATTGGAACAAGAAAAAGAGAAAAGGAAAAAGCAAAAAAGAAAAAGAAAGAAAGAACGCTTGAAAAA
GAAGGGAACTTTTAACTAAATCCCAGAGAGAAGCCAGAGCCAGAGCCGAAGCTACTCTTAACTGCTACAAGCT
CAGGGTGTTGAAGTGCCATCAAAAGACTCTTTGCCAAAGAGAGGCCAATTTATGAAGATAAAAAAGAGGAAAAA
ATACCACAGCAGCTAGAAAGTAAAGAGTGCTCTGAATCAATGGAATTATGTGCTGCTGTAGAAGTTATGGAACAA
GGAGTACCAGAAAAGGAAGAGACACCCTCCTGTTGAACCAGAAGAAGAAGATACTGAGGATGCTGGATTG
GATGATTGGGAAGCTATGGCCAGTGATGAGGAGACAGAAAAAGTAGAAGGAAACAAAGTTTATATAGAAGTAAAA
GAAAACCTGAAGAGGAGGAGGAGGAGGAAGAAGAGGAAGAAGATGAAGAAAGTGAAGAAGAGGAGGAAGAG
GAGGGAGAAAGTGAAGGCAGTGAAGGTGATGAGGAAGATGAAAAGGTGTGATGAGAAGGATTGAGGAAGACA
TTAGATAAAAAGCCAAGTAAAGAAATGAGCTCAGATTCTGAATATGACTCTGATGATGATCGGACTAAAGAAGAA
AGGGCTTATGACAAAGCAAAACGGAGGATTGAGAAACGGCGACTTGAACATAGTAAAAATGTAAACACCGAAAAG
CTAAGAGCCCCCTATTATCTGCGTACTTGGGCATGTGGACACAGGGAAGACAAAAATTCTAGATAAGCTCCGTAC
ACACATGTACAAGATGGTGAAGCAGGTGGTATCACACAACAAATTGGGGCCACCAATGTTCTCTTGAAGCTATT
AATGAACAGACTAAGATGATTAAAAATTTGATAGAGAGAATGTACGGATTCCAGGAATGCTAATTATTGATACT
CCTGGGCATGAATCTTTCAGTAATCTGAGAAAAGAGGAAAGCTCTCTTTGTGACATTGCCATTTTAGTTGTTGAT
ATTATGCATGGTTTGGAGCCCCAGACAATTGAGTCTATCAACCTTCTCAAATCTAAAAAATGTCCTTCTTGAAGT
GCACTCAATAAGATTGATAGGTTATATGATTGAAAAAGAGTCTGACTCTGATGTGGCTGCTACTTTTAAAGAAG
CAGAAAAAGAATACAAAAGATGAATTTGAGGAGCGAGCAAAGGCTATTATTGTAGAATTTGCACAGCAGGGTTTG
AATGCTGCTTTGTTTTATGAGAATAAAGATCCCCGCACTTTTGTGCTTTGGTACCTACCTCTGCACATACTGGT
GATGGCATGGGAAGTCTGATCTACCTTCTGTAGAGTTAAGTACAGACCATGTTGAGCAAGAGACTTGCACACTGT
GAAGAGCTGAGAGCACAGGTGATGGAGGTTAAAGCTCTCCCGGGATGGGCACCACTATAGATGTCATCTTGATC
AATGGGCGTTTGAAGGAAGGAGATACAATCATTGTTCTGGAGTAGAAGGGCCATTGTAAGTCAAGATTCGAGGC
CTCCTGTTACCTCCTCTATGAAGGAATTACGAGTGAAGAACAGTATGAAAAGCATAAAGAAGTAGAAGCAGCT
CAGGGGGTAAAGATTCTTGAAAAGACCTGGAGAAAAACATTGGCTGGTTTACCCCTCCTTGTGGCTTATAAAGAA
GATGAAATCCCTGTTCTTAAAGATGAATTGATCCATGAGTTAAAGCAGACACTAAATGCTATCAAATTAGAAGAA
AAAGGAGTCTATGTCCAGGCATCTACACTGGGTTCTTTGGAAGCTCTACTGGAATTTCTGAAAACATCAGAAGTG
CCCTATGCAGGAATTAACATTGGCCAGTGATGATAAAAAAGATGTTATGAAGGCTTCAGTGATGTTGGAACATGAC
CCTCAGTATGCAGTAATTTTGGCCTTCGATGTGAGAAATTGAACGAGATGCACAAGAAATGGCTGATAGTTTAGGA
GTTAGAATTTTGTAGTCAGAAATTATTTATCATTATTTGATGCCTTTACAAAATATAGACAAGACTACAAGAAA
CAGAAACAAGAAGAAATTAAGCACATAGCAGTATTTCCCTGCAAGATAAAAAATCCTCCCTCAGTACATTTTAAAT
TCTCGAGATCCGATAGTGATGGGGTGACGGTGAAGCAGGTGAGGTGAACAGGGGACACCCATGTGTGTCCCA
AGCAAAAAATTTTGTGACATCGGAATAGTAACAAGTATTGAAATAAACCATAAACAAGTGGATGTTGCAAAAAA

WO 2004/030615

PCT/US2003/028547

894/6881

FIGURE 831B

GGACAAGAAGTTTGTGTAAAAATAGAACCTATCCCTGGTGAGTCACCCAAAATGTTTGGAAGACATTTTGAAGCT
ACAGATATTCTTGTAGTAAGATCAGCCGGCAGTCCATTGATGCACTCAAAGACTGGTTCAGAGATGAAATGCAG
AAGAGTGACTGGCAGCTTATTGTGGAGCTGAAGAAAGTATTTGAAATCATCTAATTTTTTTCACATGGAGCAGGAA
CTGGAGTAAATGCAATACTGTGTTGTAATATCCCAACAAAAATCAGACAAAAAATGGAACAGACGTATTTGGACA
CTGATGGACTTAAGTATGGAAGGAAGAAAAATAGGTGTATAAAATGTTTTCCATGAGAAACCAAGAACTTACAC
TGGTTTGACAGTGGTCAGTTACATGTCCCCACAGTTCCAATGTGCCTGTTCACTCACCTCTCCCTTCCCCAACCC
TTCTCTACTTGGCTGCTGTTTTAAAGTTTGCCCTTCCCCAAATTTGGATTTTTATTACAGATCTAAAGCTCTTTC
GATTTTATACTGATTAAATCAGTACTGCAGTATTTGATTAAACC

WO 2004/030615

PCT/US2003/028547

895/6881
FIGURE 832

CTTCCTTTCCAACCTGGACGCTGCAGAAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCC
ATCAACGAAGTGGTAACCCGAGAATACACCATCAACATTACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGT
GCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGAACCTCCAGATGTGCGCATTGACACC
AGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAA
CGTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAAT
CTACAGACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAATTGC

WO 2004/030615

PCT/US2003/028547

896/6881
FIGURE 833

MAPAKKGGEKKKGRSAINEVVTREYTTINIHKRIHGVGFKKRAPRALKEIRKFAMKEMGTPDVRIDTRLNKAVWAK
GIRNVPIRIRVRLSRKRNEDEDSPNKLYTLVTYVPVTTFKNLQTVNVN DEN

WO 2004/030615

PCT/US2003/028547

897/6881
FIGURE 834

ATGCCCCGGCGGAGGGGCGAGCGCGGCGTCTGGCCGGCTTCTCACCGCCGCGGAGCAAAGAGGGTCCCGGGAAGCG
GCAGGGTCGGCGTCCAGGAGCGGCTTCGGGGGCTCCGGCGGCGGAGGCGGAGCAAGCGGCCCCGGGTCCGGG
AGCGGAGGCCCTGGGGGCCCCGCGGGCAGGATGAGCTTGACCCCGAAGGAGCTCTCGAGCCTGCTGAGCATCATA
TCGGAGGAGGCGGGCGGCGGCAGCACCTTCGAGGGCCTGTCCACCGCCTTCCACCACTACTTCAGCAAGGCCGAC
CACTTCCGCTGGGCTCGGTGCTCGTCAATGCTGCTCCAGCAGCCCGACCTGCTGCCTAGCGCGGCGCAGCGCCTC
ACGGCGCTCTACCTGCTCTGGGAGATGTACCGCACCGAGCCGCTGGCCGCCAACCCCTTCGCCGCCAGCTTCGCG
CACCTGCTCAACCCCGCGCCGCCCGCCCGCGGGCGGCCAGGAACCCGACCGCCCTCCGCTCTCAGGATTTTTACCT
CCTATAACTCCACCAGAAAAGTTTTTTCTTTCCAGCTGATGCTGGCACCCCCACGGGAACCTTTCAAAAAGACG
CCTCGCCAGATTGCACTGATGGACGTTGGAACATGGGCCAGTCTGTGGACATTAGTGGGCTTCAGTTAGCCTTG
GCCGAACGCCAATCTGAATTGCCAACGCAAAGCAAAGCGAGCTTCCCCAGTATTCTCAGTGACCCAGACCCGGAT
TCTTCTAATTCTGGATTTGACAGCTCAGTTGCCTCTCAGATCACAGAAGCTTTAGTCAGCGGACCAAAGCCACCT
ATTGAAAGCCATTTTCGACCAGAGTTTATTTCGTCCACCGCCTCCACTCCACATTTGTGAGGATGAACTTGCTTGG
CTAAACCCACGGAGCCTGACCACGCGATCAGTGGGATAAATCGATGTGTGTTAAGAATAGCACTGGTGTGGAG
ATCAAACGAATAATGGCCAAAGCCTTCAAAAGCCCCTTATCCTCTCCCCAACAAACACAGCTACTTGGTGAGTTG
GAAAAAGACCCCAAACCTTGTCTACCATATTGGCCTCACCCAGCCAAACTTCCTGACCTTGTGAAAAACAACCCT
TTAGTCGCTATAGAAATGTTGCTGAAATTAATGCAGTCAAGCCAGATCACTGAGTATTTCTCTGTCTGCTGCTCAAT
ATGGACATGTCTTTACATTCAATGGAAGTTGTAAATCGACTAACTACAGCTGTTGATCTACCTCCTGAATTTATT
CACCTTTATATATCAAATTGCATCTCTACTTGTGAACAGATTAAGGATAAATATATGCAGAATCGGTTGGTGCGT
CTTGTGTGTGTGTTTCTCCAATCCTTGATCCGTAACAAAATTATTAATGTACAGGATTTGTTTATAGAAGTGCAG
GCATTCTGTATTGAATTCAGTAGGATACGAGAAGCTGCTGGTCTTTTCCGGTTGTTGAAGACATTGGATACTGGG
GAAACACCTTCTGAGACCAAAATGTCAAAATTAA

WO 2004/030615

PCT/US2003/028547

898/6881
FIGURE 835

MPGGGASAASGRLLTAAEQRGSREAAGSASRSFGGSGGGRRGGASGPGSGSGGPGGPAGRMSLTPKELSSLLSI
SEEAGGGSTFEGGLSTAFHHYFSKADHFRLGSLVLMQLQPDLLPSAAQRLTALYLLWEMYRTEPLAANPFAASFA
HLLNPAPPARGGQEPDRPPLSGFLPPIITPEKFFLSQLMLAPPRELKKTTPRQIALMDVGNMGQSVDISGLQLAL
AERQSELPTQSKASFPSILSDPDPSNSGFDSSVASQITEALVSGPKPIESHFRPEFIRPPPPLHICEDELAW
LNPTEPDHAIQWDKSMCVKNSTGVEIKRIMAKAFKSPLSSPQQTQLLGELEKDPKLVYHIGLTPAKLPDLVENNP
LVAIEMLLKLMQSSQITEYFSVLVNMDMSLHSMEEVNRLLTAVDLPPEFIHLYISNCISTCEQIKDKYMQNRLVR
LVCVFLQSLIRNKIINVQDLFIEVQAFCEFSRIREAAGLFRLKTLDTGETPSETKMSK

WO 2004/030615

PCT/US2003/028547

899/6881
FIGURE 836

AGGGTACGGGCGGGACCGCCGAGCCGGGGCGGGGGCACGGCAACCGCGAGGCCTGGGGGCGCCCGCCCCCGG
CGCCCCACGCCCCGGTGCCAGCGAGCCGAGGCGTGTCATCTCCTTATATGGTCAAATGACACGGCGGGGTTTCTCGA
GGGCGGGAGCTGCGCAGCGCTCCACTCGGCCGGCAGCGGAGCCGCGAGCCACCAGCCGCCCGCGCCCTCCAGCCCC
GTCCGGGAGTCCCCGGCCCGCTGCGGTGCCGTGAGTACCTCCAACCCCTGCGCCCCGGAGGGAGGCCGAGGGGC
TTAGCCACCAGGGCTCGGAAGTGGGGGCCGAATCCGGTGCGAGACCCAAGGAGAGGGGAGCAGAGCCGGAGTTGG
GGAGACTGTGGCTGAAAAGTGTGTCTTCTGAGAGTACCTGAGCTGGCATTGACTTTGGGACGGAGTCTCGCTTG
TCGCCCAGGCTGGAGTGCACTGGCACGATCTCAGCTCACTGCAAGCTCTACCTCTTGGTTCACGCCATTCTCCTG
CCCCAGCCTCCCAAGTAGCTGGGACTACAGGTTGCTGAAAAGCCAGGAGTCAAATGACTGAGCGCTTTGACTGC
CACCATTGCAACGAATCTCTCTTTGGCAAGAAGTACATCCTGCGGGAGGAGAGCCCTACTGCGTGGTGTGCTTT
GAGACCCTGTTTCGCCAACACCTGCGAGGAGTGTGGGAAGCCATCGGCTGTGACTGCAAGGACTTGTCTTACAAG
GACCGGCACTGGCATGAAGCCTGTTTCCACTGCTCGCAGTGCAGAACTCACTGGTGGACAAGCCCTTTGCTGCC
AAGGAGGACCAGCTGCTCTGTACAGACTGCTATTCCAACGAGTACTCATCCAAGTGCCAGGAATGCAAGAAGACC
ATCATGCCAGGTACCCGCAAGATGGAGTACAAGGGCAGCAGCTGGCATGAGACCTGCTTCATCTGCCACCGCTGC
CAGCAGCCAATTGGAACCAAGAGTTTATCCCCAAAGACAATCAGAATTTCTGTGTGCCCTGCTATGAGAAACAA
CATGCCATGCAGTGCCTTCAGTGCAAAAAGCCCATCACCACGGGAGGGGTCACTTACCGGGAGCAGCCCTGGCAC
AAGGAGTGCTTCGTGTGCACCGCCTGCAGGAAGCAGCTGTCTGGGCAGCGCTTCACAGCTCGCGATGACTTTGCC
TACTGCCTGAACTGCTTCTGTGACTTGTATGCCAAGAAGTGTGCTGGGTGCACCAACCCCATCAGCGGACTTGGT
GGCACAATAACATCTCCTTTGAGGAACGGCAGTGGCATAACGACTGCTTTAACTGTAAGAAGTGTCTCCCTCTCA
CTGGTGGGGCGTGCTTCTCTACAGAGAGGGACGACATCCTGTGCCCCGACTGTGGGAAAGACATCTGAATTCAA
CACAGAGAAGTTGCTGCTTGTGATCTCACACACAGATTTTATGTTTTCTTTCTACCCAGGCAATCTTGCTTC
TGGTTTCTTCCAGCCACATTGAGACTTTCTTCTAGTGCTTTTCAGTGATACTCACGTTTGCTTAAACCTTTAGT
GCTTTGTGATAGTTTCACTCCCAGGGAAAGAGAAAAGTCTGCCCTAGGCCCTAGGTGGGAAGATGGTTTGAAATTTT
TGTAATCGAGTAAGGCACACCCAAATGTAAAAATCCTTTGAATGATGCCTTTATAAATCTTTCTCTCACGTCT
ATTTAAGTGCAATTAACATATGTCACGAAGTTTGAAGTTTCTAAACTCAATAAGGTAATGACCAGTTGTTATTT
ACAGCTCTGTAACCTCCCGTTGCGTCAAGTCTAAACCAAGATTATGTGACTTGCAATAAAGTTATTTCAGAACAGA
AAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

900/6881
FIGURE 837

MTERFDCHHCNESLFGKKYILREESPYCVVCFETLFANTCEECKPIGCDCKDLSYKDRHWHEACFHCSQCRNSL
VDKPFAAKEDQLLCTDCYSNEYSSKCQECKKTIMPGTRKMEYKGSSWHETCFICHRCQQPIGTSFIPKDNQNF
VPCYEKQHAMQCVQCKKPITGGVITYREQFWHKECFVCTACRKQLSGQRFTARDDFAYCLNCFCDLYAKKCAGCT
NPISGLGGTKYISFEERQWHNDCFNCKKCSLSLVGRGFLTERDDILCPDCGKDI

WO 2004/030615

PCT/US2003/028547

901/6881
FIGURE 838

AGTCTTCTGGCCCCGAGAGGGAGAGGTGGGGATAGGACCTTCCTTTAGTCCCCTCCGTAGTGGAACGAAGGATTC
TTTATGGTCATCTGTGGTGTTTCATTTTCGTAAAGAAGCATCTGCAGGGTAAGAAGGAAAAACGTCCACCTTGCAAA
TATATCCCAGGCACATGCCTCCTGAGAAGTGACCCCCCTCCTCCCTCCGCCTCCCCGGCACGTCTGGGGCTTCT
CCAGTCTCCCGCTCCTGGGACCAGGCAGAGATCCCGCGTGGGCAGACCCCTGCCACCGCGCCAGGCCCTCGTCC
GAAACTCGCGCCCGAGAGCCCACGCCGGAGGCGACGCTCCCGATACTACTGTGCTCCCAAGACCCGGAGGGCAC
GAAGAAAGGAGCCCTGGCAAACAAAGGGTTGCTGAAAAGCCAGGAGTCAAATGACTGAGCGCTTTGACTGCCAC
CATTGCAACGAATCTCTCTTTGGCAAGAAGTACATCCTGCGGGAGGAGAGCCCCCTACTGCGTGGTGTGCTTTGAG
ACCCTGTTGCGCAACACCTGCGAGGAGTGTGGGAAGCCCATCGGCTGTGACTGCAAGGTACCTGCTGCGGGCCTC
TGCGGGTCCCCGGCGCTCCCCTAGGAAACACGGGTTTCTCTGTGGTTTGTGCTGAAGCCCTGATCCACCACTGAA
GTCTGTCTCTTGAGCCCCCTCTGAGGGGCGTGGACCCTGCGTGTAGCCTTTCGGAAGCTTCTTCCCTCTAGCGAA
TGTGATCTCTGCCCACAAGCACTGGGTGAGGGCCTTGCCAGGACTTTGTGCTTAGTATCTCTAAGTACATTTTC
TGTATTCTAGCAATTAGTGCCCTTATCTAACTACCCAGCTGCCTACCAATACTGGAACCTTCTTAAGGGTGGTGC
TCTCTTCTCTTGTCTGTTTGCCCCGTGGTGAGTAACGTGGAGCAGGTGCTGTGCTCAGTCAATATTTGATGAAT
GAATGTGTACATGAGAGAACCAGAGTTGGTTCCTGGATAAATGGGCACATAAAAGCACAAAGTCCTTGG

WO 2004/030615

PCT/US2003/028547

902/6881
FIGURE 839

AAGGACTCCATGAAAGATGACAGAAGAAGTTATTGTGATAGCCAAGTGGGACTACACCGCCCAGCAGGACCAGGA
GCTGGACATCAAGAAGAACGAGCGGCTGTGGTTGCTGGACGACTCCAAGACGTGGTGGCGGGTGAGGAACGCGGC
CAACAGGACGGGCTATGTACCGTCCAACCTACGTGGAGCGGAAGAACAGCCTGAAGAAGGGCTCCCTCGTGAAGAA
CCTGAAGGACACACTAGGCCTCGGCAAGACGCGCAGGAAGACCAGCGCGGGGATGCGTCCCCACGCCCAGCAC
GGACGCCGAGTACCCCGCCAATGGCAGCGGCGCCGACCGCATCTACGACCTCAACATCCCGGCCTTCGTCAAGTT
CGCCTATGTGGCCGAGCGGGAGGATGAGTTGTCCCTGGTGAAGGGGTGCGCGGTCACCGTCATGGAGAAGTGCAG
CGACGGTTGGTGGCGGGGAGCTACAACGGGCAGATCGGCTGGTTCCCTCCAACCTACGTCTTGGAGGAGGTGGA
CGAGCGGCTGCGGAGTCCCAAGCTTCCTGAGCCTGCGCAAGGGCGCCTCGCTGAGCAATGGCCAGGGCTCCCG
CGTGCTGCATGTGGTCCAGACGCTGTACCCCTTCAGCTCAGTCACCGAGGAGGAGCTCAACTTCGAGAAGGGGGA
GACCATGGAGGTGATTGAGAAGCCGAGAACGACCCCGAGTGGTGGAAATGCAAAAATGCCCGGGGCCAGGTGGG
CCTCGTCCCCAAAACTACGTGGTGGTCTCAGTGACGGGCCTGCCCTGCACCCTGCGCACGCCCCACAGATAAG
CTACACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAGTGGTACTACGGGAACGTGACGCGGCACCAGGC
CGAGTGCGCCCTCAACGAGCGGGGCGTGGAGGGCGACTTCCTCATTAGGGACAGCGAGTCCTCGCCCAGCGACTT
CTCCGTGTCCCTTAAAGCGTCAGGGAAGAACAACACTTCAAGGTGCAGCTCGTGGACAATGTCTACTGCATTGG
GCAGCGGCGCTTCCACACCATGGACGAGCTGGTGGAACTACAAAAAGGCGCCCATCTTCACCAGCGAGCACGG
GGAGAAGCTCTACCTCGTCAGGGCCCTGCAGTGACGGCGCCCCGCCCCACACTCGCCTCCCGGGCCCCACGGTG
GAGCTGCCCCCGGCCCTTGTGGCAGAGGCTCCTCCCGCGGGGACGGCCCCGACGGCTTCTCTG

WO 2004/030615

PCT/US2003/028547

903/6881
FIGURE 840

MTEEVIVIAKWDYTAQQDQELDIKKNERLWLLDDSKTWVRNAANRTGYVPSNYVERKNSLKKGSLVKNLKD TL
GLGKTRRKTSARDASPTPSTDAEYPANGSGADRIYDLNIPAFVKFAYVAEREDELSLVKGSRVTVMEKCS DGWWR
GSYNGQIGWFPSNYVLEEVDAAAESPFLSLRK GASLSNGQGSRLHVVTLYPFSSVTEELNFEKGETMEVI
EKPENDEPWWKCKNARGQVGLVPKNYVVVLS DGPALHPAHAPQISYTG PSSSGRFAGREWYYGNVTRHQAECALN
ERGV EGD FLIRDSESSP SDFS VSLKASGKNKHFKVQLVDNVYCI GQRRFHTMDELVEHYKKAPIFTSEHGEKLYL
VRALQ

WO 2004/030615

PCT/US2003/028547

904/6881
FIGURE 841

TGGAACCATGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAAGTACAAGCCCTTGACCTGCC
TCTCCAGGATGTCTACAAAATTGGTGGTATTGGTAGTGTTCCTGTTGGCCGAGTGGAGACTGGTGTTCCTCAAACC
TGGTATGGTGGTCACCTTTGCTCCAGTCAACGTACAACAGAAGTAAATCTGTCGAAATGCACCATGAAGCTTT
GAGTGAAGCTCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCTGGCAA
CGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGTTTCACTGCTCAGGTGATTATCCTGAACCA
TCCAGGCCAAATAAGCACTGGCTATGCCCTGTATTGGATTGCCACACGGCTCATATTGCATGCAAGTTTGCTGA
GCTGAAGGAAAAGATTGATCACCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTCTTTGGGTTGCTTTG
CTGTTCTGTGATATGAGACAGATAGTT

WO 2004/030615

PCT/US2003/028547

905/6881
FIGURE 842

AAAAGCCAAAATGGGAAAGGAAAAGACTCATACCAACATTGTCGTCATTGGACACATAGATTCTGGGCAAGTCCAC
CACTACTGGCCATCTGATCTACAAAGGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGC
TGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGTGTGAACATGGTATCAC
CATTGATACCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCGTTGATGCCCCAGGACACAGAGA
CTTCATCAAAAACATGATTACAGAGACATCTCAGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTGGTGA
ATTTGAAGCTGGTATCTCCAAGAATGGGCAAACCCAAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACA
ACTAATTGTTGGTGTTAACAAAATGGATTCTACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAACTACAAA
ATTGGTGGTATTGGTAGTGTTCCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCTGGTATGGTGGTCACCTTT
GCTCCAGTCAACGTTACAACAGAAGTAAAATCTGTGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCTGGG
GACAATGTGG

WO 2004/030615

PCT/US2003/028547

906/6881
FIGURE 843

AACAGATCTTCATGAATGTCGCTATCTTTGAGGATGAAGTTTTTGCTGGAGTTACCACACACCAGGAACCTCTTTC
CACACAGCCTGCTGAGTGTGATTGCCAATTCATCCCTTTCTCTGATCTCAACCAGAGTCCACGGAACATGTACC
AATGCCAGATGGGTAAGCAAACCTATGGGCTTCCACTTCTCACTTATCAAGACCGATCGGATAACAACTGTATC
GTCTTCAGACTCCTCAGAGTCCCTTGGTGAGACCTCCATGTATGATTATTATGACATGGATAACTATCCAATTG
GGACCAATGCCATCGTTGCTGTGATTCTTACACTGGCTATGATATGGAAGATGCCATGATTGTGAATAAGGCCT
CTTGGGAACGAGGCTTTGCCATGGAAGTGTCTACAAGTCTGAGTTCATAGACCTCTCTGAAAAAATTAAACAAG
GAGATAGTAGCCTGGTGTGTTGGCATCAAACCTGGTGACCCACGCGTTCTGCAGAAGTTAGATGACGATGGATTGC
CGTTTATAGGAGCAAACCTGCAGTACGGAGATCCGTATTACAGCTACCTCAACCTCAACACCGGGGAAAGTTTTG
TGATGTACTATAAGAGTAAAGAAAATTGTGTGTGGATAACATCAAAGTGTGCAGTAATGACACTGGGAGTGGAA
AATTCAAGTGTGTTTGCATCACTATGAGAGTGCCTCGGAACCCAACTATCGGAGATAAATTTGCCAGTCGCCATG
GGCAGAAGGGCATTTTAAGCAGATTGTGGCCGGCTGAGGACATGCCTTTTACTGAGAGTGGGATGGTCCCAGACA
TTCTGTTCAATCCCATGGTTTTCCATCCCGCATGACCATTTGGGATGTTAATTGAGAGTATGGCCGGGAAGTCTG
CAGCTTTGCATGGTCTCTGCCATGATGCTACACCTTCATCTTCTCAGAGGAGAACTCGGCCTTAGAATACTTTG
GTGAGATGTTAAAGGCTGCTGGCTACAATTTCTATGGCACCCGAGAGGTTATATAGTGGCATCAGTGGGCTAGAAC
TGGAAGCAGACATCTTCATAGGAGTGGTTTATTATCAGCGCTTACGCCATATGGTCTCAGACAAATTTCAAGTAA
GGACAACCTGGAGCCCGAGACAGAGTCACCAACCAGCCTATTGGGGGAAGAAATGTCCAGGGTGAATCCGTTTTG
GGGAGATGGAACGGGATGCGCTTTTAGCTCATGGTACATCTTTCTCCTTCATGACCGCCTCTTCAACTGCTCAG
ATCGGTGCGGTAGCCCATGTGTGTGAAGTGTGGCAGTTTACTCTCTCCACTGTTGGAGAAGCCACCCCTTCTTGG
TCTGCCATGCGCAACAGAAAATACAACCTGTACTCTGTGTAGTTCGCGAGTGACACTATCGATACTGTTTCTGTGCCT
TATGTTTTTCGGTATTTTGTAGCTGAACCTGGCAGCTATGAACATCAAAGTGAACTGGATGTTGTTTAACTTGAT
GTTGACCTTTTGGATTAAAGGGGACTATCAGATTAAAGCAAATGTAATTTTAAATCAATGAAGATATCATTACCA
GGTACTCTTGAGATTTTCAACGGTGTTAGAACTCTCAACCAAGACCTGAAAACCAAGTATGCAAGGTTTCTGA
ATCTCTCTGGTAGATTAACTATTGACAAATGATTTTCTGTTATCTTTGTTCAAAAAGTTTATGTCTTCTCAAAATA
TGAAATATTGATAAATGGAAGAGCATAACGGTGACAAGTCTCCTTTCCAACCCAGGTTCCCTACACCCTGCTCTC
AGCAGGCAGTGAGTGTACACACCTGTTAATCCATCTTGAGCAGGACAGTACTATACAAATAGAATGCAAGCTGT
AATGTAATTTTATATTTTCTTATAGCCACGTTGAAGTAAAAACAAACAGGTACAGTGTTTTTTACCAGCTTTATA
GAAGTACAGTTGTTACATATTTAATGAATACAATTTGATGGGTCTGACTATATGCACACACCTTTGATACCATCA
CCACAATCAGGGTAATAAACATACCTGTCTCCACAAGTTTCTCCTGCCCCCTTGTTTTTTGCTTTTTGGTT
GCTGTTGAGTTTTTGTGTTTGTCTTCTGTGGTAAGAACTTAACCTCAAGACCTACCCTCTTAACAAATCTTTAAG
TGCACGATATAGTATTGTTAATCCAGGCACCATGTTGTACAACAGATCTTTAGACCTTACTTGTCTTGCATAAC
TGAAGCTTTATACCTGTTGAACAACTCTCCATTCCCTGGCCCCCTAGCAACCACCTTCTACCCTGTTTCTATGA
GTTTGACTATTACAGATATCTCATATAGTGGGATCATGCAATATTTGTCCTGTGACTGGCTTATTTCACTTAGCA
TAGTGAATAAGATTTCATCCATTTTGAAGCCAGGCATGGTGTGTGCATCTATAGTCCCTGCTATTTGAGAGGC
TGAGGTGGGAGGATCATTTGAGTGCAGGAGTCAAGGACAGCCTGGGTAATATAGGAAGACCTGTCTTGAAGAC
CCTGACCTCAAGTGATCCACCCACCTCGGCCTCCGAAAGTGCTAGGATTACAGGTGTGAGCCACTGTGCCTGGCC
TCCGGTGAGTATTTTATATTTAGTCTACACTCCATACTTGGCTTTTTTCTGCTTTTATGTTGATCTGCTTTTCTAT
AGCAGTGTGTAGAGTGCCACTTATGTTTTCTTCTGTGTACAGTATTTTATTGTATGGATTTACCATCCCCTGT
GTATTTAAGTTGTTCCATTCTTTGGCCATTATAACTTTTTCTGCAAATATTCTGGTGACTTATCTTTGGCCATT
ATAAACTGTTGATAATAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

907/6881
FIGURE 844

MNVAIFEDEVFAGVTTHQELFPHSLLSVIANFIPFSDLNQSPRNMYYQCMGKQTMGFPLLTYYQDRSDNKLYRLQT
PQSPLVRPSMYDYYDMDNYP IGTNAIVAVISYTGDMEDAMIVNKASWERGFAHGSVYKSEFIDLSEKIKQGDSS
LVFGIKPGDPRVLQKLDDDGLPFI GAKLQYGDPIYSYLLNLNTGESFVMYYKSKENCVVDNIKVCSNDTGSGKFKC
VCITMRVPRNPTIGDKFASRHGQKGILSRLWPAEDMPFTESGMVPDILFNPHGFPSRMTIGMLIESMAGKSAALH
GLCHDATPFI SEENSALEYFGEMLKAAGYNFYGTERLYSGISGLELEADIFIGVVYYQRLRHMVSDKFQVRTTG
ARDRVNTQPI GGRNVQGGIRFGEMERDALLAHGTSFLLHDRLFNCSDRSVAHVCEVWQFTLSTVGEATPFLVCHA
QQKIQLYSV

WO 2004/030615

PCT/US2003/028547

908/6881
FIGURE 845

GAGCTGTCCCCGGTGCCGCCGACCCGGGCGGTGTGCCCGTGGCTCCAGCCGCTGTGCGCTCGATCTCCTCGTCTC
CCGCTCCGCCCTCCCTTTTCCCTGGATGAACCTGCGTCCTTTCTCTTCTCCGCCATGGAATTCTGCTCCGTGCTT
TTAGCCCTCCTGAGCCAAAGAAACCCAGACAACAGATGCCATACGCAGCGTATAGCAGTAACCTCCCCAGCTCG
GTTTCTGTCCGTAGTTTACAGTATTTAATTTTATATAATATATATTATTATTATAGCATTTTTGATACCTCAT
ATTCTGTTTACACATCTTGAAAGGCGCTCAGTAGTCTCTTACTAAACAACCACTACTCCAGAGAATGGCAACGC
TGATTACCAGTACTACAGCTGCTACCGCCGCTTCTGGTCCTTTGGTGGACTACCTATGGATGCTCATCCTGGGCT
TCATTATTGCATTTGTCTTGGCATTCTCCGTGGGAGCCAATGATGTAGCAAATTCTTTTGGTACAGCTGTGGGCT
CAGGTGTAGTGACCCTGAAGCAAGCCTGCATCCTAGCTAGCATCTTTGAAACAGTGGGCTCTGTCTTACTGGGGG
CCAAAGTGAGCGAAACCATCCGGAAGGGCTTGATTGACGTGGAGATGTACAACCTCGACTCAAGGGCTGCTGATGG
CCGGCTCAGTCAGTGCTATGTTTGGTTCTGCTGTGTGGCAACTCGTGGCTTCGTTTTTGAAGCTCCCTATTTCTG
GAACCCATTGTATTGTTGGTGCAACTATTGGTTTCTCCCTCGTGGCAAAGGGGCGAGGAGGGTGTCAAGTGGTCTG
AACTGATAAAAATTGTGATGTCTTGGTTCTGTGCCCACTGCTTCTGGAATTATGTCTGGAATTTTATTCTTCC
TGGTTCTGTGATTTCCTCCATAAGGCAGATCCAGTTCCTAATGGTTTGCAGCTTTGCCAGTTTTCTATGCCT
GCACAGTTGGAATAAACCTCTTTTCCATCATGTATACTGGAGCACCGTTGCTGGGCTTTGACAAACTTCCTCTGT
GGGGTACCATCCTCATCTCGGTGGGATGTGCAGTTTTCTGTGCCCTTATCGTCTGGTTCTTTGTATGTCCCAGGA
TGAAGAGAAAAATTGAACGAGAAATAAAGTGTAGTCCTTCTGAAAGCCCCCTTAATGGAAAAAAGAATAGCTTGA
AAGAAGACCATGAAGAAACAAAGTTGTCTGTTGGTGATTTGAAAACAAGCATCCTGTTTCTGAGGTAGGGCCTG
CCACTGTGCCCTCCAGGCTGTGGTGGAGGAGAGAACAGTCTCATTCAAACCTGGAGATTTGGAGGAAGCTCCAG
AGAGAGAGAGGCTTCCCAGCGTGGACTTGAAAGAGGAAACCAGCATAGATAGCACCGTGAATGGTGCAGTGCAGT
TGCCTAATGGGAACCTTGTCAGTTCAGTCAAGCCGTGAGCAACCAAATAAACTCCAGTGGCCACTACCAGTATC
ACACCGTGATAAGGATTCCGGCCTGTACAAAGAGCTACTCCATAAATTACATCTTGCCAAGGTGGGAGATTGCA
TGGGAGACTCCGGTGACAAACCCTTAAGGCGCAATAATAGCTATACTTCCTATACCATGGCAATATGTGGCATGC
CTCTGGATTCAATCCGTGCCAAAGAAGGTGAACAGAAGGGCGAAGAAATGGAGAAGCTGACATGGCCTAATGCAG
ACTCCAAGAAGCGAATTGCAATGGACAGTTACACCAGTTACTGCAATGCTGTGTCTGACCTTCACTCAGCATCTG
AGATAGACATGAGTGTCAAGGCAGAGATGGGTCTAGGTGACAGAAAAGGAAGTAATGGCTCTCTAGAAGAATGGT
ATGACCAGGATAAGCCTGAAGTCTCTCTCCTCTTCCAGTTCCCTGCAGATCCTTACAGCCTGCTTTGGGTCAATCG
CCCATGGTGGCAATGACGTAAGCAATGCCATTGGGCCTCTGGTTGCTTTATATTGGTTTATGACACAGGAGATG
TTTCTTCAAAGTGGCAACACCAATATGGCTTCTACTCTATGGTGGTGTGGTATCTGTGTTGGTCTGTGGGTTT
GGGGAAGAAGAGTTATCCAGACCATGGGGAAGGATCTGACACCGATCACACCTCTAGTGGCTTCAGTATTGAAC
TGGCATCTGCCCTCACTGTGGTGATTGCATCAAATATTGGCCTTCCCATCAGTACAACACATTGTAAAGTGGGCT
CTGTTGTGTCTGTTGGCTGGCTCCGGTCCAAGAAGGCTGTGACTGGCGTCTCTTTCGTAACATTTTTATGGCCT
GGTTTGTACAGTCCCCATTTCTGGAGTTATCAGTGCTGCCATCATGGCAATCTTCAGATATGTCATCCTCAGAA
TGTGAAGCTGTTTGAGATTAAATTTGTGTCAATGTTTGGGACCATCTTAGGTATTCTGCTCCCCCTGAAGAATG
ATTACAGTGTTAACAGAAGACTGACAAGAGTCTTTTATTTGGGAGCCAGAGGAGGAAGTGTTACTTGTGCTAT
AACTGCTTTTGTGCTAAATATGAATTGTCTCAAAATAGCTGTGTAAATAGCCCGGGTCCACTGGCTCCTGCT
GAGGTCCCCTTTCTTCTGGGCTGTGAATCCTGTACATATTCTCTACTTTTTGTATCAGGCTTCAATTCCATT
ATGTTTTAATGTTGTCTCTGAAGATGACTGTGATTTTTTTTCTTTTTTTAAACCATGAAGAGCCGTTTGACA
GAGCATGCTCTGCGTTGTTGGTTTACCAGCTTCTGCCCTCACATGCACAGGGATTAAACAACAAAAATATAACT
ACAACCTCCCTTGTAGTCTCTTATATAAGTAGAGTCCCTGGTACTCTGCCCTCCTGTGAGTAGTGGCAGGATCTA
TTGGCATATTCGGGAGCTTCTTAGAGGGATGAGGTCTTTGAACACAGTGAAAATTTAAATTAGTAACTTTTTTG
CAAGCAGTTTATTGACTGTTATTGCTAAGAAGAAGTAAGAAAGAAAAGCCTGTTGGCAATCTTGGTTATTTCTT
TAAGATTTCTGGCAGTGTGGGATGGATGAATGAAGTGAATGTGAACTTGGGCAAGTTAAGTGGGACAGCCTTC
CATGTTCAATTTGTCTACCTCTTAACGAATAAAAAAGCCTACAGTTTTTAG

WO 2004/030615

PCT/US2003/028547

909/6881
FIGURE 846

MATLITSTTAATAASGPLVDYLWMLILGFIIAFVLAFSVGANDVANSFGTAVGSGVVTLKQACILASIFETVGSV
LLGAKVSETIRKGLIDVEMYNSTQGLLMAGSVSAMFGSAVWQLVASFLKLPISGTHCIVGATIGFSLVAKGQEGV
KWSELIKIVMSWFVSPLLSGIMSGILFFLVRAFILHKADVPVNGLRALPVFYACTVGINLFSIMYTGAPLLGFDK
LPLWGTILISVGCAVFCALIVWFFVCPRMKRKIEREIKCSPSESPLMEKKNSLKEDHEETKLSVGDIENKHPVSE
VGPATVPLQAVVEERTVSFKLGDLEEAPERERLPSVDLKEETSIDSTVNGAVQLPNGNLVQFSQAVSNQINSSGH
YQYHTVHKDSGLYKELLHKLHLAKVGDCMGDSGDKPLRRNNSYTSYTMAICGMPLDSFRAKEGEQKGEEMEKLW
PNADSKKRIRMDSYTSYCNVSDLHSAEIDMSVKAEMGLGDRKGSNGSLEEWYDQDKPEVSLLFQFLQILTACF
GSFAHGGNDVSNAIGPLVALYLVDYTDGVSSKVATPIWLLLYGGVGICVGLWVWGRRVIQTMGKDLTPITPSSGF
SIELASALTVVIASNIGLPISTHCKVGSVSVGWLRSSKAVDWRFLFRNIFMAWFVTVPISGVISAAIMAIFRYV
ILRM

WO 2004/030615

PCT/US2003/028547

910/6881
FIGURE 847

ACCAACCTCTTCGAGGCACAAGGCACAACAGGCTGCTCTGGGATTCTCTTCAGCCAATCTTCATTGCTCAAGTGT
CTGAAGCAGCCATGGCAGAAGTACCTGAGCTCGCCAGTGAAATGATGGCTTATTACAGTGGCAATGAGGATGACT
TGTTCTTTGAAGCTGATGGCCCTAAACAGATGAAGTGCTCCTTCCAGGACCTGGACCTCTGCCCTCTGGATGGCG
GCATCCAGCTACGAATCTCCGACCACCACTACAGCAAGGGCTTCAGGCAGGCCGCGTCAGTTGTTGTGGCCATGG
ACAAGCTGAGGAAGATGCTGGTTCCCTGCCCACAGACCTTCCAGGAGAATGACCTGAGCACCTTCTTTCCCTTCA
TCTTTGAAGAAGAACCTATCTTCTTCGACACATGGGATAACGAGGCTTATGTGCACGATGCACCTGTACGATCAC
TGAAGTGCACGCTCCGGGACTCACAGCAAAAAAGCTTGGTGATGTCTGGTCCATATGAACTGAAAGCTCTCCACC
TCCAGGGACAGGATATGGAGCAACAAGTGGTGTCTCCATGTCCTTTGTACAAGGAGAAGAAAGTAATGACAAAA
TACCTGTGGCCTTGGGCCTCAAGGAAAAGAATCTGTACCTGTCCTGCGTGTTGAAAGATGATAAGCCCACTCTAC
AGCTGGAGAGTGTAGATCCCAAAAATTACCCAAAGAAGAAGATGGAAAAGCGATTTGTCTTCAACAAGATAGAAA
TCAATAACAAGCTGGAATTTGAGTCTGCCAGTTCCCCAACTGGTACATCAGCACCTCTCAAGCAGAAAACATGC
CCGTCTTCTGGGAGGGACCAAAGGCGGCCAGGATATAACTGACTTCACCATGCAATTTGTGTCTTCTTAAGAG
AGCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGGAACAGAAAGGTTTT
TGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCCCAACTGCCTGCCTTAGGGTAGTGCTAAGA
GGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTTCAGGGCCAATCCCCAGCCCTTTTGTGAGCCAG
GCCTCTCTCACCTCTCTACTCACTTAAAGCCCCGCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCT
CTGTCATTGCTCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTTGTGTTTATTCA
TTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTAGTTTTTAATAGCTATGGAAT
CAATTCATTTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATT
ATTTAAATGGGAATATTTATAAATGAGCAAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCTCTGAAG

WO 2004/030615

PCT/US2003/028547

911/6881
FIGURE 848

MAEVP ELASEMMAYYS GNEDDLFFEADGPKQMKCSFQDL DLCPLDGGIQLRISDHHSKGF RQAASVVVAMDKLR
KMLVPCPQTFQENDLSTFFPFI FEEEP IFFDTWDNEAYVHDAPVRS LNCTLRDSQQKSLVMSGPYELKALHLQGO
DMEQQVVFMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINN
LEFESAQFPNWI STSQAENMPVFLGGTKGGQDITDFTMQFVSS

WO 2004/030615

PCT/US2003/028547

912/6881
FIGURE 849

AGGCACCATGACTCCTGTGAGGATGCAGCACTCCCTGGCAGGTCAGACCTATGCCGTGCCCCCTCATCCAGCCAGA
CCTGCGGTGAGAGGAGGCCGTCCAGCAGATGGCAGATGCCCTGCAGTACCTGCAGAAGGTCTCTGGAGACATCTT
CAGCAGTGAGAGCGGCCTTGCTGCGGCCAAAGAACATGGAAAAGCATGAGTGGGGTGATGTGTGCCTTAAAGCAT
CAGACACTTGGGCCCTCGGGCATCAGGAGCCAGCCACAGGGATGTCTGGGGAAATGGCGTTCCATGAGATGCAAGC
ACACAAGAATGCACTTGGCACATCTGGGGAAACAGCAGGCAGCTGATATCACTGGGCCCCACCCTGCACCAGGGAGG
ATGGAAGCAGGTAGAGCAGAGCCGGAGCCAGGTGCAGGCCATTGGAGAGAAGGTCTCCTTGGCCCAGGCCAAGAT
TGAGAAGATCAAGGGCAGCAAGAAGGCCATCAAGGTGTTCTCCAGTGCCAAGTACCCTGCTCCAGAGCGCCTGCA
GGAATATGGCTCCATCTTCACGGGCGCCCAGGACCCTGGCCTGCAGAGACGCCCCCGCCACAGGATCCAGAGCAA
GCACCGCCCCCTGGACGAGCGGGCCCTGCAGGAGAAGCTGAAGGACTTTCTGTGTGCGTGAGCACCAAGCCGGA
GCCCCAGGACGATGCAGAAAGAGGGACTTGGGGGTCTTCCCAGCAACATCAGCTCTGTCAGCTCCTTGCTGCTCTT
CAACACCACCTAGAACCT

WO 2004/030615

PCT/US2003/028547

913/6881
FIGURE 850

AGCGCGGGGAACCGGAGGCTGCAGGATGGTCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCA
ACGCAGTGC GCGACCGGGAGCTGGACCTCCGGGGGTATAAAATCCCGTCATTGAAAATCTAGGTGCTACGTTAG
ACCAAGTTTGATGCTATTGATTTTTCTGACAATGAGATCAGGAACTGGATGGTTTTCTTTGTTGAGAAGACTGA
AAACATTGTTAGGGAACAACAACAGAATATGCCGTATAGGTGAGGGACTGATCAGGCTCTGCCCTGTCTGACAG
AACTCATTCTACCAATAATAGGCTCGTGGAAGTGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTT
ACCTAAGTATCCTAAGAAATCTGGTAACCAATAAGAAGCATTACAGATTGTATGTGATTATATAAAGTTCCGCAAG
TCAGAGTACTGGATTTCCAGAAAGTGAACTAAAAGTTTTAATCCAGGTGCTGGTTTGCCAACTGACAAAAAGAA
AGGTGGGCCATCGCCAGGGGATGTAGAAACAATCAAGAATGCTATAGCAAATGCTTCAACTCTGGCTGAAGTGGA
GCGGCTGAAGGGTTGCTGCAGTCTGGTCAGATCCCTGGCAGAGAACGCAAATCGGGGCC

WO 2004/030615

PCT/US2003/028547

914/6881
FIGURE 851A

GATGGGCTGTGCAAAGGGCGCGGCTGCTGAGGACAGGGCTGTGGCTGGAGAACCTGCTGCTTCTGAAAGCCGAGC
CCCACCCTAAAGGACCGAGAGCACAGGCCATGGGAGAGGAATCGAGTAGGGATGCAGAGCCTGGTGGCACTGTCC
TGAGAGAGGAGGAGGCTGGGCGAGGGCCCCGGCGCTGGAGAGGTGCCCTGCATATGGGACCTCTCAGAGGTGCACA
AGAGCTGTGTGCCAGGTACCCCTGTCTCTCTCTCTCTCTCCAGCCCCCAGCCTACTCTCTTAATGGTCTGTGTCT
TTCAGGGATGAGATTTACTGCCAGATCTGCAAGCAGCTCTCGGAGAACTTCAAACAAGCAGCCTGGCCCCGGGC
TGGATCCTGCTCAGCCTCTGCCTCGGCTGCTTCCCACCCTCAGAGAGGTTTATGAAGTATCTACTGAACTTCATC
GGCCAAAGGGCCGGCGACCTACGGCCCCCTTCTGTGCCGAGCGCCTGAGACGCACCTATGCCAATGGGGTGCCTGCG
GAGCCCCCACCTGGCTGGAGCTGCAGGCTGTCAAGTCCAAGAAGCACATCCCCATCCAAGTCATCTTGCCCACT
GGAGAGAGCCTAACCGTCCCCGTGGACTCAGCCTCCACATCTCGGGAATGTGCATGCACATCGCTCACAAGCAG
GGCCTCAGCGACCACTGGGCTTCTCCCTCCAGGTGCGCGTGTACGACAAGTTCTGGTCCCTGGGCAGCGGGCGC
GACCACATGATGGATGCCATCGCCCGGTGTGAGCAGATGGCCAGGAGAGGGGCGAGAGCCAGCGCCAGTCACCC
TGGCGCATCTACTTCCGGAAGGAATTCTTACCCCTGGCACGACTCCCGGAGGACCTGTGAGCAGCGAGCTT
ATTTACCGCAAGTCTCCGAGGAGTCTGGTCTGGCGAGTACAGCTTCGAGAAGGAGGAAGAGCTGGTTGAGCTG
CTGGCCCGGCACTGCTACGTGCAGCTCGGCGCCTCAGCAGAGAGCAAGGCTGTCCAGGAGCTGCTGCCAGCTGC
ATCCCCACAAGCTGTACAGGACCAAGCCCCCAGACAGGTGGGCGAGCCTCGTCACTGCCGCTGCGCCAAGGCC
CCATACACTCAGAAGCAAGTCACACCACTGGCCGTGCGAGAGCAGGTGGTGGACGCCCGCCGCTGCAGTGGCCG
CTGCTCTTCTCCCGCTCTTCAAGTCATCACACTCTCAGGCCCGCCCTGCCAAGACGCAGCTGATCTTGGCT
GTTAACTGGAAGGGGCTTTGCTTCTTGACCAGCAGGAGAAGATGCTGCTGGAATCTCTTTCCAGAGGTCATG
GGTCTGGCCACCAACAGGGAGGCCAGGGCGGGCAGAGGCTGCTGCTCTCCACGATGCATGAGGAGTACGAGTTT
GTGTACCCAGCAGTGTGGCCATCGCTGAGCTGGTGGCCCTGTTCTTGAGGGCTGAAGGAGAGGTCCATTTT
GCCATGGCCCTGAGGACAGGAAGGCCACAGATGACACCACCTCCTGGCCTTCAAGAAGGGGGACCTGTTGGTC
CTCACAAGAAGCAGGGGCTGCTGGCCTCTGAGAACTGGACCTCGGCCAGAACGACAGGACAGGCAAGACGGGG
CTGGTGGCCATGGCCTGCCTCTACACCATCCCCACGGTCACTAAGCCCTCGGCACAGCTGCTGAGCTTGCTTGC
ATGTACACAGAGAAGAGGAAGCTGGCGGCTCAGGAGGGGCAAGTTCACAGAGCCACGTCTCTGAGGAGCCACCAAG
GAAAAGCTGCACACCCTGGAGGAGTTCTCTATGAGTTCTTCAGGGCTCCAGAGAAGGACATGGTGAGCATGGCC
GTGCTGCCCCCTGGCCCGTGGCCGTGGCCACCTGTGGGCTATTCTGCGAGCCGCTGCGACAGCCGCTGCTCAAG
CGAGTCCACGCCAACGTGACCTCTGGGACATCGCCTGCCAGATCTTGTGCGCATCCTCCGGTACATGGGCGAC
TACCCTTCTCGGCAGGCTGGCCACCTGGAGCTCACCGACCAGATCTTCACTGAGCCCTGCAGACCCGCC
CTCCAGGACGAGGTCTACTGCCAGATCTTGAAGCAGTGACGCACAACCTCCAACAGGCACAGCAAGAGCGGGG
TGGCAGCTGCTGTGGCTGTGACGGGCTCTTCCGCCCAGCAAGGGGCTGCTGCCCCATGCCAGAAAGTTTATA
GACACTCGGAGGGGGAAGCTGCTGGCCCCGACTGCAGCCGCCGAATCCAGAAGGTCTGAGGACGGGGCCCCGG
AAGCAGCCCCCGCACAGGTGGAGGTGGAGGCCGAGCAGAAGCTCTCCGCTCTGCCACAAGATCTACTTC
CCCAATGACACCAGTGAGATGCTGGAGGTGGTTGCCAACACACAGGCTGCGGGATGTGTGTGACAGCATTGCCACC
AGGCTGCAGCTGGCCTCTGGGAGGGCTGCAGCCTCTTCATCAAGATTTACAGACAAGGTGGGCCGGGCTGGGGCT
GGGCAGACGGTGGGCGGACGGGCAGTGAGCGAGGCCCTAGGTGCTGCCTGTGGGGGCTCAGCCTACCAGGGGCA
CCCATGCTGGACCAGGCTGCACGGCCAGGGCTGCTGGGACAGAGGTAGGTGGGGTCTGGAGCAGAGCCAGCTCC
ACACGCCAATAGCCACGCACAGCCGACTCCAGCGCAGCAGCCAGGCCGTAGGCGGCCACTGGACCAGAAGCCAG
CAGGTTCTCAGGAGGACAGTCCCCGGAAGCCACCAACTTCCCTGTACCTTCCCCCTTCCCCAGGTCATCAGCCAG
AAGGAGGGAGACTTCTTCTTTGATTCTTGGAGGAGGTGTCTGACTGGGTGAAGAAGAACAAGCCCCAGAAAGAA
GGGGCCCCCGTGACGCTCCCCCTACCAGGTGACTTCATGCGGAAATGTGGCTCAACATATCTCCAGGGAAGGAT
GTGAATGCAGACACCATACTCCATTACCACCAGGAGCTGCCAAGTACCTGCGCGGATTCCACAAGTGTTTCGCGG
GAGGATGCCATCCACCTGGCGGGCCTCATCTACAAGGCCAGTTCAACAACGACCGGTCCCAGCTGGCTAGTGTC
CCCAAGATCCTGAGGGAAGTGGTGCCTGAGAACCTCACACGCTGATGTCTCGGAGGAGTGGAAGAAAGAGCATC
CTTCTAGCCTATGACAAGCATAAGGACAAGACAGTGGAGGAGGCCAAGGTGGCCTTCTGAAAGTGATCTGCCGG
TGGCCACCTTCGGATCCGCCCTTCTTCAGAGTGAAGCAAACCTCGGAGCCTTCTTACCCGGACGTATCCTCATC
GCCATCAACCGACATGGGGTTCTGCTCATCCACCCCAAGACCAAGGACCTGCTCACCACCTATCCCTTACCAAG
ATCTCCAGCTGGAGCAGCGGCAGCACCTACTTCCACATGGCGCTGGGGAGCCTGGGCGGTGGCAGCCGCTGCTG
TGCGAGACCTCCCTGGGCTATAAGATGGATGACCTGCTGACCTCATATGTGCAGCAGCTCCTGAGTGCCATGAAC

WO 2004/030615

PCT/US2003/028547

915/6881

FIGURE 851B

AAGCAGCGGGGCTCCAAGGCCCCAGCCCTGGCCAGCACCTAGCAGCGGATGCTGGCGTGTCTGCTCAGGCGCCCT
TCCCGACCTCTAGCCTGGCGGCACCTTCCCAGGCCCTCTCAACCCAGGGCCTGTCCTTGGCGGGCAGCCTTCCAT
GCTGCCCCCATACAAAGCCCACTCAGCCCCGCAGGCGGGCCCCCTCTGTCTTGGGCGCTGCCCAGGGAGGCCAAA
AGACGGGCCCAGAATGGGGTCGGGAGTCTCGGACCCCCAGGCTATTGGTGGATGACTGACTGACAGGACACCTCC
CAACCCACCCACCCACCAGAATGTTCAATAAAAACTCCTGGAGCAGGA

WO 2004/030615

PCT/US2003/028547

916/6881
FIGURE 852

MKYLLNF IGQGPATYGPFC AERLRRTYANGVRAEPPTWLELQAVKSKKHIPIQVILATGESLTVPVDSASTSREM
CMHIAHKQGLSDHLGFSLQVAVYDKFWSLGSGRDHMDAIARCEQMAQERGESQRQSPWRIYFRKEFFTPWHDSR
EDPVSTELIYRQVLRGVWSGEYSFEKEEELVELLARHCYVQLGASAESKAVQELLPSCIPHKLYRTKPPDRWASL
VTAACAKAPYTQKQVTPLAVREQVVDAA RLQWPLLF SRLFEVITLSGPRLPKTQLILAVNWKGLCFDQQEKMLL
ELSFPEVMGLATNREAQGGQRLLLSTMHEEYEFVSPSSVAIAELVALFLEGLKERSIFAMALQDRKATDDTTLLA
FKKGDLLVLTKKQGLLASENWTLGQNDRTGKTGLVPMACLYTIPTVTKPSAQLLSLLAMSPEKRKLAAQEGQFTE
PRPEEPPKEKLHTLEEF SYEFFRAPEKDMVSM AVLPLARARGHLWAYSC EPLRQPLLKRVHANVDLWDIACQIFV
AILRYMGDYP SRQAWPTLELTDQIFTLALQHPALQDEVYCQILKQLTHNSNRHSEERGWQLLWLCTGLFPFSKGL
LPHAQKFIDTRRGKLLAPDCSRRIQKVLRTGPRKQPPHQVEVEAAEQNVSRICHKIYFPNDTSEMLEVVANTRVR
DVCD SIATRLQLASWEGCSLFIKISDKVGRAGAGQTVGGRVSEALGAACGGLSLPGAPMLDQAARPGLLGQR

WO 2004/030615

PCT/US2003/028547

917/6881
FIGURE 853

AAGTGCATGACTCAGGACTGGGTGGGAGGGGGCTGTCCCTGAGGCCCTGGTCTCCCCAGCCAAGTCCTGGCAGG
GGGATGCTGTTCTTCAGGATCCCATGACCTGGGGCTCTTGGGGAGCCCCAGCCCGGAGAGTGACCTGTGGCTTTG
CTGGGGAAAGGGGCTTGGAGGGTACAGGGCAGTGTCCAGGATTGCAGTCTCAAATCCGAGGCCCCACAGGGGAGCT
GCCTCTGTGATCGCCATTAAGGCTGTGGCCTGGGGTCTCAGGGCAGCCCAGGAACCAAAAATAGCCTGTAACTTG
TCACTTTGTAAGTCCTGCCCTCCAGACACACTTCCCTTTCTTCTCCCCAAGCCTCTCTTCCCAGTTAGCTCCCCCT
GACTTGGAGTCACCTCTAAGCCTTGGCCCAGGGCCCTCTGCAGTGAGATGGAGGGACTCATCCCCCGGAGAGTGG
CATCTGCAGGCCCCACTGGCTGCCTGTGGTCACCCCTAGGGTTCTAGCGGGGCTGCCTCCCCATTTTCTCAGAGC
ATCCCTGCCAGCTGGCTGGTTCTCACTCTCCTGTTTTCTAGGAAAAGAAAGTGGGGAGAGACAGGAACAGGGTCC
GGAGCAGCCCCAGCAGCAGCATTGAGGTGGAGCAATATGTCGGACGCCTTGGCCAACGCCGTGTGCCAGCGCTGC
CAGGCCCCGCTTCTCCCCCGCGAGCGCATTGTCAACAGCAATGGGGAGCTGTACCATGAGCACTGCTTCGTGTGT
GCCCAGTGCTTCCGGCCCTTCCCCGAGGGGCTCTTCTATGAGTTTGAAGGCCGGAAGTACTGCGAACACGACTTC
CAAATGCTGTTTTGCTCCGTGCTGTGGATCCTGCGGTGAGTTCATCATTTGGCCGCGTCATCAAGGCCATGAACAAC
AACTGGCACCCGGGCTGCTTCCGCTGCGAGCTGTGTGATGTGGAGCTGGCTGACCTGGGGCTTTGTGAAGAATGCC
GGCAGGCATCTCTGCCGGCCTTGCCACAACCGTGAGAAGGCCAAGGGCCTGGGCAAGTACATCTGCCAGCGGTGC
CACCTGGTCATCGACGAGCAGCCCCCTCATGTTCAAGAGCGACGCCTACCACCCTGACCACCTTCAACTGCACCCAC
TGTGGGAAGGAGCTGACAGCCGAGGCCCGCGAGCTGAAGGGTGAGCTCTACTGCCTGCCCTGCCATGACAAGATG
GGCGTCCCCATCTGCGGGGCTGCGCGCGGCCCATCGAGGGCCGAGTGGTCAACGCGCTGGGCAAGCAGTGGCAC
GTGGAGCACTTTGTCTGTGCCAAGTGTGAGAAGCCATTCTGGGGCACCAGGCACTATGAGAAGAAGGGCCTGGCC
TACTGCGAGACTCACTACAACCAGCTCTTCGGGGAGCTCTGCTACAACCTGCAGCCATGTGATTGAAGGCGATGTG
GTGTGCGGCCCTCAACAAGGCCTGGTGTGTGAGCTGCTTCTCCTGCTCCACCTGCAACAGCAAGCTCACCTGAAG
AACAAGTTTGTGGAGTTCGACATGAAGCCCGTGTGTAAGAGGTGCTACGAGAAGTTCCCGCTGGAGCTGAAGAAG
CGGCTGAAGAAGCTGTGCGAGCTGACCTCCCGCAAGCCCAGCCCAAGGCCACAGACCTCAACTCTGCCTGAAGGC
CCTCTTGCGCAGTGCTCTCGGCCCCCTCCGCTTCTCCCCCTCCTGCTGTCCATGCTTGGCCCCCTCGTCCCCATC
CACCTGTGUCCTCCGCATCTTACCCTCCCTTTCTCTTTCTCATTGCCTTCTCCCTTCTGTTCCCTCATCTCTG
CCTTCCCCATGTCTCTCCTCTCCTTGGCCGTGGCTTCTGTCTGTGAGGAGGCAGGAGCTGGGGAGTGGGAGCCTA
TGACCCACAGTCTGACAGCCATGTCCACCTGTGCCACAGCTTCCGCCCACAGACCTCCAGGGACAGGAGCAAAT
TGCACCACAGTCTCCCGCCTGGCCTGGCCCTCCCCAGGCGGCTCAGTGGCTCATGCTGTCTGTGAGAGCCCCTG
CCCCAGAGCGGCCCCACTAAGCGCATGTGGCTCCTGGGCTACCCACAGCCAGGGCAGCCTGCTGGAGCCACAGGG
CCAGGGCCATGCAGATGGAGGCCTCTGGGAGCCACCTCCAATCCCTCACCCTCACTCAACCAGTGGCACAGTGT
CCTTGTGCCACACTGAGCCAGCAAGTCTGTGTCCACACCCACAAGCTACCTGGAGGGACAGGACCCACCTCC
ATCCTTCGGAAGGCCTTCTGGAATCCACCTTGGCCTCCGCCCTCGGTTCCGCCCCGCCCCCTCTCCCCCGACC
TTGGGGCTTGTGTGAGCCCTTGGGTGGGGCCAGGAGGAGGTGATGGCGTCAGAGGAGGTGTGGTCAGAGGTGAC
TTGTTCCACCTCCAGGGAGGACGCTTCGTCTTCGGCCAGCGCAGACCTGGTGTGTTGTTTGGGCTCACGCTT
GCACAATGAAGGCTTGTTCACAC

WO 2004/030615

PCT/US2003/028547

918/6881
FIGURE 854

CCGACACCCACGGGCGGAGATCACCTGCTGCCCCGCAGACCCCTGTCCCTTCCTCCCGGACCAGCAGCTAGAGGA
TGTCCAAACGGAGTTGGTGGGCTGGATCCAGAAAGCCCCAAGAGAGATGCTGAAACTCTCAGGCTCTGACTCCA
GCCAAAGCATGAATGGCCTTGAAGTGGCTCCCCAGGTCTGATCACCAACTTCTCCCTGGCCACGGCAGAGCAAT
GTGGCCAGGAGACGCCACTGGAGAACATGCTGTTGCCTCCTTCTACCTTCTGGATTTTATCCTGGCTTTAGTTG
GCAATACCCTGGCTCTGTGGCTTTTCATCCGAGACCACAAGTCCGGGACCCCGGCCAACGTGTTTCTGATGCATC
TGGCCGTGGCCGACTTGTGCTGCGTGTGGTCTGCCCCACCCGCTGGTCTACCACTTCTCTGGGAACCACTGGC
CATTTGGGGAAATCGCATGCCGTCTACCGGCTTCCTCTTCTACCTCAACATGTACGCCAGCATCTACTTCCTCA
CCTGCATCAGCGCCGACCCTTTCCTGGCCATTGTGACCCGGTCAAGTCCCTCAAGCTCCGCAGGCCCCCTCTACG
CACACCTGGCCTGTGCCTTCCTGTGGGTGGTGGTGGCTGTGGCCATGGCCCCGCTGCTGGTGAGCCACAGACCG
TGCAGACCAACCACACGGTGGTCTGCCTGCAGCTGTACCGGGAGAAGGCCTCCCAACATGCCCTGGTGTCCCTGG
CAGTGGCCTTCACCTTCCCGTTCATCACACGGTCACTGCTACCTGCTGATCATCCGCAGCCTGCGGCAGGGCC
TGCCTGTGGAGAAGCGCCTCAAGACCAAGGCAGTGCAGATGATCGCCATAGTGCTGGCCATCTTCTGGTCTGCT
TCGTGCCCTACCACGTCAACCGCTCCGTCTACGTGCTGCACTACCGCAGCCATGGGGCCTCCTGCGCCACCCAGC
GCATCCTGGCCCTGGCAAACCGCATCACCTCCTGCCTCACACGCTCAACGGGGCACTCGACCCCATCATGTATT
TCTTCGTGGCTGAGAAGTTCCGCCACGCCCTGTGCAACTTGCTCTGTGGCAAAGGCTCAAGGGCCCGCCCCCA
GCTTCGAAGGGAAAACCAACGAGAGCTCGCTGAGTGCCAAGTCAGAGCTGTCAGCGGGGGGCGCCGTCCAGGCCG
AGCGCAGACTGTTTAGGACTCAGCAGACCCAGCAAGAGGCATCTGCCCTTCCCCAGCCACCTCCCCAGCAAGCA
ACCTGAAATCTCAGCAGATGCCCACCATTTCTCTAGATCGCCTAGTCTCAACCCATAAAAAGGAAGAACTGACAA
AGGGGATCCATCGGCCACCCCTCTGCAGGGGCTTGTGATGGCTACAATGGCTCCTAGACACTCAACGACTTCATC
TGTGGCAGGGAGAGAGAGGGCCGGAAGAACAACCCCTGAACAATGGAGGCCTTTCTTTCCCGCTAGGCTCCCAGC
CTCCTTCCCGCTACAGAATCGCTCATCGGCGAGGCTCAGCAGAAAGACCCTGAAGGCAGGCTGCAAATGACCCAG
AAGAGGGACCTGGGAGTCTGGTGGGGACGGGGAGGGAGTCTCAATACTCCTTTGCAGCGCAAGGTACTCTGAGT
CCCCCTCTGTAGTGCTCTGCCAGACACACACTGCCTGAGTTGAAGAGACACAGGCCACACATTTAGGCTGGTTG
CCAGCGGACGTCAGCACTCACGGCCTGCGGGGACTCAGCACAGCTCTGGATTCTGGATCTCTCCTGCTGTAACCC
CACGCACAAGCCTGCAACCCCCAGAGCTCTTTGACAGGCTCCCAGGCCTCCCAGTCCTGGACAAGCATGTGCAGT
CACGGGAGCTCAGCTCAGGCCAGGGCTGGGCTGTGCACCTGCCTCCCACTGACCCAGACCCACTTCCTCCAGAGA
GGCCTCTCTCCGCCTGAGCTATTTCCCTTGCTAGTGTGCAGATATTTCCCTAACATGTCCTTTTTTGATTTGTT
TGTACGGACCATAAATATAACTGTAGCTTTAAGACTAAAAA

WO 2004/030615

PCT/US2003/028547

919/6881
FIGURE 855

MSKRSWWAGSRKPPREMLKLSGSDSSQSMNGLEVAPPGLITNFSLATAEQCGQETPLENMLFASFYLLDFILALV
GNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFL
TCISADRFLAIVHPVKSLKLRPLYAHLACAFWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSL
AVAFTFPFITTVTCYLLIIRSLRQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYRSHGASCATQ
RILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEGKTNESSLSAKSEL

WO 2004/030615

PCT/US2003/028547

920/6881
FIGURE 856A

GGGGAAGATGGCGGCTGCTCCTTTGGAGGAGCGGGATTGAGAGGATCGGGGTGGGGAGACCAACAAGAGAGACA
TTTCTGGCTCTGAAGGCGAACGCTTCGCTGGCCATTTAGGAGCTCTGCTCAAAGCCAGACGTATCCTAGAAGGAA
AACATCACCATGGCTACAGAAATTGGTTCTCCTCCTCGTTTTTCCATATGCCAAGGTTCCAGCACCAGGCACCT
CGACAGCTGTTTTATAAGCGACCTGATTTTGCACAACAGCAAGCAATGCAACAGCTTACTTTTGATGGAAAACGA
ATGAGAAAAGCTGTGAACCGAAAAACCATAGACTACAATCCATCTGTAATTAAGTATTTGGAGAACAGAATATGG
CAAAGAGACCAGAGAGATATGCGGGCAATTGAGCCTGATGCAGGTTATTACAATGATCTGGTCCCACCTATAGGA
ATGTTGAATAATCCTATGAATGCAGTAACAACAAATTTGTTTCGGACATCAACAAATAAAGTAAAGTGTCCTGTA
TTTGTTGTTAGGTGGACTCCAGAAGGAAGACGCTTGGTCACTGGAGCTTCTAGTGGGGAGTTTACCTGTGGAAT
GGACTCACTTTCAATTTTGAACAATATTACAGGCTCACGACAGCCAGTGAGGGCCATGACGTGGTCACATAAT
GACATGTGGATGTTGACAGCAGACCACGGAGGATATGTGAAATATTGGCAGTCGAACATGAACAACGTCAAGATG
TTCCAGGCACATAAGGAGGCGATTAGAGAGGCCAGTTTCTCACCACGGATAATAAATTTGCTACATGCTCTGAT
GACGGCACTGTTAGAATCTGGGACTTTCTTCGTTGCCATGAGGAAAGAATTCTCCGAGGGCATGGTGCTGATGTG
AAATGTGTAGACTGGCATCCAACCAAGGGTGTAGTTGTTTCAGGAAGTAAAGATAGTCAACAGCCAATCAAGTTC
TGGGATCCCAAGACTGGGCAGAGTCTTGCAACACTTCATGCCATAAAAACACAGTAATGGAAGTGAAATTAAC
CTCAATGGCAATTGGCTACTCACAGCATCACGTGATCATCTCTGTAACTTTTGTATATCAGAAACCTAAAAGAA
GAGCTTCAAGTCTTCCGAGGTCATAAGAAAGAAGCCACAGCTGTGGCCTGGCATCCTGTTTCATGAAGGACTTTT
GCCAGTGGAGGGTCTGATGGTTCTTTGTTATTCTGGCATGTTGGGGTAGAGAAGGAAGTGGGTGGGATGGAGATG
GCTCACGAAGGGATGATCTGGAGTCTGGCTTGGCATCCTCTTGGGCATATTCTCTGCTCAGGCTCAAATGACCAT
ACTAGCAAATTCTGGACTCGAAACCGACCAGGTGATAAAATGCGAGATCGATATAATCTAAACCTTTTACCTGGA
ATGTCTGAAGATGGAGTAGAATATGATGACCTCGAACCTAATAGCCTGGCAGTAATTCCAGGAATGGGAATACCA
GAACAATAAAATAGCTATGGAACAAGAACAGATGGGGAAAGATGAATCAAATGAAATGAAATGACAATTCCA
GGTTTAGA'TTGGGGAATGGAGGAAGTGATGCAAAAGGATCAGAAAAAGTACCTCAGAAGAAAGTTCCTTATGCA
AAACCCATTCTCTCAGTTCCAGCAGGCTTGGATGCAAAATAAAGTTCCAATTCTGCTCCAATGAGGTGCTG
AATGACAGAAAAGAAGACATTAAATTGGAAGAGAAGAAAAACACAAGCAGAAATTGAGCAAGAAATGGCTACA
TTACAATATACTAACCACAACCTTCTGGAGCAACTTAAATTTGAAAGACTTGACACAGAAACAAGTTGAGCAAAAT
CAGCCTCCTCCCTCATCTGGCACCCCTCTCCTCGGACCCAGCCTTTTCCAGGACAAGGTCCAATGTCTCAGATT
CCTCAAGGTTTTCAACAGCCCCATCCATCTCAGCAGATGCCAATGAACATGGCTCAAATGGGGCCTCCAGGTCCA
CAGGGACAGTTTAGGCCTCCTGGACCCAGGGACAAATGGGACCACAAGGTCTCCACTGCATCAGGAGGGTGGG
GGGCCACAAGGAATGCAGAGGCATCCTGGACCTCATGGCCCTTTGGGACCTCAAGGGCCACCTGGACCACAAGGT
AGTTCTGGTCCTCAAGGTCAATGAGGTCTCAGGGTCCACCTGGCCACAGGGTCACATAGGCCCCCAAGGCCCG
CCTGGCCCTCAGGGTCACTTGGGCCACAGGGGCCTCCGGGTACTCAAGGTATGCAAGGGACCCTGGTCCCAGA
GGAATGCAAGGGCCTCCTCATCCTCATGGGATCCAAGGCGGACCAGGGTCTCAAGGGATCCAAGGTCTGTGTCT
CAGGGACCTCTGATGGGATTGAATCCAAGAGGAATGCAGGGGCCTCCAGGCCCCCGGAGAAACAGGGTCTGTCT
CCCCAAGGGATGATTATGGGCCACCCGCCTCAAGAGATGAGAGGACCTCACCTCCAGGTGGACTACTGGGACAC
GGCCCTCAGGAAATGAGAGGTCTCAGGAGATCCGAGGCATGCAGGGGCCTCCACCCCAAGGATCAATGCTGGGA
CCTCCCCAGGAATTGCGAGGGCCTCCAGGCTCACAAAGTCAGCAGGGGCCGCCCCAGGGCTCTTTAGGACCTCCA
CCCCAGGGTGGCATGCAAGGACCCCCCGACCTCAGGGACAGCAGAACCCAGCAAGAGGGCCACATCCATCTCAA
GGGCCAATACCATTCCAGCAACAGAAAACGCCTCTGCTAGGTGATGGGCCCCGGGCCCCCTTCAACCAGGAAGGA
CAGAGCACAGGCCCCCACCCTGATACCAGGCCTAGGGCAGCAGGGAGCACAAGGTGCGATTCCCCCTCTGAAC
CCCGGACAAGGACCTGGCCCCAACAAAGTTTTCAGAAGAGGAGCCCCGCCGAGGCATGAGGGCCGTGCTCCCCCA
GAGGAAGGGATGGTTTTCTGTTCTGAAGACTTTGGTCCAGAGGAGAATTTTGATGCTTCTGAGGAAGCGGCC
GAGGACGAGATCTCAGAGGTCGAGGTCGGGGTACCCACAGAGGAGGAAGGAAGGGTTTACTTCCACTCCTGACG
AGTTCCCTCGCTTTGAAGGAGGGCGGAAGCCAGATTCTTGGGATGGAAACAGAGAGCCTGGGCCAGGTGATGAAC
ATTTTCGTGATACTCCCCGCCCTGATCATCCCCCTCACGACGGTCATTCCCAGCCAGCAGAGAACGCTCCTCTT
CTCTCCAAGGCATGGACATGGCATCCCTACCTCCCCGAAAGCGCCCTGGCATGATGGCCCAGGCACTTCTGAGC
ACAGAGAGATGGAGGCCCCAGGAGGCCCTTCTGAAGACCGAGGAGGCAAAGGCCGAGGGGGCCAGGACCTGCTC
AGAGAGTGCCCAATCTGGGCGTTCCAGCTCCTTAGACGGAGAGCACCACGATGGATACCACAGAGATGAACCTT

WO 2004/030615

PCT/US2003/028547

921/6881
FIGURE 856B

TTGGGGGCCCTCCAGGCAGTGGCACCCCTTCTCGAGGGGGCCGGAGTGGCAGTAACTGGGGTAGAGGGAGTAACA
TGAACCTCTGGCCCGCCGAGGCGAGGAGCTTCACGGGGTGGTGGAGGGGTCGGTAGAAGCTGGAACTGAGTACCC
TGAGGCCTCTCTGGACAGTATGTAAGAACTTCTTGTGGACTCACCAAGAGAAAACAAAAGGAAGCCTGCACCATTG
TAGCCCTGAACCTCTTTTCTGGGCACCTGAATCCCAGGAACCCCTCAATGAGGTCTTCAAGATGAAGAGACTGCTGC
CAGCTACCAGCCTGGCTGGCCCTGTCTGTCCACCCTCATTGCCCCAACTCCCATGTTGTTTTGTGAAGATAAAA
GCTGGGATCTTTTTCTTTTTTTTTAAGTCTCACAAGACATGGGGCATCTCCACAAATTTAAGTTCTGTCCATTTG
GAAATTTGTTTCTATGTGTACAGTTTGTCTAGAGAAAAACAAAGTTTTTGTATGAATAACAGAATGTGATTTACGCA
AGAATTGACAGAAAACCTAGTTGTGAAGTGCTTGCCTTAAGGAAACCTTTGGTTTCCATCGCATCCCATCTGCCAA
GGAATGCACGGTTGTTGCTGATGTTTCATGAGCATATTAACCACTAGGTTATCTAAATTAATCTCAGCTGTGAAC
TTGTGTTTTTCAACACATTCTGTACACCATTTTTGTGACAGAAAAATACTTGAAAAATTATTCTAATGTAGTTTG
TAGTAGGTTCAAATTTTTATTTCAGACATGCTCTGACAGATGGAAAAATTGACTCTGAAGAGAAAAATGCAATCTTC
TGGATGTCCAACGAGGGAGCTTCCCCTTGGAAAGCATCTCCTAAGAATCACAGTTTAGGTTTGAATCGCCTTGTTA
TGATGAGGAGAGGAACCTTGATGTTAGTCAGAAATAAAGTCACATGCCCTTAGATAACTTGAAATCACACATGGA
GTTGATAAGGAATGGACCAAAATAGGTCCTCAAACAATTTGCAACACTTAATTAAGTTTTCTCTCTTCTCTCTT
CCATACTATGTGGAATACCAGTGTTACGGCAGGGCGTACTTCTAACTCACAGTAAGCCAGATAGATCTTGTCCA
TGGCAAATTCCTTGTTTAAATAAACATAACATTTAGCCAGTTTGGATTGGAAGCCAAAAATTCAGTTTGTTAT
ATACCCCATGATACTTTCTATACTGACCTTTATTTTGGTTTTACATGGAAGCTTTTATTAAGGAGTGTCTCTAT
GGCCACCTTAACATTTTATTACATTGGCAGCTTCAGTTTTGGCATCAGTCAAATTTATTTGGCAAATTTAGTGGT
GCTGGAAGTTTCTTTTTTCTTTTTCTTTTTTGACAGAGTCTTGCTCTGTCACCCAGCCAGGAGTGCAGTGGTGC
AATCACGGCTCAGTTTACGCTTTGACCTGCTCAGCCTCCCTAGTAGCTAGGACTACAGGCATATGCCACCATGC
CCAGCTAATTTTTTGTGTGTGTGTGTTTTTGTAGAGATGGAGTTTCAACACTTTGTCTATGCTGGTTTCAAACCTC
TGGGCTCAAGCGGTCCACCTGCTGTGGCCTCCCAAGTGCTGGGATTGCAGATCTGAGCCACAGTACCTGGCCGC
TGGTGCTGGAAGTTTCAATGGTTGCTTAGAAAAGGCATACTGATATAGTTTAAACAGGATATGAAAATTTAACTGG
TTCTCTATGAATGTAAAAACAGCAAAAGCTAATTGATTTCTGTGGAGTGAGAAAATGTCAGCCATATACACTGC
TTTTCAGTGTTAGAATCTAGAGACTATTTTTTTTTTAACTTTGAAATTACAGCTTATTTAATCAGCGCTCCACCA
TAAACATGCTATTAGGAGGCTCAAGATTGCTTTAGGTTATGGGTATTTCTTCACTCACCCCAACTGGTATAGCT
TAAAGAGAGAGAACTGTAATCAAATTTTCATGAAGCTAAAACCGGATCCAGAGACCAAAACCATATCAAGATTAG
ACTTTTTTCCCTGAGATTCTAGTGGAATAATTTTCATTATTTTGGGCTTTAACTTTAGAAACATAGTATCTCAG
TAAGCAGATAACCATACATTTAAAAATTTTCATTTTACCTTGAAGCTCTACTGGACTTGACAGATCACATTT
TGAGAGTGAATTCATTTAAACAATAAACCTCTACATTATACTTAT

WO 2004/030615

PCT/US2003/028547

922/6881
FIGURE 857

AGAACATCCAGTCACGGATAAAAAATGAGCTGGTTTCAGAAGGCCAAACTGGCCGAGCAGGCTGAGCAATATGATGA
CATGGCAGCCTGCATGAAGTCTGTAACCTAAGCAAGGAGCTGAATTATCCAATGAGGAGAGGAATCTTCTCTCAGT
TGCTTATAAAAAATGTTGTAGGAGCCCGTAAGTCATCTTGGAGGGTCGTCTCAAGTATTGAACAAAAACGGAAGG
TGCTGAGAAAAACAGCAGATGGCTCGAGAACACAGAGAGAAAAATTGAGACGGAGCTAAGAGATATCTGTAATGA
TGTATTGTCTCTTTTGGAAAAGTTCTTGATCCCAATGCTTCACAAGCAGAGAGCAAAGTCTTCTATTTGAAAAAT
GAAAGGAGATTACTACCGTTACTTGACTGAGGTTACTGCTGGTGATGACAAGATAGGGATTGTGGATCAGTCACA
ACAAGCATACCAAGAAGCTTTTGAATCAGCAAAAAAGAAATGCAACCAACACATCCTGTCAGATTGGGTCTGGC
CCTTAACCTTCTGTGTTCTATTATGAGATTCTGAACTCCCCAGAGAAAGCCTGCTGTCTTGCAAAGACCGCTTTTG
ATGAAGCCATTGCTGAACTTGATACATTAAAGTGAAGAGTCATACAAAGACAGCATGCTAATAATGCAATTACTGA
GAGACAACCTTGACATTGTGGACATCGGATACCAAGGAGACGAAGCTGAAGCAGGAGAAGGAGGGGAAAAATTAAC
CGGCCCTTCCAACCTTTTGTCTGCCTCATTCTAAAAATTTACACAGTAGACCATTTGTCTCATCCATGCTGTCCCAAAA
TAGTTTTTTGTTTTATGATTTATGACAGGTTTATGTTACTTCTATTTGGATTTCTATATTTCCCATGTGGTTTTTA
TGTTTTAATATTAAAGGGAGTAGAGCCAGTCAACATTTAGGGAGGTATCTGTTTTTCATCTTGAGGTGGCCAATATTG
GGATGTGGAATTTTTATACAAGTTATAAATGTTTGGCATAGTACTTTTGGTACATTGTGGCTTCACAAGGGCCAG
TGTAACCTGCTTCCATGTCTAAGCAAGAAAACTGCCTACATATTGGTTTGTCTGGTGGAGAATAAAAGGGAT
CATTGATTCCAGTCAGAGGTGTAGTAATTGTGGGTACTTTTAAAGGTTTGGAGCACTTTACAAGGCTGTGGTAGAA
ACATACCCCATGGATACCACATGTTAAACCATGTATATCTGTGGAATACTCAGTCTCATTGTGCACACCTTTGAC
TACAGCTGCAGAAGTTTTCCTTTAGATAAAGTTGTGACCCATTTTACTCTGGATAAGGGCAGAAACAGTTTCACAT
TCCATTATTTGTAAAGTTACCTGCTGTTAGCTTTTATTATTTTGTCTACACTCATTTTATTTGTATTTAAATGTT
TTAGGCAACCTAAGAACAAATGTAAAGTAAAGATGCAGTAAAAATGAATTGCTTGGTATTCTATTGCTTCATGTA
TATCAAGCACAGCAGTAAACAAAAACCCATGTATTTAACTTTTTTTTAGGTTTTTGTCTTTGTGATTTTTTTT
TGATACTTGCCTAACATGCATGTGCTGTAAAAATAGTTAACAAGGAAATAACTTGAGATGATGGCTAGCTTTGTT
TAATGTCTTATGAAATGTTTCGTGGATAATCCAAGCATAATTGTTAAGAACACGTGTATTAAATTCATGTAAGTGG
AATAAAAGTTTTATGAATGGACTTTTCACTACTTTCTCTACAGCTTTTCGTGTAAATTAGTCTTTTGGTTCTGA
AATTTCTCTAAAGGAAATTGTACATTTTGAATTTATTCCTTATTCCTCTTGGCAGCTAATGGGCTTTTAGTA
AGTTTAAACAAAAAATTTATCATAACAACAAAAATACTACTAATACTACTGTTTCCATGTCCCATGATCCC
GTCTCTTCTCCCTCCCTGAAAAAATGAGTTCCTATTTTTCTGGGAGAGGGGAGATTAATTGGAAAAAATG
TTAATAGTTCCATTTAAATTTTGGTATATGGCATTCTTAACCTAAGAAGCCACAATGTTCTTGGCCATCAT
GACAATGGGTAGCATTAACATAAGTTTTGTGCTTCCAAATCACTTTTCGGTTTTTAAGAATTTCTTGATACTCC
TACAGCCTGCCTTCGATTTTGATCCTTTATTCTGTTTGTGTCAGGTGCACAAGATTACCTTCCTTTTTTAGCCATCT
GTCTTGTCAACCAACCATTCCCTACTTGGTGGCCATGTACTTGGAAAAAGGCCGATGATCTTTCTGGCTCCACTCA
ATGCTAAGGCACCTGCTTCCTTTGCTTGCATCCCACAGACTATTTCCCTCATCCTATTTACTGCAGCAATTGT
CTCCTTAGTTGACGAGATTGTGTTTATCTCCCTTTAAACCCCTACCTATCCTGAATGATCTGTCTATTGTCTGCCT
TTAAATCCTTCCTCTTTCTTCTCTATTCTCTAAATAATGATGGGGCTAAATTATACCCAAAGCTCACTTT
ACAAAAATTTCTCAGTACTTTGCAGAAAACACCAAAACAAAAATGCCATTTTAAAGAGGTGTATTTTTCTTT
TAGAATGTTAGAATGTAAGCTCCTCAAAAGCAGGGACAATGTTTTCCGTATGTTCTACTGTGCCTAGTATACTGT
AAATGCTCAATAAAATACTGATGATGGGAGGCAGTGAGTCTTGATGATAAGGGTGAGAAACCGAAATCCC

WO 2004/030615

PCT/US2003/028547

923/6881
FIGURE 858

GATGACATGGCAGCCTGCATGAAGTCTGTAACTAAGCAAGGAGCTGAATTATCCAATGAGGAGAGGAATCTTCTC
TCAGTTGCTTATAAAAAATGTTGTAGGAGCCCGTAAGTCATCTTGGAGGGTCGTCTCAAGTATTGAACAAAAACG
GAAGGTGCTGAGAAAAACAGCAGATGGCTCGAGAACACAGAGAGAAAATTGAGACGGAGCTAAGAGATATCTGT
AATGATGTATTGTCTCTTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCAAAGTCTTCTATTTG
AAAATGAAAGGAGATTACTACCGTTACTTGACTGAGGTTACTGCTGGTGATGACAAGATAGGGATTGTGGATCAG
TCACAACAAGCATACCAAGAAGCTTTTGAATCAGCAAAAAAGAAATGCAACCAACACATCCTGTCAGATTGGGT
CTGGCCCTTAACTTCTGTGTTCTATTATGAGATTCTGAACTCCCCAGAGAAAAGCCTGCTGTCTTGCAAAGACCGC
TTTTGATGAAGCCATTGCTGAACTTGATACATTAAGTGAAGAGTCATACAAAGACAGCATGCTAATAATGCAATT
ACTGAGAGACAACCTTGACAATGTGGTTTTTATGTTTAATATTAAGGGAGTAGAGCCAGTCAACATTTAGGGAGGT
ATCTGTTTTTCATCTTGAGGTGGCCAATATTGGGATGTGGAATTTTTATACAAGTTATAAATGTTTGGCATAGTAC
TTTTG

WO 2004/030615

PCT/US2003/028547

924/6881
FIGURE 859A

TTTTCGGCGCCGTGGCGGAATGGCGGCTTCCATCTCTGAGGCGAGCGACGCTATGGATCCCACAGTGGTTTTGCTA
AGAAGGCCATTTTCAACTCTCCACTGGAGGCTGCTATGGCGTTCCTTCACCTGCAGCAGCCAGCTTTCTACTGG
CTAGCCTGAAAGCTGACTCTATAAATAAGCCCTTTGCACAGCAGTGCCAAGACTTGGTTAAAGTCATTGAGGACT
TTCCAGCAAAGGAGCTGCACACCATCTCCCATGGCTGGTAGAAAGCATTTTTGGCAGCCTAGATGGTGTCTCTCG
TTGGCTGGAACCTCCGCTGCTTACAGGGGCGCGTGAATCCTGTGGAGTACAGCATCGTGATGGAATTTCTCGACC
CTGGTGGCCCAATGATGAAGTTGGTTTATAAGCTTCAAGCTGAAGACTATAAGTTGACTTTTCTGTCTCTCTACT
TGCTGGTCTGTGAAGGCGTCCATCCAGGAGTGTCATCCTCCCTGACAGTCTCTGTACCACAACAAGGTCCAGT
TCACCCCTACTGGGGGCTTGGTCTGAACCTGGCCCTGAATCCGTTTCGAGTATTACATATTCTTCTTTGCTTGA
GCCTCATCACTCAGAAGCCACTTCCTGTGTCCCTCCACGTCCGTACTTCAGACTGTGCCTATTTTCATCCTGGTGG
ACAGGTACCTGTCTATGGTTTCTGCCACCCGAAGGCAGTGTGCCCCCACCCTCTCCTCCAGCCAGGGGGGACCA
GCCCCCTACCACCTCCCAGGACACCAGCCATACCCCTTTGCTTCTATGGCCTCCACCACACTAGCCTCTTAAAGC
GACACATCTCTCATCAGACGCTGTGTGAATGCAGACCCCGCTCCACGAGATCTGGAGGTCAGAACTCTGTCTC
AGGTTTTTGTGAAATGTGGCTTCATCACTATTCTTGGAGATGTATCAAAAAATGCAGTCCCCTCATGCCAAGG
AGTCGTTACAGCCTACTGAGGAGCATGTGTTGGTGGTGCCTGCTGTGAAGCACCTGCACGCCTTTGCCAACA
GCCTGAAGCCAGAGCAGGCTCACCCTCCGCCACTCCCACGCCACCAGCCCCCTGGAGGAGTTCAAACGGGCTG
CTGTCCCGAGGTTCTGTCAGCAGAACTCTACCTCTTCTTGACGATTGCTTTGGCCACTGGCCCCCTGGACGCAT
CGTTCAGAGCTGTCTGGAGATGTGGCTGAGCTACCTGCAGCCGTGGCGGTACGCGCCTGACAAGCAGGCTCCGG
GCAGCGACTCCCAGCCCCGGTGTGTGTCGGAGAAATGGGCACCCTTTGTCCAGGAGAACCTGTGTATGTACACCA
AGTTGTTTGTGGGCTTTCTGAACCGCGCGCTCCGCACAGACCTGGTCAGCCCCAAGCACGCGCTCATGGTGTTC
GAGTGGCCAAAGTCTTTGCCAGCCCAACCTGGCTGAGATGATTAGAAAGGTGAGCAGCTATTCTGGAGCCAG
AGCTGGTCATCCCCACCGCCAGCACCAGCTCTTACGGCCCCCACATTCACTGGGAGCTTCTGTCAACCCTGGC
CACCAGCGGTCACTGATGCCCTCTTCAAGGTGAAGAGCCACGTCTACAGCCTGGAGGGCCAGGACTGCAAGTACA
CCCCGATGTTTGGGCCCCGAGGCCCGCACCTGGTCTGCGCCTCGCTCAGCTCATCACACAGGCCAAACACACAG
CCAAGTCCATCTCCGACCAGTGTGCGGAGAGCCCGCTGGCCACTCCTTCTCTCATGGCTGGGCTTTAGCTCCA
TGGACACCAATGGCTCCTACACAGCCAACGACCTGGACGAGATGGGGCAAGACAGTGTCCGGAAGACAGATGAAT
ACCTGGAGAAGGCCCTGGAGTACCTGCGCCAGATATTCCGGCTCAGCGAAGCGCAGCTCAGGCAGTTCACTCTG
CCTTGGGCACCAACCAGGATGAGAATGGAAAAAGCAACTCCCCGACTGCATCGTGGGTGAGGACGGACTATCC
TTACGCCCCCTGGGCGGTACCAGATCATCAATGGGCTGCGAAGGTTTGAAATTGAGTACCAGGGGACCCGGAGC
TGCAGCCCATCCGGAGCTATGAGATCGCCAGCTTGGTCCGCACACTCTTTAGGCTGTCTGCTGCCATCAACCACA
GATTTGCAGGACAGATGGCGGCTCTGTGTTCCCGGGATGACTTCTCAGCAGCTTCTGTCTGCTACCACTCACAG
AACCTGGGCTGGCCAGCAGGCACCTGCTGAGCCCTGTGGGCGGAGGCAGGTGGCCGGCCACACCCGCGGCCCA
GGCTCAGCCTGCGCTTCTGGGCAGTTACCGGACGCTGGTCTCGCTGCTGGCCTTCTTCTGTGGCCTCTCTGT
TCTGCGTGGGCCCCCTCCATGCACGCTGCTGCTCACCCTGGGCTATGTCTCTACGCTCTGCCATGACACTGC
TGACCGAGCGGGGAAGCTGCACAGCCCTGGAAGGTCTCAGCTGCCTTCAGAGCAGGCTGGAGGGATTGCCACA
CAGCCCCACCCTTGGGCTGAGAGGACCTGGGAAGCCCCCTCAGGAGGGAACACGGTCATCTCGGGCTTCTGGAG
CGGGGTCTCTGCAGCCGCAGAGGCATCTGGAGGAAACGCAACCAAGAAAGGAAGGCAGGTGGGCCCCAGCAAAGG
AGTAGCTGCCAGGGCTCAACAGCTACGCTCTGTGACAGCGCAGAGCTCAGCGGCGGCCTTTCCCTCCCTCCGCCA
AGGACTCACGGCCAAGCCAGCTCTCGGGGCTTTTTTCCACTGCCATTTGGCTACTCTGCTGCACCAAGCTTGG
GAGCCAGCTGCCAACAGCCACCTGGGCTGGCCTCCCCACTGGCTGGCCTTGGGTTGGCAGAGTGGGTTGTGG
CGCTTCTCTCTGTGTGGGACCAGGACAGTGGCTTAAGTCTCCACTCCAGGAAAGAATCAAAGTTTCTAGAGT
TGTGAGAAAACCAGAGAGTGGCTGTCTGATTCTTCACTGTGAGGGGCGTTCTTCTATGTTCTCCCAGCTGTTCCA
AGACTGGGCCGTAGAATTCCATGTTTCAGGAGCCTAAGACCCTCCAGAGCCCAGGGGCTTACCAGCAGACCCCA
AGCCATTGAGCACATCACCCAAAGCAGTGGCCAACATCGCGGACCCCTGTGCCTTGTACAGATGGGTGCTGGTC
CTCAGGCGTTGGGGACACTGTGGGTGATGGGGTGGATTCTGCCAGTTTCTGCTCTGCAGCCAAAGATGGTCA
GAAGCATTGTCACTTCAGTAACATCAAGTGTCTAAAGACATGGCAACCGTTCAAGTGGTACTTAAGTATTCAAAT
ATACAACACAGATTCTCTGACAGAAACCAGCACGGGGTCTTACCTTCATTACCCACAGGCGACATGCGAGG
GAGAACAGCATCTCAGTGGTGATTTCCAAACCAAGCCTTTGTTTTCGGTGTGGGGTTTTGGGGTTTTGCTTTAAT
GTTTTTGAAATTGTAAATGTTGGGCTTTGTATTTTGATGTAAACTGAGCATAATGGCATTTTAGGGCCTGTGACC

WO 2004/030615

PCT/US2003/028547

925/6881
FIGURE 859B

AAAATGAAGCTTGTAACGACCCATGGATCTGAATAAACATGTCCTTGCTTCTGAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

WO 2004/030615

PCT/US2003/028547

926/6881
FIGURE 860

MAFPHLQQPSFLLASLKADSINKPFAQQCQDLVKVIEDFFPAKELHTIFPWLVESIFGSLDGVLVGWNLRCLQGRV
NPVEYSIVMEFLDPGGPMMKLVYKLQAEDYKFDFPVSYLPGPVKASIQECILPDSPLYHNKVQFTPTGGLGLNLA
LNPFEYYIFFFALSILITQKPLPVSLHVRTSDCAYFILVDRLSWFLPTEGSPVPPPLSSSPGGTSPSPPPRTPAIP
FASYGLHHTSLLKRHISHQTSVNADPASHEIWRSETLLQVFVEMWLHHYSLEMYQKMQSPHAKESFTPTTEHVLV
VRLLLKHLHAFANSLKPEQASPSAHSHATSPLLEEFKRAAVPRFVQQKLYLFLQHCFGHWPLDASFRAVLEMWLSY
LQPWRYAPDKQAPGSDSQPRCVSEKWAPFVQENLLMYTKLFVGFLNRALRTDLVSPKHALMVFRVAKVFAQPNLA
EMIQKGEQLFLEPELVIPHRQHRLFTAPTFTGSFLSPWPPAVTDASFVKVSHVYSLEGQDCKYTPMFGPĒARTLV
LRLAQLITQAKHTAKSISDQCAESPAGHSFLSWLGFSSMDTNGSYTANDLDEMGSVRKTDYLEKALEYLRQI
FRLSEAQLRQFTLALGTTQDENGKKQLPDCIVGEDGLILTPLGRYQIINGLRRFEIEYQGDPELQPIRSYEIASL
VRTLFRLLSSAINHRFAGQMAALCSRDDFLGSFCRYHLTEPGLASRHLLSPVGRRQVAGHTRGPRLSLRFLGSYRT
LVSLLLAFFVASLFCVGPLPCTLLLTLYVLYASAMTLLTERGKLHQP

WO 2004/030615

PCT/US2003/028547

927/6881
FIGURE 861

GGCGCCGAGTAGCCGGGCCGGGGCCGGAGCGCGGGCGGCGGGGAGGCAGCTGCGCCCCGCGCCTCCTGCCCTCCCA
GGCCCCGCGCCCCGCGCCCCGGGCCCGGCGATGGTGACACATGCGGCGGGCGGCGCCGGCGGGCAGGACCATGGT
TGAGCGCGCCAGCAAGTTCGTGCTGGTGGTGGCGGGCTCGGTGTGCTTCATGCTCATCTTGTAACAGTACGCGGG
CCCAGGACTGAGCCTGGGCGCGCCCGGCGGGCCGCGCGCCCGCCGACGACCTGGACCTGTTCCCCACGCCCCGACCC
CCACTACGAGAAGAAGTACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGCTTCGACATGAAGGGCGACGA
CGTGATCGTCTTCTGACATCCAGAAGACGGGCGGCACCACCTTCGGCCGCCACCTCGTGAGAACGTACGCCT
CGAGGTGCCGTGCGACTGCCGGCCCGGCCAGAAGAAGTGACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCT
CTTCTCCCGCTTCTCCACCGGTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTACCAACTGCGTGCCCCG
CGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCAGGAAGTTCTACTACATCACCTGCTACGAGACCC
CGTGTCGCCGTACCTGAGCGAGTGGCGGCATGTGCAGAGGGGTGCCACGTGGAAGACGTGCTTGACATATGTGTGA
TGGGCGCACGCCCACGCCTGAGGAGCTGCCGCCCTGCTACGAGGGCACGGACTGGTGGGCTGCACGCTACAGGA
GTTTCATGGACTGCCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGCTG
CTACAACCTGTCCTTCATCCCCGAGGGCAAGCGGGCCGAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGG
CATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCGAGTACCTGTTGAGCGGACGTTCAACCTCAAGTT
CATCCGGCCCTTCATGCAGTACAATAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAAGACACCATCCGGCGCAT
CGAGGAGCTCAACGACCTGGACATGCAGCTGTACGACTACGCCAAGGACCTCTTCCAGCAGCGCTACCAGTACAA
GCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCACT
GCCGCGGGAGGATGCCGACGAGCCGGGCGCGTGCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGGTA
GTGGCGGTGGTGGCCACGGGGAGGCCCTCTTGGGGGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAA
GACTGTCAAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCCTGAAAAAAACAGAGCAGGGATG
TAGTGGGGCTGGGCAGGGATGGGGCTTGAGAAATCAACAGGTGCAGCCAGTGGGTGAGGAAAGCGTGCTCG
AAGGATGCCATGGTCAGGGCAGGGCTCCAGAGCAGGTGTTGTGCTGAGCTGCTCTCCTGGCCTCCTTGGATT
TATCGCAAAAACCTGAAGGTTTGCGCAAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCC
TCACCAACTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAA
CTGCCCCAGCTCCAGGCCATCCCATAGCCCCCTCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCC
CAGCTACCCATCTGTAGCTCCCTCAAAGTCAGGGCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCC
CAGGAAGCCTGCTCCCCTCTCTGGCCCATGGTCTCTCATGCTTTGGGTGAGGAGGCCAAAGCTGATGTTTACG
GCCCCACCCACTCCCTACAGTCCCTCAGACC

WO 2004/030615

PCT/US2003/028547

928/6881
FIGURE 862

GA CTG C C C G T A C A A C C T G G C C A A C A A C C G C C A G G T G C G C A T G C T G G C C G A C C T G A G C C T G G T G G G C T G C T A C A A C
C T G T C C T T C A T C C C C G A G G G C A A G C G G G C C C A G C T G C T G C T C G A G A G C G C C A A G A A A C C T G C G G G G C A T G G C C
T T C T T C G G C C T G A C C G A G T T C C A G C G C A A G A C G C A G T A C C T G T T C G A G C G G A C G T T C A A C C T C A A G T T C A T C C G G
C C C T T C A T G C A G T A C A A T A G C A C G C G G G C G G G C G G C T G G A G G T G G A T G A A G A C A C C A T C C G G C G C A T C G A G G A G
C T C A A C G A C C T G G A C A T G C A G C T G T A C G A C T A C G C C A A G G A C C T C T T C C A G C A G C G C T A C C A G T A C A A G C G G C A G
C T G G A G C G C A G G G A G C A G C G C C T G A G G A G C C G C A G G A G C G T C T G C T G C A C C G G G C C A A G G A G G C A C T G C C G C G G
G A G G A T G C C G A C G A G C C G G G C C G C G T G C C C A C C G A G G A C T A C A T G A G C C A C A T C A T T G A G A A G T G G T A G T G G C G G
T G G T G G C C A C G G G G A G G C C T C T T G G G G G T G T G G G G G A T A A A A C A G G A C A G A C G A C A G G T C C A C C C A A G A C T G T C
A A G G G A T G A G C A T C C C A A A C C T G C T C C A C A G A G G T A G C T G C G T C C T G A A A A A A A C A G A G C A G G G A T G T A G T G G G
G C T G G G C A G G G A T G G G G G C T T G A G A A A T C A A C A G G T G C A G C C C A G T G G G T C A G A G G A A A G C G T G C T C G A A G G A T G
C C A T G G T C A G G G C A G G G C C T C C A G A G C A G G T G T T G T G C C T G G A G C T G C T C T C T G G C C T C C T T G G A T T T A T C G C A
A A A C T G A A G G T T T G C G C A A G A G A C G A G G A C A G C G G A A A G T G G A C C T G C C A G G C C G G G A G T G T G T C C C T C A C C A A
C T A T G C A C A C A G C A C T C G C T C T T A G C T C C T C T G T C C G G G C T A C T A G G A G T G A G A C C A G C T T C T G G C A A C T G C C C C
A G C T C C A G G C C A T C C C A T A G C C C C T C C T C T T C T G G C T G C C C C A A T G C C C C G A G G C C T G G G G A G C C C C C A G C T C A
C C C A T C T G T A G C T C C C T C A A A G T C A G G G C C C A C C C C A T C T G A G G C A G A G A A G A C T C G A G T C C A G C C C C C A G G A A G
C C T G C T C C C C T C T C T G G C C C A T G G T C C T G C T T A T G C T T T G G G T C A G G A G G C C A A A G C T G A T G T T C A G G C C C C A C
C C A C T C C C T A C A G T C C T C A G A C C A A G G A G G G T T T G G G T A G T A G G C C C G A G C T G C A T T G C C G G C C T T C C T C G G G C
C A A C T G G C A G C C C A G G A G T G G G G A G G C T T T G G C C A G G G A T G C T G C C A C T T G T G C G T G A G T C C G C G G C T G G C C C T T
G G A G G T G A C C A T C C A G G C A G G C C T G G C T C A G A C T G G A A G G G C T G G G G A C C G A G G G C T C C C C T G C C T C T G T T C T C C
T T T C T G A C C C A C T G G G A T T T G C T A G C A G G C T G C C C C A G C C C C A T C A C C G A A C A C A T A C T C A A G A G C T C A A A T A C
C A C T G C T C C C A C C A G C G T A C G G A T T A A G T T C A T C A G G C T T C C A T C G G C T G G A G C A T G G G A C C A T A G C C C C T G C C C
A G G A G C C G T A C C C T C G G A C C A C A G T G G C T C T G T A T G G C C A G G A A C T G G G A C T C G A G C T T T C A G A T T C T C A A C T A G
C C T T G G C A A A C A G C T G T A G G T G G C C T C C C T G A C A A C A G A C A C T C A G C C C T C C C C A C C C T G G C T C T C C T T G C A T T
T C C C C A T G C T C C C C A C C C C T G G C A A A A G G C T G G C C A T G C T C T G T T C C C A G C A G C C G C G C A G G T T T C C C C A C T G G
C T G C A A T G G C C C T A C C A A A A G C C A T G T T G C A T A T C C G T T G T A A G C A C G T G C C C T G T G C C C T G T C C C C A T T C C T T A
T G C C C T A G G A G G C C A A G C T G G T G T C T C T A G G A G G G C C C A C A C A G G C A C C C T G G A T C C C C A G A G A T A G A T T G G T
G T G C T C A G G C C G C A G G C T G A C T C A G A G G T A G G G C A G T G G G C T C T G C A G G C C A C C T G G C T G G G G T T G G T G G G G G T C
C T C T C C T G C C C C A G C T T C C A C T C A G C C A C C A C A G T T G C C A C A C C A T G G G G T G G A G A C G T G G G T C A C C A C G G G C
T T G G G A G C A A G C G C C T T C T G C A G C A C A G G A A G C C G A A G C T G G G G T C A G G T G A G G T C G C T A C C C C T G G A G G T C T G G
C A T A A G G G C C C C A C C C T C A G G T C T C C T A C A C T G G C C C C A T T T T A C T T T G G G G T C C A A G G A C A G G A T G G T C A A C A G
G G C A G G G T G G A C A G C G T G C C A G C G C C G C G C A G G G C A C C T C C C T G G G T G G A T G C A T C A C A C T A A G G A A G T G A G T G
G G G G T G G G T G C A C T C C T T G G A G G A G G A A C A C G T T C A G G G G A T T G T G A G G T C T T G C A C A A G C C A C G T G G G G C A
C C T T G G C T T C C C G G C A G G A G G T G G A C A C C C A G C C A G A G G C C T G G C T C A A G G T G A C C T C A C C T T C A C C A T G G G C T T
C C T G G G T G C G C G G G C C T G A G C G C A G G T T G T T T T G T A C A T A T T G G A A T A T G T G T T A A C T T A T G C C C C G C A T C C C A A
C T C A C A C G G A A G C A C G G G T C T T G T C T C A G T C T C T T C G C T G C A T T T T G G A A A G C A G T C T C C T C T C G G G C C A G C G C G
G G C T G A G G T G T C C A G A G G C G G C G G C A G C T G G C A G T G C C C T C A G C C C C C A A G T G T C C A G C C T G G C A C T T C C C A T T C
A G G C C A C C T G C T T T G G G T C A A C A G T T C C T T T G C C A G C A G C A T C T C C T A A A T T G T A A G G A C T C T G T C C A C C G G G G C
C C T C C C A G G G C T G T G A G G A C G G A A A C A G G C A G G G A G T G G A G C T A A C A G C T T A G T C A C C A G G A C C C C C A G A C C T G C
A A A C G T C C C C T C C T G G A A G G G G A A G C C A G G A A C A G C A G A A C T G C C C A C A A A A C A A G G C T G T G A C T T T T C G G G A A
C T G G A A C T G T T T A A C T T G A A C C C A G G A T T G T T T A A A G C T T T A T T T A T T A T A G C T T C T T C T T A A A A A A A A G T G T T
G A A G A A A T T T T T T G G T T A T T C A T A C A A A A A A T G A G T T G A T G A T G G A A A G C A A G T C A T A A T C A T C T A A T T G T T T
T T G T C T A G G T C G A G A A T G A A T G T T A G C T G A T G A A A T A A C C C T G A C A A G G

WO 2004/030615

PCT/US2003/028547

929/6881
FIGURE 863

MLADLSLVGCYNLSFIPGKRAQLLLESAKKNLRGMAFFGLTEFQRKTQYLFERTFNLKFIRPFMQYNSTRAGGV
EVDEDTIRRIEELNDLDMQLYDYAKDLFQORYQYKRQLERREQRLRSREERLLHRAKEALPREDADPEGRVPTD
YMSHIIKW

WO 2004/030615

PCT/US2003/028547

930/6881
FIGURE 864

GGAAAAAGCGACTTGTGGCGGTTCGAGCGTGGCGCAGGCGAATCCTCGGCACTAAGCAAATATGGACCTCGCGGC
GGCAGCGGAGCCGGGCGCCGGCAGCCAGCACCTGGAGGTCCGCGACGAGGTGGCCGAGAAGTGCCAGAACTGTT
CCTGGACTTCTTGGAGGAGTTTCAGAGCAGCGATGGAGAAATTAATACTTGCAATTAGCAGAGGAAGTGAATTCG
TCCTGAGAGAAACACATTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCCACCACCATTCA
AGAGGAGTTCTATAGAGTTTACCCTTACCTGTGTGCGGCCTTGAAAACATTCGTCAAAGACCGTAAAGAGATCCC
TCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAGACACAAGATTCGAGAGCTCACCTCATCCAG
AATTGGTTTGTCTACTCGCATCAGTGGGCAGGTGGTGGGACTCACCCAGTTCACCCAGAGCTTGTGAGCGGAAC
TTTTCTGTGCTTGGACTGTCAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCAAACATCTG
CCGAAATCCAGTTTGTGCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATTTGTTGATTTTCAAAA
GGTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTATCCCCGAGTTTAGAAGTAATTTTAAGGGC
TGAAGCTGTGGAATCAGCTCAAGCTGGTGACAAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTC
CAAGCTTAGCACACCAGGAGCACGTGCAGAACTAATTCCTGTGTCAGTGGTGTGATGGATATGAGACAGAAGG
CATTCGAGGACTCCGGGCCCTTGGTGTAGGGACCTTCTTATAGGCTGGTCTTCTTGCTGTGTGTTGCGCC
AACCAACCCAAGTTTGGGGGAAAGAGCTCAGAGATGAGGAACAGACAGCTGAGAGCATTAAAGAACCAATGAC
TGTGAAAGAATGGGAGAAAGTGTGAGATGAGTCAAGATAAAAACTATACCACAATCTTTGTACCAGCCTGTT
CCCTACTATACATGGCAATGATGAAGTAAACGGGGTGCTCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAAC
AGGAGAAGGGACCTCTCTTCGAGGGGACATAAATGTTTGCAATTGTTGGTGACCCAAGTACAGCTAAGAGCCAATT
TCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAGTGGTAAAGCGTCCAGTGTGCTGGCTTAAC
AGCAGCTGTTGTGAGAGATGAAGAATCTCATGAGTTTGTCAATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGG
TGTTGTTGTTGATTGATGAATTTGATAAGATGGACGTGCGGGATCAAGTTGCTATTTCATGAAGCTATGGAACAGCA
GACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCCGACGTCCATTTTGGCAGCAGCAAACCC
AATCAGTGGACACTATGACAGATCAAAATCATTGAAACAGAATATAAATTTGTCAGCTCCCATCATGTCCCGATT
CGATCTCTCTTTATCCTTGTGGATGAATGTAATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTT
GCATTCAAGAATTGAGGAATCAATTGATCGTGTCTATTCCCTCGATGATATCAGAAGATATCTTCTCTTTGCAAG
ACAGTTTAAACCCAAGATTTCCAAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACATCTCCGCCAGAGAGA
TGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCGACAGCTTGAGAGCATGATTTCGTCTCTCTGAAGC
TATGGCTCGGATGCACTGCTGTGATGAGGTCCAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATC
AATCATCCGTGTGGAACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGC
TGGTGGCATCAATGGTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAATGAAGACATAAATCA
AGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGGCTTCTCTGAGTACTGCCGAATCTCTAACCTTATTGTGCTTCA
CCTCAGAAAGGTGGAAGAAGAAGAGGACGAGTCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGA
AATCGAATCAGAGATAGACTCTGAAGAAGAACTTATAAATAAAAAAAGAATCATAGAGAAAGTTATTTCATCGACT
CACACACTATGATCATGTTCTAATTGAGCTCACCCAGGCTGGATTGAAAGGCTCCACAGAGGGAAGTGAGAGCTA
TGAAGAAGATCCCTACTTGGTAGTTAACCTAACTACTTGCTCGAAGATTGAGATAGTGAAGTAAGTGAAGGAG
GCTGAGGAAGTGTGGCACAGCACCTCGTGGCCTGGAGCCTGGCTGGAGCTCTGCTAGGGACAGAAGTGTCTCTGG
AAGTGATGCTTCCAGGATTTGTTTTAGAAACAAGAATTGAGTTGATGGTCTATGTGTACATTATCACAGGT
TTCATACCAACACAGGCTTCAGCACTTCCTTGGTGTGTTTCTGTCCCAGTGAAGTTGGAACCAATAATGTGT
AGTCTCTATAACCAATACCTTTGTTTTATGTGTAAGAAAAGGCCCATTAATTTAAGGTATGTGCTGTCTATT
GAGCAATAACTTTTTTCAATTGCCAGCTACTGCTTTTATTTCATCAAAATAAAATAACTTGTCTG

WO 2004/030615

PCT/US2003/028547

931/6881
FIGURE 865

MDLAAAEPGAGSQHLEVRDEVAEKCQKLFDFLEEFQSSDGEIKYLQLAEELIRPERNTLVVSFVDLEQFNQQL
STTIQEEFYRVYPYLCRALKTFVKDRKEIPLAKDFYVAFQDLPTRHKIRELTSSRIGLLTRISGQVVRTHPVHPE
LVSGTFLCLDCQTVIRDVEQQFKYTQPNICRNPVCANRRRFLDITNKSREVDQKVRIQETQAEIPRGSIPRSLE
VILRAEAVESAQAGDKCDFTGTLIVVPDVSKLSTPGARAETNSRVSGVDGYETEGIRGLRALGVRDLSYRLVFLA
CCVAPTNPFRGGKELRDEEQTAESIKNQMTVKEWEKVFEMSQDKNLYHNLCTSLFPTIHGNDEVKRGVLLMLFGG
VPKTTGEGTSLRGDINVCIVGDPSTAKSQFLKHVEEFSPRAVYTSKGASSAAGLTAAVVRDEESHEFVIEAGALM
LADNGVCCIDEFDKMDVRDQVAIHEAMEQQTISITKAGVKATLNARTSILAAANPISGHYDRSKSLKQNINLSAP
IMSRFDLFFILVDECNEVTDYAIARRIVDLHSRIEESIDRVYSLDDIRRYLLFARQFKPKISKESEDFIVEQYKH
LRQRDGGSGVTKSSWRITVRQLESMIRLSEAMARMHCCDEVQPKHVKEAFRLNKSIIRVETPDVNLDQEEEIOME
VDEGAGGINGHADSPAPVNGINGYNEDINQESAPKASLRGSEYCRISNLIVLHLRKVEEEEDSALKRSELVN
WYLKEIESEIDSEEELINKKRIIEKVIHRLTHYDHVLIETQAGLKGSTEGSESYEEDPYLVVNPNYLLED

WO 2004/030615

PCT/US2003/028547

932/6881
FIGURE 866

CCGGGATCTCGAGATAGCCGCAGCTCTCGCGATCTTTCTGGAGCCGCACCTCCACGCGGAGTCCGAGCGCGTGTG
CTGAGACCCCAGGGTCGGGAGGGCGGAGACTGGGAGGGAGGGAGAAGCCCCTTTGGCCTGCCTTACGGAAGCCTG
CGAGGGAGGGTGGTGTCCACTGCCAGTTCCGTGTCCCGATGCCAGCGCCAGCGCCAGCCGCAAGAGTCAGGAG
AAGCCGCGGGAGATCATGGACGCGGCGGAAGATTATGCTAAAGAGAGATATGGAATATCTTCAATGATACAATCA
CAAGAAAAACCAGATCGAGTTTTGGTTCGGGTTAGAGACTTGACAATACAAAAAGCTGATGAAGTTGTTTGGGTA
CGTGCAAGAGTTTCATACAAGCAGAGCTAAAGGGAAACAGTGCTTCTTAGTCCTACGTCAGCAGCAGTTTAAATGTC
CAGGCTCTTGTGGCGGTGGGAGACCATGCAAGCAAGCAGATGGTTAAATTTGCTGCCAACATCAACAAAGAGAGC
ATTGTGGATGTAGAAGGTGTTGTGAGAAAAGTGAAATCAGAAAATTGGAAGCTGTACACAGCAAGACGTTGAGTTA
CATGTTCAGAAGATTTATGTGATCAGTTTGGCTGAACCCCGTCTGCCCTGCAGCTGGATGATGCTGTTTCGGCCT
GAGGCAGAAGGAGAAGAGGAAGGAAGAGCTACTGTTAACCAGGATACAAGATTAGACAACAGAGTCATTGATCTT
AGGACATCAACTAGTCAGGCAGTCTTCCGTCTCCAGTCTGGCATCTGCCATCTCTTCCGAGAACTTTAATTAAC
AAAGGTTTTGTGGAAATCCAACTCCTAAAAATTATTTAGCTGCCAGTGAAGGAGGAGCCAATGTTTTTACTGTG
TCATATTTTAAAAATAATGCATACCTGGCTCAGTCCCCACAGCTATATAAGCAAATGTGCATTTGTGCTGATTTT
GAGAAGGTTTTCTCTATTGGACCAGTATTCAGAGCGGAAGACTCTAATACCCATAGACATCTAACTGAGTTTGT
GGTTTGGACATTGAAATGGCTTTTAATTACCATTACCACGAAGTTATGGAAGAAATTGCTGACACCATGGTACAA
ATATTCAAAGGACTTCAAGAAAGGTTTCAGACTGAAATTCAAAACAGTGAATAAACAGTTCCCATGTGAGCCATTC
AAATTTTGGAGCCAACCTCTAAGACTAGAATATTGTGAAGCATTGGCTATGCTTAGGGAAGCTGGAGTCGAAATG
GGAGATGAAGACGATCTGAGCACACCAAATGAAAAGCTGTTGGGTCAATTTGGTAAAGGAAAAGTATGATACAGAT
TTTTATATTCTTGATAAATATCCATTGGCTGTAAGACCTTTCTATACCATGCCTGACCCAAGAAATCCCAAACAG
TCCAACCTCTTACGATATGTTTCATGAGAGGAGAAGAAATATTGTGAGGAGCTCAAAGAATACATGATCCTCAACTG
CTAACAGAGAGAGCTTTACATCATGGAATTGATTTGGAGAAAATTAAGGCTTACATTGATTCTTCCGCTTTGGA
GCCCCCTCTCATGCTGGTGGAGGCATTGGATTGGAACGAGTTACTATGCTGTTTCTGGGATTGCATAATGTTTCTG
CAGACCTCCATGTTCCCTCGTGATCCCAAACGACTCACTCCTTAAATTACACTTTGCCACTTAACTCCAGTGTG
GATGACAGAGCGAGACCCCTGCCCTCAAAAAAAAAAAAAAAAAAGAAAGCCACACTTATTCTTTTTCAGTAACCTGC
TAGTGACAGAGGCTGTACTTTAGGTACTTAAATATGCACTAGAATAAATTGCAAGGCCCTAAATATCACTGTT
ATTTTTGGAGTAATTCAGTATAGGTTTCGTTTAAAGAGATTTTTATACTTCAGACATGCATCAGTAGGAAATAA
CTTGAGAAATTCATATGGTTATGTTACAAATTCATATTCTGTTACTACAGTAAACGTTAAGAGTTTTAAACAGTT
AAGATTGTACAATTTTTCTTCTTTCTATATTACAAGGGCCCCAGTGTTAATGTCTTAGATTTTTCAGTATTTGAA
CTTATTTTTTTAAATTCTGTCATTGAGATAAGAATAATTCAGGTAGCATCTGAAATTTTAAATGAATGTATAATTG
GCATATCATGGAAAATTAACCAGAAAGTATCAGTTCTTAAAGTTATGCCTAGAAATTATGTAAAGCTAACTAC
TGGTTAGAAAGTATTCAGTGTAATATTGTATTAATTTGTTAAATTCTAAACTTGAATTTCAATAAAATTTTAAAG
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WO 2004/030615

PCT/US2003/028547

933/6881
FIGURE 867

ATGACAAAGAAAAATGCCTGCATGGGCCTTGTTTTCCAGATTCAATCAAGGCTCAAAGCTTTTATCTTGTTCTTA
ATAGCACCTTGACCCGATAGAGCCCGCAAGGCTTTGCGGGCCTTAATTATTTCCCAAGATCGATGAGACCCCT
CAGCCCCCTGGGCAGCAGCATCCCACGGCAGTTTTCCAGATGGATGAGCTGCGTCGAAAGCTGCAGAGCAGACAG
GGATGCAGACAAGGTCCAGCACGCCAGCAGAGCCTGCGGCCTGCGGGTTCTCGGGCGGATGGCACTGCAAAAT
TCAGCCCTTAATTCAATCAATATGTGCTTCGAGGAGTTTATAGTCATGGTTTGGTATGGTGGTATGTGATGCA
CACAAAGCAGAGACAGCTGCATGTAGAAGGGCAGGGGAGCATGGAGGCCCCAGTACAGCCAGGAGGCCCTGGAG
CTTCAGGCAGCAGGACATGGGTCTGGATCTGTAGTCAGAGGGGAGGTGAGGAAAGAGCTTGTACACCAGCAAAAG
ATTGGATCCTGTGGTTCTCAAACCTTATTAGTCCTGGAGCTGTGTTTCAAGGAAATTCTGCAGAAGAACAGCAG
TTCCCTTGCAAGGATGACCCAGGGCCCTGGTTCCCAGCAGCTCCAAGATGAGATGGCAGAAAGGGAGAGGGGG
AACCAGGAGAGGGGAAGGAGGAAATATATTAGTCGAGCTGCCCCAACGTCCCTCAAGGACAAGCACAAAGGGGT
GGTGTGGACAAGCATAATGCAATTGGCCCAGGGACAGGCCATAGACCCCACTTCCAAACCCATTTCTCCTCACA
GCCCAGGGCCTGAAGGGAACCCGCTGGATGCAAAGCCGAGGTCAACCAGAGATGGAGGTGGACAGACAGTGTGGG
ATGGCCCTGCACCTGAACTCCCAGGCACTACCTTGCAATTGTGAGTTTCTAATTTTACACACACTGGGGAGAGG
TCTGCTGTGGGCCAGGCTGGCCACCAGCGCTGGGTAAGTAGGGACTGGCCTAGCCACAGGCCTCAAGGATGCCGA
AGTCTGGTGGGGGAGACAAGCATGGAGAGAGACAGAGATGGCAGAGGCCAGGACAGGAAGCCTCTGGGCATCCTG
GCTGAGGACAGGGTGGCACACCCAGAGGAGAGTGAATCGTGAAATGCCGAAAGCTAAAGAGAAGATTCCCACCA
GAGATCACAGAGCAGAACATGCAAAAGTATAAAATTGCCCAACCACCGTCACTCACGGACCCCTTTGTCCCCTTC
TCTTCCCCTCCACCCCATAGAAGTTTGCTGACAACACGGGTTTCATACCACATTTCCACATATGGGAAGAACTCT
GTGGCCAGAGTGGTTACATTAGAGCACCTCCTCCCCTGAGAGCCACACAAGGGCCCATACCACTTCCAGTTCA
TGGCTCCACCTTTGTCTGCTCTCACAACCTTCCCAGACCTGGCCTATACCCACATGTTATTAATAATCTTCTA
GATATGCCCTTTAGGATTTGCTGCAAAGACACTTGAGATAAAGTATCTGTCAGAACCACTGGGATGTAGCCAAA
GCTAAGGAATATGTCCTGTTCTGTGGAGAGCAGATGATCAATAGGTGGTTCCCAGCTAATGGAGTGAAGTGGAGCA
AGGCTCATAGGCCCTTCAGTTCCATCAAAGGAAGATAAGTCCCCACTCATTGTCCCTGGAGGAACTGTGAGGTC
TTCTTATATTTGCATGTATGTGCCAAAGAGAGACATGTAAAAACCAGAGCCCGGAGACATAGAGAAGATCATTCA
AAAGCACATGCCAAGCTAAAGACAATACCAGGGACAGGACCTCATCTTCTGACTCTTGGTCCAGTTCTCCCTCCA
ACTCAGCAAACAGCCTTTGGATTCCACTTGGGAAATATGGAACTGAACAGCCAGAAGAAACCTTCCCTAACACT
GAAACCAGTGGTGAATTTGGTAAACGCCCTGCAGAAGATATGGAAGAGGAACAAGCATTAAAGATCTAGAAAC
ACTGATGAGATGGTTGAATTACCCATTCTGCTTCAGAGCAAGAATGCTGGAGCAGTGAAGTGGAAAAGGAGGCAAG
AATATTAAGGCTCTCCATACAGACTACAACGCCAGCATTTTCAGTTCTAGACAGCAGTGGCCCCAGCATATATTG
CATATCAGTGTGATATCGAAACAATTGGAGAAATTCTGAAGAAAATCATCACTACCTTGAAGAGGGCCCGCAG
TTGCCATCACCCACTGCAACCAGCCAGCTCCCGCTCGAATCTGATGCTGTGGAATACTTAAATTACCAACAATAT
AAAGGAAGGGACTTTGACTGCGAGTTGAGGCTGTTGATTTCATCAGAGTCTAGCAGGAGGAATTATTGGGGAATGT
TGCTCTCAATTTCACTGATAGAGTTGTTCTTATTGGAGGAAAACCAATAGGGTTGTAGAGTGCATAAAGATCATC
CTTGATCTTATTTCTGAGTCTCCCATCAAAGGACATGCACAGCCTTATGATCCCAATTTTACGATGAAACCTAT
GATTATGGTGGTTTTACAATGGTGTGTTGCTGACGACCGTGGACGCCAGGGGAGACCTCATGACCTATAACAGA
AAAGGGAGACCTGGAACCGTTACGACGGCGTGGTTGATTTCACTGCTGATGAACTTGGGGCTCTGCAATAGAT
ACATGGAACGCATCAGAATGGCAGATGGCTTATGAACCACAGGGTGGCTCCAGATATGATTATTCCTATGCAGGG
TGTCATGGCTCATATGGTGATCTTGGTGGACCTATTATTACTACACAAGGAGCTTTGATCAAAATTGATGAGCCT
TTAGAAGGATCCGAAGATCGGATCATTACCATTACAGGAACACAGGACCAGATACAGAATGCACAGTATTTGCCG
CAGAAATAGTGTGAAGCAGTATTCTGGAAAGTTTTCTAA

WO 2004/030615

PCT/US2003/028547

934/6881
FIGURE 868

MTKKNACMGLVFQIQSRLKAFILFLIAPCTDRARQGFAGLNYFPKIDETPQPPGQQHPTAVFQMDLRRKLQSRQ
GCRQGPAPPAEPAACGFLGRMALQNSALNSINMCLRGVYSHGLVWLVCDAHKAETAACRRAGEHGGPSTARRPLE
LQAAGHGSGSVVRGEVRKELVHQQKIGSCGSQTILSPGAVFQGNSAEEQQFPCKDDPRAPGSQQLQDEMAERERG
NQGEGRRKYIQSCPNVPQQAQRGGVDKHNAIGPGTGHRPHFQTPFLLTAQGLKGTRWMQSRGHPPEMEVDROCG
MALHPETPRHYLALSVSNTHTGERSAVGQAGHQRWVSRDWP SHRPQGCRSLVGETSMERDRDGRGQDRKPLGIL
AEDRVAPHEESESWKCRKLKRRFPPEITEQNMQKYKIAQPPSLTDFVVFSSPPPHRSLADNHGFIPHFHIWEES
VAQSGYIRAPPPLRATQGP IPPSSSWLHLCPALTTFPDLAYTHMLLNLLDMPLGFAAKTLEIKYLSEPTWVAK
AKEYVLFCEQMINRWFPANGVTGARLIGLSVPSKEDKSPLIVPGGNCEVFLYLHVCAKERHVKTRARRHREDHS
KAHAKLKTIPGTGPHLLTLGPVLPPTQQTAFGFHLGNMETEQPEETFPNTETS GEFGKRPAEDMEEEQAFKRSRN
TDEMVELPILLQSKNAGAVTGKGGKNIKALHTDYNASISVLDSSGPQHILHISADIETIGEILKKIITTTLEEGPQ
LPSPTATSQLPLESDAVEYLYNYQQYKGRDFDCELRLLIHQSLAGGIIGECCPHFTDRVVLIGGKPNRVVECIKII
LDLISESPIKGAQPYDPNFYDETYDYGGFTMVFADDRGRPGGDLMTYNRKGRPGNRYDGVVDFSADETWGS
TWNASEWQAMAYEPQGGSRDYDYSYAGCHGSYGD LGGP IITTTQ GALIKIDEPLEGSEDRIITTTGTQDQIQNAQYLP
QNSVKQYSGKFF

WO 2004/030615

PCT/US2003/028547

935/6881
FIGURE 869

ATGAAGCAGTTAATTACCCCTGCTAAACAGCAGGAAGCATTGAGCAAAACTCTGCTCACCTTCCTCAATCAGA
GGACATTTCTGCTCATCAGTCAAGCAGGCAGACCACAGGACTCTCAGACAAAGGCTGAGAGGTAGACTGATGAGG
AGGAGACTGTCAGTGAGCACAAAGGCCTTAAGATTAGCGACTGAAGGCTCCTGGAATGAGTATGTGGTTAGAGAC
TGGAATACTCAGGAGTTTCCCTAGGTCTGCTCCAAATAGCACAAAGCAATGGATGATGAAGGATCCATGTTAATA
GCAGTGGATCCACAGTGCAGATTTTCAGGTGATCTGCTCCCTACGACTCACTAATTGGAGTCCCATTGGCCCCC
CATGTGACCCCTCTTGGATAAAAATCAAAATGGCTCTCGTCTTGTTGTTTCTCCTGTTTGCCCCCAGTCAGGGCT
GGCACAGAGTGGCAGCTCTCTGCTCTCCACAGGGCTCCCGCTCCACCCAGCCCGATAAAGCATGCCGACTGGGC
TACAAAGCCAAGCAAGGTTACATTATATATAGGATTTGTGTTTCGCCGTGAGGAGCAAGCTGGACACCACTGTGGG
GCTCTAAGAGTCCTGAATTCGTACTGGGTTGGTGAAGATTCCACATACAAATTTTTTGAGGTTATCCTCATTGAT
CCATTCCATAAAGCTATCAGAAGAAATCCTGACACCCAGTGGATCACCAAACAGTCCACAAGCACAGGGAAATG
CGTGGGCTGACATCTGCAGGCTGA

WO 2004/030615

PCT/US2003/028547

936/6881
FIGURE 870

MKQLITPAKQQEAFEQKLCSPSSIRGHFCSSVKQADHRTLQRLRGRLMRRRLSVSTKALRLATEGSWNEYVVRD
WNYSGVSLGLLQIAQAMDDEGSMLIAVDPQCRFSGDLLPYDSLIGVPLAPHVTLLDKNQNGSRLVCFSCLPVRA
GTEWQLSALHRAPRSTQPDKACRLGYKAKQGYIIYRICVRREEQAGHHCGALRVLNSYWVGEDSTYKFFEVLID
PFHKAIRRNPDQTQWITKPVHKhREMRGLTSAG

WO 2004/030615

PCT/US2003/028547

937/6881
FIGURE 871

ATGTGGGGCGACCTCTGGCTCCTCCCGCCTGCCTCTGCCAATCCGGGCACTGGGACAGAGGCTGAGTTTGAGAAA
GCTGCAGAGGAGGTTAGGCACCTTAAGACCAAGCCATCGGATGAGGAGATGCTGTTCATCTATGGCCACTACAAA
CAAGCAACTGTGGGCGACATAAATACAGAACGGCCCCGGGATGTTGGACTTCACGGGCAAGGCCAAGTGGGATGCC
TGGAATGAGCTGAAAGGGACTTCCAAGGAAGATGCCATGAAAGCTTACATCAACAAAGTAGAAGAGCTAAAGAAA
AAATACGGGATATTGAGAGACTGGATTTGGTTACTGTGCCATGTGTTTATCCTAAACTGAGACAATGCCTTGTTTT
TTTCTAATACCGTGGATGGTGGGAATTCGGGAAAATAACCAGTTAAACCAGCTACTCAAGGCTGCTCACCATACG
GCTCTAACAGATTAGGGGCTAAAACGATTACTGACTTTCCTTGAGTAGTTTTTATCTGAAATCAATTAAAAGTGT
ATTTGTTACTTT

WO 2004/030615

PCT/US2003/028547

938/6881
FIGURE 872

MWGDLWLLPPASANPGTGTEAEFEKAAEEVRHLKTKPSDEEMLFIYGHYKQATVGDINTERPGMLDFTGKAKWDA
WNELKGTSKEDAMKAYINKVEELKKKYGI

WO 2004/030615

PCT/US2003/028547

939/6881

FIGURE 873

GTTTAGGGGCTGGTACAAAGGATGAATTGCACATTGTTGAAGTAGAGGCAATGAATTACAAAGGCAGTCCAATTA
AAGTAACACTGGCAACTTTGAAAATGTCTGTACAGCCAAAGGATTCCCTTGGAGGCTTTGAAATCACACCACCAG
TGGTCTTACGGTTGAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTGTGGAGGAAGATG
CAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAACTCTTAAGTGTATCTGGAAAGCGGTCTGGCCCGTGGAGGTG
GTAGCAAGATTCCACAGAAAAAGTAAAAGTTGCTGCTGATGAAGATGAAGATGATGATGAGGATTTTGATG
ATGGGGAAGCTGAAGAAAAAGCGCCGGTGAAGAAATCCATACGAGATACTCCAGCCAAAAATGCACAAAAGTCAA
ATCAGAATGGAAGAACTCAAACCGTCAACACCAAGATCAAAAGGACAAGACTCCTTCAAAAAACAGGAAAAA
ACTTCTAAACACCGAAAGGACCTAGTTCCATAGAAGACATTAAAGCGAAAATGCAAGCAAGTATAGAAAAAGCG
CATTGAACAGTCCTGGGCACTGCTGGTAAATTAAGCCCAAAGATGGGGAGAAAGGAAAAGGAGAGACAAATATAG
TCCATACTGAG

WO 2004/030615

PCT/US2003/028547

940/6881
FIGURE 874

MNYKGSPIKVTLATLKMSVQPKDSLGGFEITPPVVLRLKCGSGPVHISGQHLVAVEEDAEESEDEEEEDVKLLSVS
GKRSARGGGSKIPQKKVKVADEDEDDDDDEDFFDDGEAEEKAPVKKSIRDTPAKNAQKSNQNGKDSKPSTPRSKGQ
DSFKKTGKNF

WO 2004/030615

PCT/US2003/028547

941/6881
FIGURE 875

AGCGGGTTTGC GGGAGCGCCGCGTGGTTAGCGTCGGCGGCTTTTGGCATGGCGACTTTTTCTGGCCCGGCTGGGC
CAATCCTGTCGCTTAATCCGCAGGAAGATGTCGAGTTTCAAAAAGGAGGTGGCGCAGGTTTCGAAGCGCATAACCC
AGCGAAAAAACAAGAACAACCTTACTCCTGGAGTAGTCTATGTGCGCCACCTACCTAACCTACTTGACGAAACCC
AGATCTTTTCATATTTCTCCAGTTTGGCACTGTGACACGGTTTCAGGCTGTCCAGAAGTAAAAGGACTGGAAATA
GCAAAGGCTATGCATTTGTGGAGTTTGTAGTCTGAGGATGTTGCCAAAATAGTTGCTGAAACAATGAACAACCTACC
TGTTTGGTGAAAGACTCTTGGAGTGTCAATTTATGCCACCTGAAAAAGTACATAAAGAACTCTTTAAAGACTGGA
ATATTCCATTTAAGCAGCCATCATATCAATCAGTGAAACGGTATAATCGGAATCGGACACTAACACAAAAGCTAC
GGATGGAGGAGCGATTTAAAAAGAAAGAAAGATTACTCAGGAAGAAATTAGCTAAAAAGGAATTGACTATGATT
TTCCTTCTTTGATTTTACAGAAAACGGAAGTATTTCAAAAACTAATCGTCAGACGTCTACAAAAGGCCAGGTTT
TACGTAAGAAGAAGAAAAAGTTTCAGGTACTCTTGACACTCCTGAGAAGACTGTGGATAGCCAGGGCCCCACAC
CAGTTTGTACACCAACATTTTGGAGAGGCGAAAAATCTCAAGTGGCTGAACTGAATGATGATAAAGATGATG
AAATAGTTTTCAAACAGCCCATATCCTGTGTAAAAAGAAGAAATACAAGAGACTCAAACACCTACACATTCACGGA
AAAAAGACGAAGAAGCAGCAATCAGTGAATTTTCAATGTATTATATTTCTTTTGAAAAATATAATATTTTATGA
GAGTGGACTTTGTATTTCACTAGGTACAATGGAATACAACCTTTGACAAGATTTTCAGAGGAAAAATACACTGTT
TGGTCAAGTTAAGGAAAGCAGTGTGTAATTTGGATTGCCTGCCCTTGGCTGAAATACAGGGGTGCATACCATCT
TGCAGTGGCTTGGCTGACATTGCCTCTTTGTCTGGCCTCTAGTTTCTTTTGATATTTCATAGCTCTCCTTAGT
TTACTCTGCCTGGATAGAAAGTTGACCACTAACTGCAGGTTTAAGTACTAACTGCAGCCTTTCTGTGCGCCAGC
AATTAAAGACCACCAATCTTGTTTGTCCATCTACATGGTTTGTGCGGGACATTTAACTCATGGAGGTGCTTTAGA
TTTCAACATCAGATGGTTGAAGCTGGAAGTTTAATTATATGTAGAGTGAGAAGGCAGTTCAGTTTTAGCACAGA
TTTGTATGTGTTTCAAGTTTAAATAGAGATTCAAAAAATGACTCATTTTACCAATAATGTTAAATTAGTTTTGG
TTGTGCTAGCATGAATTAATAACCACCATTTTATACCAGTATCATCAGTGAAGAATTGTATTTCAAGATTCAAAC
AATAACCAGCAATTAACTTTTTTCTACAATGTATTTGTTTGCAGTAGGACTTGGGAGTCATTGGAAAAA
ATAATAAATTTTCCCCTTCATTAACAAAAA

WO 2004/030615

PCT/US2003/028547

942/6881
FIGURE 876

MATFSGPAGPILSLNPQEDVEFQKEVAQVRKRITQRKKQEQLTPGVVYVRHLPNLLDETQIFS YFSQFGTVTRFR
LSRSKRTGNSKGYAFVEFESEDVAKIVAETMNNYLFGERLLECHFMPPEKVHKELFKDWNIPFKQPSYQSVKRYN
RNRTLQKLRMEERFKKKERLLRKKLAKKGIDYDFPSLILQKTESISKTNRQTSTKGQVLRKKKKKVSGTLDTPE
KTVDSQGPTPVCTPTFLERRKSQVAELNDDDKDDEIVFKQPI SCVKEEIQETQTPTHSRKKRRRSSNQ

WO 2004/030615

PCT/US2003/028547

943/6881
FIGURE 877

CCGCGGCGTCCACACTCGCCGCGCGCGCGCGCGGCGGCTGGACCTTGCTGGCCCCGCGGCGCCATGAGCCGCAGC
CTGGACTCGGCGCGGAGCTTCTTGAGCGGCTGGAAGCGCGGGGCGGCGGGAGGGGGCAGTCCTCGCCGGCGAG
TTCAGCGACATCCAGGCCTGCTCGCCGCGCTGGAAGGCTGACGGCGTGTGCTCCACCGTGGCCGGCAGTCGGCCA
GAGAACGTGAGGAAGAACCCTACAAAGACGTGCTGCCTTATGATCAGACGCGAGTAATCCTCTCCCTGCTCCAG
GAAGAGGGACACAGCGACTACATTAATGGCAACTTCATCCGGGGCGTGGATGGAAGCCTGGCCTACATTGCCACG
CAAGGACCCTTGCCCTCACACCCTGCTAGACTTCTGGAGACTGGTCTGGGAGTTTGGGGTCAAGGTGATCCTGATG
GCCTGTGAGAGATAGAGAATGGGCGGAAAAGGTGTGAGCGGTACTGGGCCCAGGAGCAGGAGCCACTGCAGACT
GGGCTTTTCTGCATCACTCTGATAAAGGAGAAGTGGCTGAATGAGGACATCATGCTCAGGACCCTCAAGGTACA
TTCCAGAAGGAGTCCCCTTCTGTGTACCACTACAGTATATGTCTGGCCAGACCGTGGGGTCCCCAGCAGTCCT
GACCACATGCTCGCCATGGTGGAGGAAGCCCGTCCGCTCCAGGGATCTGGCCCTGAACCCCTCTGTGTCCACTGC
AGTGCGGGTGTGGGCGAACAGGCGTCTGTGCACCGTGGATTATGTGAGGCAGCTGCTCCTGACCCAGATGATC
CCACCTGACTTCAGTCTCTTTGATGTGGTCTTAAGATGAGGAAGCAGCGGCCTGCGGCCGTGCAGACAGAGGAG
CAGTACAGGTTCTGTACCAACGCTGGCTCAGATGTTCTGCTCCACACTCCAGAATGCCAGCCCCCACTACCAG
AACATCAAAGAGAATTGTGCCCACTCTACGACGATGCCCTCTTCTCCGACTCCCCAGGCACCTTCTCGCCATA
CCCCGCCCACCAGGAGGGGTCTCAGGAGCATCTCTGTGCCCGGGTCCCCGGGCCACGCCATGGCTGACACCTAC
GCGGTGGTGCAGAAGCGCGGGGCTCCAGCGGGCGCCGGGAGTGGGACGCAGACGGGGACGGGGACGGGGACGGGG
GCGCGCAGCGCGGAGGAGGCGCCGCTCTACAGCAAGGTGACGCCGCGCGCCAGCGACCCGGGGCGCACGCGGAG
GACGCGAGGGGGACGCTGCCCTGGCCGCGTTCTCTGCTGACCAAAGTCTGCGGATCTGGCGCCTACGAGGACGTG
GCGGGTGGAGCTCAGACCGGTGGGCTAGGTTTCAACCTGCGCATTGGGAGGCCGAAGGTCCCCGGGACCCGCCT
GCTGAGTGGACCCGGGTGTAAGTCTAACGCCAGTTCCTGCTGTGCTCTTGTGAGCTCGGACTGCTGATGCC
CGGTGCTGCTGAGCGCCGTGCGCAGAATGGAAACAGTGGGCTGGATCAAAGTTAAAGTTTCTCAGGGTGGGAAA
TGTGGGGGCTTTGCCCAATGACTGTAGCATTCAAGGCTTGAGGCTGGAGGAGGTAGCTAGGGTATAGTGGCTGG
TGAGGCTGCACAGAGCAGATTCAAGAAAGAAGATCAGGAAGGGGCATGACCCCTGAGTTATGAAGGGGAGAAGGG
ACAGATGAGCTTCCGGAGACTGCTCTCCTCACACACAGCACTAGTCCATCCTCAGCACCTGAGCCTCCCTCACT
TGGACACTCAGGGGACCACACAGAGAAGTGGATGGACACTTCGCCATCCAGGCAGAACTAAGCCAGGCATAACCA
CAGCCAAGCAGATTAACCCAGGCAGACCGATAAAAAGACCTCCAGATAGGCAGACAGACAGATGGACCACCAAC
CTGGACAGACAGCCAAAGCTTCAGAGATACAGTCCACAGGTGGACAAAGGGATCCCCAGCCAGAGAGAGAGAGAC
CAGCCAACAGCTTGATAGACAGTGCAGCCAGAGAGACCACAAACAGAGCCCCCAAAGACAGACATCTCTGCT
AGCTGGACAGCCAGGTGGACCCCTAAGTTAGATTACTAGACAGATATAAACAGATCCCCCTGCTGAACAGATACA
CAGAGTTCTCAGACCCCAACCCCAACCTCAGGTGGGCTGGCTGGCTGACAGACCTTCTGGCCAGACAGACTCCTA
ACCAACCAGATGGACTGCCAGACAGGCAGACATCAGCCACATGGAATCCTGACATCCCAGCCAGCCGGCCAGACT
CTCATCTTGATGTCTTGATGGATGGACCCAGCTAGTCAGACATGATCCTCCAGATTGACAGACAAGTCCCCAA
ATGAGTACACATCTCCAGCTATTCAGACAGATGGACCCCAAGCAATCAGGACCTATCTAGGCAGACCCAGCCA
GACCCCGCCAGACAGACTCCCAACCAGACTGACCCCTTACTATTACACAGCCTGCCGAGTAGCTGGGACTACA
GGTCTAATTTTTTTTTTTTTTAAGAAATGAGTTTTTGCCATGTTGCCAGACTGGTCTTGAACCTCCAACCTCAA
GCAATCCTCCTGCCTCAGCCTCCCAAGTGCTGAGATTACAGGTGTGAGCCACCAGGCTCAGCCCCCTAAGATTT
GAAACACTTTAAATGGCCCATGGTAGGGTTCTGCTAGGATAAAACATTAAGCGGCTGTTAAAAGAAATAAAGG
AGGACACGTCTCTGTGC

WO 2004/030615

PCT/US2003/028547

944/6881
FIGURE 878

TGGAAGCGGCACTCAAGATGCTGCGCCGCGAGGCCCGCCTGCGCCGCGAGTACCTGTACCGCAAGGCCCGGGAGG
AGGCGCAGCGCTCAGCCCAGGAGAGGAAGGAGCGGCTGCGGCGCGCGCTGGAAGAAAACCGCCTGATTCCCACTG
AGTTACGCCGAGAGGCTCTGGCCTTACAGGGGTCCCTGGAGTTTGATGATGCTGGAGGTGAAGGTGTGACCAGCC
ACGTGGATGATGAATACCGATGGGCAGGAGTCGAGGATCCCAAGGTTATGATCACTACCTCCCGAGACCCCACTT
CCCGCCTCAAGATGTTTGCAAAGGAGCTGAAGCTGGTGTTCCTGGGCGGCCAGCGAATGAACCGAGGTGACATG
AAGTGGGGGCACTGGTGCAGCCTGCAAAGCCAACGGCGTCACCGATCTGCTGGTTCGTTACGAGCATCGGGGCA
CACCTGTGGGGCTCATCGTCAGCCACCTGCCCTTTGGTCCTACTGCCTACTTCACGCTGTGCAATGTGGTCATGC
GGCATGACATCCAGACCTGGGCACCATGTGCGAGGCCAAGCCCCACCTCATCACACACGGCTTCTCCTCCCGCC
TGGGCAAGCGGGTCTCTGACATCCTCCGATACCTATTTCCCGTGCCCAAAGATGACAGCCACCGGGTCATCACCT
TCGCAAACCAGGACGACTACATATCATTCCGGCACCATGTGTATAAGAAGACAGACCACCGCAACGTGGAGCTCA
CTGAGGTCGGGCCCCGCTTTGAGCTGAAGCTGTACATGATCCGTCTGGGCACGCTGGAGCAGGAGGCCACAGCAG
ACGTGGAGTGGCGCTGGCACCCCTTACACCAATACCGCACGCAAGAGAGTCTTCCTGAGCACCGAGTGAGCACACT
CACCCTCAGTCAGGACATGGACTTGGAATCAGGATGGGGCTGTCATAGACAGACCCACAGTAGGAAGTGTCA
CAGAATGGCCTGCTGAATGGGATGTGGAATGTGGCGGGTGGAGAGGTCTGAATAAACCGTCTGTGTGTCATGGCA
AAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

945/6881
FIGURE 879

MLRREARLRREYLYRKAREEAQRSAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGVTSHVDDEY
RWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGAQRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLI
VSHLPFGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRVSDILRYLFPVPKDDSHRVITFANQDD
YISFRHHVYKKT DHRNVELTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTN TARKRVFLSTE

WO 2004/030615

PCT/US2003/028547

946/6881
FIGURE 880

GGCGGCGGCAGCGGGTTCGGTTGCGCGTGACGCACGGGGTGGGAGCGGAGCCCAGGCCGGGAGCAGGCGCCTCTG
CCAGAGACCATGGGGAACGTGTTGGCCGCCAGGTCGCCGCCCGCAGGGCCGCCACCGCCGCCTGCGCCGGCCCTC
GTGGAGCTGCCGCCACCTCCGCCCTCGCCGCCGGGCTTCACGCTGCCGCCGCTGGGAGGCGGCCTGGGCGCCGGC
ACCAGTACGAGTCGAGGTTTCGGAAC TGACCCCCGGGGCTGCAACTGCCAGCGCCTCAGGGGCCGCCGAGGATGGG
GCCTGCGGGCTGCCTGCCCAACCCGGGCACATTTCGGGGAGTGCCACCGGAAGTGCAAGGAGCTGTTTCCCATTAG
ATGGAGGGTGTCAAGCTCATAGTCAACAAAGGGTTGAGTAACCATTTCCAGGTGAACCACACAGTAGCCCTCAGC
ACAATCAGGGAGTCCAGCTACCACTTCGGGGTCACGTATGTGGGGACAAAGCAGCTGAGTCCCACAGAGGCGTTC
CTTGTATTGGTGGGTGACATGGACAACAGCGGCAGTCTCAACGCTCAGGTCATTACCACTGAGGCCCCCGCCTC
AGGTCCAAGATGGCCATCCAGACCCAGCAGTCGAAGTTTGTGAACTGGCAGGTGGACGGGGAGTATCGGGGCTCT
GACTCACAGCAGCCGTAACCC TGGGGAACCCAGACGTCCTCGTGGGTTCAGGAATCCTCGTAGCCCACTACCTC
CAGAGCATCACGCCTTGCC TGGCCCTGGGCAGAATGCTGGTCTACCAACAGCAGCCTGGGGAGGAGGGCACTGTC
ATGTCTCTAGCTGGGAAATACACATTGAACAAC TGGTTGGCAACGGTAACGTTGGGCCAGGCGGGCATGCACGCA
ACATACTACCACAAAGCCAGTGACCAGCTGCAGGTGGGTGTGGAGTTTGAGGCCAGCACAAAGGATGCAGGACACC
AGCGTCTCCTTCGGGTACCAGCTGGACCTGCCCAAGGCCAAAGGCTCTGTGGATAGCAACTGGATCGTGTGTGCC
ACGTTGGAGAAGAAGCTCCCGCCCC TGGCCCTGACACTGGCCCTTGGGGCCTTCCTGAATCAC

WO 2004/030615

PCT/US2003/028547

947/6881

FIGURE 881

AAGAACTGGCCTGTACATTTTCAAGGAATTCTTGAGAGGTTCTTGGAGAGATTCTGGGAGCCAAACACTCCATTG
GGATCCTAGCTGTTTTAGAGAACAACCTTGTAATGAGAGCCTTCATCTCTTGAGCTGCCGGCTGACACAGTGCAGCG
CATTGCGGCTGAACTCAAATGCCACCCAACGGATGAGAGGGTGGCTCTCCACCTAGATGAGGAAGATAAGCTGAG
GCACCTTCAGGGAGTGCTTTTATATTCCCAAATACAGGATCTGCCTCCAGTTGATTTATCATTAGTGAATAAAGA
TGAAAATGCCATCTATTTCTTGGGAAATTCTCTTGGCCTTCAACCAAAAATGGTTAAAACATATCTTGAAGAAGA
ACTAGATAAGTGGGCCAAAATAGCAGCCTATGGTCATGAAGTGGGGAAGCGTCCTTGGATTACAGGAGATGAGAG
TATTGTAGGCCTTATGAAGGACATTGTAGGAGCCAATGAGAAAGAAATAGCCCTAATGAATGCTTTGACTGTAAA
TTTACATCTTCTAATGTTATCATTTTTTTAAGCCTACGCCAAAACGATATAAAAATTCTTCTAGAAGCCAAAGCCTT
CCCTTCTGATCATTATGCTATTGAGTCACAACCTACAACCTTACGGACTTAACATTGAAGAAAGTATGCGGATGAT
AAAGCCAAGAGAGGGGGGAAGAAACCTTAAGAATAGAGGATATCCTTGAAGTAATTGAGAAGGAAGGAGACTCAAT
TGCAGTGATCCTGTTTCAGTGGGGTGCATTTTTACACTGGACAGCACTTTAATATTCCTGCCATCACAAAAGCTGG
ACAAGCGAAGGGTGTATGTTGGCTTTGATCTAGCACATGCAGTTGGAAATGTTGAACCTCTACTTACATGACTG
GGGAGTTGATTTTGCTGCTGGTGTTCCTACAAGTATTTAAATGCAGGAGCAGGAGGAATTGCTGGTGCCTTCAT
TCATGAAAAGCATGCCCATACGATTAAACCTGCATTAGTGGGATGGTTTGGCCATGAACTCAGCACCAGATTTAA
GATGGATAACAACTGCAGTTAATCCCTGGGGTCTGTGGATTCCGAATTTCAAATCCTCCCATTTTGTGGTCTG
TTCTTGATGCTAGTTTAGAGATCTTTAAGCAAGCGACAATGAAGGCATTGCGGAAAAAATCTGTTTTGCTAAC
TGGCTAICTGGAATACCTGATCAAGCATAACTATGGCAAAGATAAAGCAGCAACCAAGAAACCAGTTGTGAACAT
AATTACTCCGTCTCATGTAGAGGAGCGGGGTGCCAGCTAACAAATAACATTTTCTGTTCCAAACAAAGATGTTTT
CCAAGAAGTAGAAAAAGAGGAGTGGTTTGTGACAAGCGGAATCCAAATGGCATTTCGAGTGGCTCCAGTTCTCT
CTATAATTCTTTCCATGATGTTTATAAATTTACCAATCTGCTCACTTCTATACTTGACTCTGCAGAAACAAAAA
TTAGCAGTGTTTTCTAGAACAACCTAAGCAAATTATACTGAAAGCTGCTGTGGTTATTTTCAGTATTATTTCGATTT
TTAATTATTGAAAGTATGTCACCATTGACCACATGTAACATAACAATAAATAATATACCTTAC

WO 2004/030615

PCT/US2003/028547

'948/6881
FIGURE 882

MEPSSLELPADTVQRIAAELKCHPTDERVALHLDEEDKLRHFRECFYIPKIQDLPPVDLSLVNKDENAIYFLGNS
LGLQPKMVKTYLEEEELDKWAKIAAYGHEVGKRPWITGDESIVGLMKDIVGANEKEIALMNALT VNLHLLMLSFFK
PTPKRYKILLEAKAFPSDHYAIESQLQLHGLNIEESMRMIKPREGEETLRIEDILEVIEKEGDSIAVILFSGVHF
YTGQHFNIPAITKAGQAKGCYVGFDLAHAVGNVELYLHDWGVDFACWCSYKYL NAGAGGIAGAFIHEKHAHTIKP
ALVGWFGHELSTRFKMDNKLQLIPGVCGRISNPPILLVCSLHASLEIFKQATMKALRKKS VLLTGYLEYLIKHN
YGKDKAATKKPVVNIITPSHVEERGCLTITFSVPNKDVFQELEKRGVVCDKRNPNGIRVAPVPLYN SFHDVYKF
TNLLTSILDSAETKN

WO 2004/030615

PCT/US2003/028547

949/6881
FIGURE 883

GTGTACGGTCCGCAGCGGCAGGTGAAGTCTAGCAGAGGACGCGGCCAGGCGATTCCGGTGAAGCGATTCTGCAGG
CGTTGGTTCCCCCTCTTTGACCTGGTAAATGCAGGCTTTTTATGCGAGAGGATTTGAATTTGTTGAAATGAGCAGTC
GTAAATCAAAGAGTAACAGCTTAATTCACACAGAGTGCCTTTCACAGGTACAAAGAATTTTACGTGAAAGATTTT
GTCGTCAGAGTCCACATAGTAACCTATTTGGAGTGCAAGTACAATACAAACACTTAAGTGAGCTGCTGAAAAGAA
CTGCTCTCCATGGAGAGAGTAACCTCTGTCCATTATTATCGGACCCCGAGGATCAGGAAAACTATGTTAATAAATC
ATGCTTTGAAAGAACTCATGGAAATAGAAGAAGTGAGTGAAAATGTATTACAAGTTCACTTAAATGGACTGCTGC
AGATCAATGACAAAATCGCCCTAAAGGAAATCACAAGGCAGTTAAATCTGGAAAATGTAGTTGGAGATAAAGTTT
TTGGAAGCTTTGCTGAAAACCTTTTCATTTCTTCTGGAAGCTTTAAAAAAGGTGACCGAACTAGCAGTTGCCAG
TGATCTTCATATTAGATGAATTTGATCTTTTTGCTCATCATAAAAACCAACACTTCTCTATAATCTTTTTGACA
TTTCTCAGTCTGCACAGACCCCAATAGCAGTTATTGGTCTTACATGTAGATTGGATATTTTGGAACTCTTAGAAA
AAAGAGTGAAGTCAAGATTTTCTCACCGGCAGATACACTTAATGAATTCATTTGGTTTTCCACAGTATGTTAAAA
TATTTAAAGAACAGTTATCTCTACCTGCAGAGTTTCCAGACAAGGTTTTTGGCTGAGAAGTGGAATGAAAATGTTT
AGTATCTCTCAGAAGATAGAAGTGTGCAAGAAGTACTACAGAAGCATTTCAATATCAGCAAAAACCTGCGGTCAT
TACACATGCTATTGATGCTTGTCTTAAATCGAGTAACAGCATCGCACCCATTTATGACTGCCGTAGATCTAATGG
AAGCAAGCCAACCTGTGTAGCATGGACTCGAAAGCAAATATTGTACATGGTCTATCAGTCTTGGAATCTGTCTTA
TAATAGCAATGAAACATTTAAATGACATCTATGAGGAAGAGCCATTTAATTTTCAAATGGTCTATAATGAGTTTC
AGAAGTTTGTTCAAAGGAAAGCACATTCGGTTTTATAATTTTGAAAAACCTGTTGTCATGAAGGCTTTTGAACACT
TGCAGCAATTAGAATTAATAAAGCCCATGGAAAGAACTTCAGGAAATTCACAGAGAGAGTACCAGCTGATGAAAC
TGCTTTTGGATAATACTCAAATTATGAATGCTCTGCAGAAATATCCCAACTGTCCTACAGATGTGAGGCAGTGGG
CAACATCCTCACTAAGCTGGTTATGAATATAACCAGTGACTTCAACTTTGGCATTTCATTACACTTCTGTAGAG
AACGGAAAACTATTGTCCATTAACATGATATGCTAAACATTCTATAAACATTCTTGTTATTTATGTGAGACTTGCC
CATCTACTGTCTTGGCTGTGCTTGCCTTTTAAATCATGAACAGTTACATGATTTATAATTTCACTGATTGAGATT
ACTTTGTAAGTAGCTGTTTCAGAAGAATAAAATATGACTGTTTTAGGGACTAGACCATGTGCTTTTTTAACACTTA
TATATATAATGGTCTATTTGAAGAGCTCACTTCAACCTAACAGCTAGATGTCTTTACAAACCTTAAACCAAAGGA
GTAAAAAACAATGGTAAGCACTGAAGTATAATAAGTAACCTTTGGTACAGCAGGTTTGCTGCAGTGTTTTTTT
CTGTCCACATGCAAAATTTTGGATTCTATCCCAGACCCAGGTTTTCTAGTTTCAAGACTAACCAGCTTAGTCAGA
AGATGGTTCCATGGAAGAAAAAGGCCAAGGAGTTTGAAGATTTTCTTCTAGACATCTCAAAATGTGGTACTCAT
ACCATCCACATCAGAATCCCTTGTAGGATTTTCTAAAATTACAGATTGTTGAGCCTACCATAGGTCAAAGGACT
GGAATTTTCTTCTTAACAAGTATAGTCATGGCACCGTAACATTTTGGTCAATGACATTGTATAAAGGGTGGT
CTCATAAGATTATACCATATTTTACTGTACCTTTTCTATGTCTAAATATACAAATGTTTTACCATTG

WO 2004/030615

PCT/US2003/028547

950/6881
FIGURE 884

MSSRKSKSNSLIHTECLSQVQRILRERFCRQSPHSNLFQVQVQYKHLSELLKRTALHGESNSVLIIGPRGSGKTM
LINHALKELMEIEEVSENVLQVHLNGLLQINDKIALKEITRQLNLENVVGDKVFGSFAENLSFLLLEALKKGDRTS
SCPVIFILDEFDLFAHHKNQTLLYNLFDISQSAQTPIAVIGLTCRLDILELLEKRVKSRFSHRQIHLMNSFGFPQ
YVKIFKEQLSLPAEFPDKVFAEKWNENVQYLSSEDRSVQEVQKHFNISKNLRSLSHMLLMALNVRTASHPFMTAV
DLMEASQLCSMDSKANIVHGLSVLEICLIIAMKHLNDIYEEEPFNFMVYNEFQKQVQRKAHSVYNFEKPVVMKA
FEHLQQLLELIKPMERTSGNSQREYQLMKLLLDNTQIMNALQKYPNCPTDVRQWATSSLSWL

WO 2004/030615

PCT/US2003/028547

951/6881

FIGURE 885

ATTTCGGCACCGCAGCGTAGGTGCTACCACCGCTGCCGTCGCCGCCGCCATTTTGATGGCAGGAAGAGTCCGGTTC
TGGGACAGCTGGAGACAGTGGTGGTGAAGTAACTTTACCAAAGGAAAGCTATTTTGCGAACTATCTTCTCC
AGCGGAGATGGCCAATGTGCTTTGTAACAGAGCCAGACTGGTTTCCTATCTCCCAGGATTTTGCTCTTTAGTTAA
AAGGGTTGTCAATCCCAAAGCCTTTTCGACTGCAGGATCATCAGGTTTCGGATGAGTCTCATGTGGCTGCTGCACC
TCCAGATATATGCTCTCGAACAGTGTGGCCTGATGAACTATGGGACCCCTTTGGACCTCAAGATCAGAGGTTCCA
GCTTCCTGGGAACATAGGTTTTGATTGTACCTCAATGGGACTGCTTCACAGAAGAAAAGCCTGGTTTCATAAAAC
TTTGCTGATGTTCTAGCAGAACCTTTATCAAGTGAAAGACATGAGTTTGTGATGGCACAATATGTGAATGAATT
TCAGGGTAATGATGCACCTGTTGAACAAGAAATTAACAGTGCAGAACTTACTTTGAAAGTGCCAGAGTAGAGTG
TGCAATACAAACATGTCCAGAATTGCTGCGAAAAGATTTTGAATCACTGTTTCCAGAAGTAGCTAATGGCAAACT
AATGATTCTGACTGTAACACAAAAAATAAGAAATGATATGACTGTTTGGAGTGAAGAAGTAGAAATTGAAAGAGA
AGTGCTCTTAGAAAAGTTTCATCAATGGTGCTAAGGAAATTTGCTATGCTCTTCGAGCTGAGGGTTATTGGGCTGA
CTTTATTGACCCATCATCTGGTTTGGCATTTTTTTGGACCATATACAAACAACACTCTTTTTTGAACCTGATGAACG
CTACCGACATTTAGGATTCTCTGTTGATGACCTTGGATGCTGTAAAGTGATTTCGTCATAGTCTCTGGGGTACCCA
TG TAGTTGTAGGGAGTATCTTCACTAATGCAACACCAGACAGCCATATTATGAAGAAATTAAGTGGAAATTAGCA
GAAATATCCATTCAATTTGCTGTACTATTTGTATGTAATATTTGGGTTGATCTATAAACACTGTCAGACTAAAGTT
TTTAAATATACTTATTTCTAAGTATTTATTTTCTAGCATTTATGAATTTGCAACATTGGCAAGTGATTTGGGATTT
TAAATTTGCAATGTTCAATTTATTCATATCATTGAATACACGTTGAACACATCCACATTGTATAGGATGTGGTAA
TTAGCTTGTAAACCAGGGTATGATCTGCTATTGTTATTTCTCCTCTTTATTGGAAAAAGGCCTCAGTTTTAATTAT
TTTCTTCCCAAATAAATCACACATTTGGTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

952/6881
FIGURE 886

MANVLCNRARLVSYLPGFCSLVKRNVNPKAFSTAGSSGSDESHVAAAPPDICSRTVWPDETMGPFQDQRFQLP
GNIGFDCHLNGTASQKKSLVHKTLPDVLAEPLSSERHEFVMAQYVNEFQGNDAPVEQEINSAETYFESARVECAI
QTCPELLRKDFESLPFEVANGKLMILTVTQTKNDMTVWSEEVEIEREVLLEKFINGAKEICYALRAEGYWADFI
DPSSGLAFFGPYTNNTLFETDERYRHLGFSVDDLGCCKVIRHSLWGTHVVVGSIFTNATPD SHIMKKLSGN

WO 2004/030615

PCT/US2003/028547

953/6881
FIGURE 887

TATCGCAAGCAGCAGTCTCTGGTCCCAGCCCCACCCCATGGCCCCCTCCCAGTCCCAGCACCACCAGCAGTAATAAC
AACAGTAGCAGCAGTAGCAACTCAGGATGGGATCAGCTCAGCAAAACGAACCTCTATATCCGAGGACTGCCTCCC
CACACCACCGACCAGGACCTGGTGAAGCTCTGTCAACCATATGGGAAAATAGTCTCCACAAAGGCAATTTTGGAT
AAGACAACGAACAAATGCAAAGGTTATGGTTTTGTCTGACTTTGACAGCCCTGCAGCAGCTCAAAAAGCTGTGTCT
GCCCTGAAGGCCAGTGGGGTTCAAGCTCAAATGGCAAAGCAACAGGAACAAGATCCTACCAACCTCTACATTTCT
AATTTGCCACTCTCCATGGATGAGCAAGAACTAGAAAAATATGCTCAAACCATTTGGACAAGTTATTTCTACAAGG
ATACTACGTGATTCCAGTGGTACAAGTCGTGGTGTGGCTTTGCTAGGATGGAATCAACAGAAAAATGTGAAGCT
GTTATTGGTCATTTTAATGGAAAAATTTATTAAGACACCACCAGGAGTTTCTGCCCCACAGAACCTTTATTGTGT
AAGTTTGCTGATGGAGGACAGAAAAAGAGACAGAACCCAAACAAATACATCCCTAATGGAAGACCATGGCATAGA
GAAGGAGAGGTGAGACTTGCTGGAATGACACTTACTTACGACCCAACTACAGCTGCTATACAGAACGGATTTTAT
CCTTCACCATAACAGTATTGCTACAAACCGAATGATCACTCAAACCTTCTATTACACCCTATATTGCATCTCCTGTA
TCTGCCTACCAGGTGCAAAGTCCTTCGTGGATGCAACCTCAACCATATATTCTACAGCACCCCTGGTGCCGTGTTA
ACTCCCTCAATGGAGCACACCATGTCACTACAGCCCGCATCAATGATCAGCCCTCTGGCCCAGCAGATGAGTCAT
CTGTCACTAGGCAGCACCGGAACATACATGCCTGCAACGTCAGCTATGCAAGGAGCCTACTTGCCACAGTATGCA
CATATGCAGACGACAGCGGTTCTGTGAGGAGGCAAGTGGTCAACAGCAGGTGGCTGTGAGACGTCATATGAC
CATTCTCCATATACCTTTCAACCTAATAAGTAACTGTGAGATGTACAGAAAGGTGTTCTTACATGAAGAAGGGTG
TGAAGGCTGAACAATCATGGATTTTCTGATCAATTGTGCTTTAGGAAATTATTGACAGTTTGCACAGGTTCTT
GAAAACGTTATTTATAATGAAATCAACTAAACTATTTTGTCTATAAGTTCTATAAGGTGCATAAAACCCTTAAA
TTCATCTAGTAGCTGTTCCCCCGAACAGGTTTATTTTAGTAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

954/6881
FIGURE 888

MAPPSPSTTSSNNNSSSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTKAILDKTTNKCKGYGFV
DFDSPAAAQKAVSALKASGVQAQMAKQQEQDPTNLYISNLPLSMDEQELENMLKPFQVISTRILRDSSGTSRGV
GFARMESTEKCEAVIGHFNGKFIKTPPGVSAPTEPLLCKFADGGQKKRQNPKNYIPNGRPWHREGEVRLAGMTLT
YDPTTAAIQNGFYPSPYSIATNRMITQTSITPYIASPVSAQVQSPSWMQPQPYILQHPGAVLTPSMEHTMSLQP
ASMISPLAQQMSHLSLGGSTGTYMPATSAMQGAYLPQYAHMQTTAVPVEEASGQQQVAVETSNHSPYTFQPNK

WO 2004/030615

PCT/US2003/028547

955/6881
FIGURE 889

AGACTTGGAACCCCAAAGTGTCCGCGACCTGACGGCAGCTCCCTTCCAGCTTCATGGGCAAAGTGTGGAAAC
AGCAGATGTACCCTCAGTACGCCACCTACTATTACCCCCAGTATCTGCAAGCCAAGTTTGGAAAGGCATTTCGGGAA
TACCAAGTGAAAAGGAAGAGTGAAGAACAGAAAAATGTTAGTGGGATGGCAAACACTGTGAACATTGCTGTTTTCT
AGTGGGCCAGAAAAATCAGTCTCTGGTCCCAGCCCACCCCATGGCCCCCTCCAGTCCCAGCACCACCAGCAGTAA
TAACAACAGTAGCAGCAGTAGCAACTCAGGATGGGATCAGCTCAGCAAAACGAACCTCTATATCCGAGGACTGCC
TCCCCACACCACCGACCAGGACCTGGTGAAGCTCTGTCAACCATATGGGAAAATAGTCTCCACAAAGGCAATTTT
GGATAAGACAACGAACAAATGCAAAGGTTATGGTTTTGTGCGACTTTGACAGCCCTGCAGCAGCTCAAAAAGCTGT
GTCTGCCCTGAAGGCCAGTGGGGTTCAGCTCAAATGGCAAAGCAACAGGAACAAGATCCTACCAACCTCTACAT
TTCTAATTTGCCACTCTCCATGGATGAGCAAGAACTAGAAAAATATGCTCAAACCATTTGGACAAGTTATTTCTAC
AAGGATACTACGTGATTCCAGTGGTACAAGTCGTGGTGTGGCTTTGCTAGGATGGAATCAACAGAAAAATGTGA
AGCTGTTATTGGTCATTTTAATGGAAAAATTTATTAAGACACCACCAGGAGTTTCTGCCCCCACAGAACCTTTATT
GTGTAAGTTTGTGATGGAGGACAGAAAAAGAGACAGAACCCAAACAAATACATCCCTAATGGAAGACCATGGCA
TAGAGAAGGAGAGGTGAGACTTGCTGGAATGACACTTACTTACGACCCAACTACAGCTGCTATACAGAACGGATT
TTATCCTTCACCATACAGTATTGCTACAAACCGAATGATCACTCAAACCTTCTATTACACCCTATATTGCATCTCC
TGTATCTGCCTACCAGGTGGCAAAGGAAACCAGAGAAAAACAAGTATCGGGGCTCTGCTATCAAGGTGCAAAGTCC
TTCGTGGATGCAACCTCAACCAATATATTCTACAGCACCCCTGGTGCCGTGTTAACTCCCTCAATGGAGCACACCAT
GTCACTACAGCCCGCATCAATGATCAGCCCTCTGGCCAGCAGATGAGTCATCTGTCACTAGGCAGCACCAGAAC
ATACATGCCTGCAACGTCAGCTATGCAAGGAGCCTACTTGCCACAGTATGCACATATGCAGACGACAGCGGTTCC
TGTTGAGGAGGCAAGTGGTCAACAGCAGGTGGCTGTGAGACGTCTAATGACCATTCTCCATATACCTTTCAACC
TAATAAGTAACTGTGAGATGTACAGAAAGGTGTTCTTACATGAAGAAGGGTGTGAAGGCTGAACAATCATGGATT
TTTCTGATCAATTGTGCTT'FAGGAAATTATTGACAGTTTTGCACAGGTTCTTGAAAACGTTATTTATAATGAAAT
CAACTAAACTATTTTTGCTATAAGTTCTATAAGGTGCATAAAACCCTTAAATTCATCTAGTAGCTGTTCCCCCG
AACAGGTTTATTTTAGTAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

956/6881
FIGURE 890

MAPPSPTTSSNNNSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTKAILDKTTNKCKGYGFV
DFDSPAAAQKAVSALKASGVQAQMAKQQEQDPTNLYISNLPLSMDEQELENMLKPFQVISTRILRDSSGTSRGV
GFARMESTEKCEAVIGHFNGKF IKTPPGVSAPTEPLLCKFADGGQKKRQNPKNYIPNGRPWHREGEVRLAGMTLT
YDPTTAAIQNGFYPSYSIATNRMITQTSITPYIASPVSAYQVAKETRENKYRGS AIKVQSPSWMQPQPYILQHP
GAVLTPSMEHTMSLQPASMISPLAQQMSHLSLGSTGTYPATSAMQAYLPQYAHMQTTAVPVEEASGQQQVAVE
TSNDHSPYTFQPNK

WO 2004/030615

PCT/US2003/028547

957/6881
FIGURE 891

GGCTAATGTAACATACTCTACCACTTGGTCTGAAGCCCAGCAGTATCTGATGGATAATCCAACTTTTGCAGAAGA
TGAGGAGTTACAAAATATGGACAAAGAAGATGCATTAATTTGCTTTGAAGAACACATTTCGGGCTTTAGAAAAGGA
GGAAGAAGAAGAAAAACAGAAGAGTTTGCTGAGAGAAAGGAGACGACAGCGAAAAAATAGGGAATCTTTCCAGAT
ATTTTTAGATGAATTACATGAACATGGACAACTGCATTCTATGTCATCTTGGATGGAATTGTATCCAACATTAG
TTCTGATATTAGATTCACTAATATGCTTGGTCAGCCTGGATCAACTGCATTGATCTTTTCAAGTTTTATGTTGA
GGATCTTAAAGCACGTTATCATGACGAGAAGAAGATAATAAAAGACATTCTAAAGGATAAAGGATTTGTAGTTGA
AGTAAACACTACTTTTGAAGATTTTGTGGCGATAATCAGTTCAACTAAAAGATCAACTACATTAGATGCTGGAAA
TATCAAATTGGCTTTCAATATTACTAGAAAAGGCAGAAGCCCGTGAACGTGAAAGAGAAAAAGAAGAGGCTCGGA
AGATGAAACGAAAAGAATCTGCATTTAAGAGTATGTTAAACAAGCTGCTCCTCCGATAGAATTGGATGCTGTCT
GGGAAGATATCCGTGAGAGATTTGTAAAAGAGCCAGCATTTGAGGACATAACTCTAGAATCTGAAAGAAAACGAA
TATTTAAAGATTTTATGCATGTGCTTGAGCATGAATGTCAGCATCATCATTCAAAGAACAAGAAACATTCTAAGA
AATCTAAAAAACATCATAGGAAACGTTCCCGCTCTCGATCGGGGTGAGATTGAGATGATGATAGCCATTCAA
AGAAAAAAGACAGCGATCAGAGTCTCGTTCTGCTTCAGAACATTCTTCTAGTGCAGAGTCTGAGAGAAGTTATA
AAAAGTCAAAAAAGCATAAGAAGAAAAGTAAGAAGAGGAGACATAAATCTGACTCTCCAGAATCCGATGCTGAGC
GAGAGAAGGATAAAAAAGAAAAGATCGGGAAAGTGAAAAAGACAGAACTAGACAAAGATCAGAATCAAAACACA
AATCGCCTAAGAAAAAGACTGGAAAGGATTCTGGTAATTGGGATACTTCTGGCAGCGAACTGAGTGAAGGGGAAT
TGGAAAAGCGCAGAAGAACCCTTTTGGAGCAACTGGATGATGATCAATAAATTATACCAAATATATGTTTACAGT
ATGATTTAAAGTCTGATTTCAGACCAGGGACTCTATTTTAAAGTTCAACTGAAATAACACTGGGTTTTAATTATATC
ACAGGAAAAAAAAGTGCATTTAAGTATTGTTATCGTGGACTTTATAAAAGCAAAGGAAATTGAAAGTAACTTTT
GATTCTGTATCAAGAATCATATTTTCATACAGTCATAACTGTCTTTCTGTGACCCCTTTCACAGGGCACTGTAGGA
TGGATTAAAGGTGGCAATTTACTGATAACTGCAGATGTCTCTACTTTGTTCTAAAATCTAAGTCATGAGGTGATT
TGATTTACTTTTATAGAAGCTGGATTTTGAAGATCTAATGAAAAATTTTTTGATAATATAGTAGTACAAAAAAGC
ACCAGCAACTGATAAAAATTGCTTTTTTGTGCGCTACCCAACCTGGTTAAAGCCAATGTGATCTTTTATGGTGAAA
CTCCTAAGAAACAGGTGGTTTTGCTGGAACTTGGTAGACCCTTAATTATAGTGGTGCTAATGAGCACTACTGTA
ATATAAAGCCACCATTATTTTTTATCAAACATCTGAATACATTTTACAAAGGCTATTGTGAGGGCATTATTTTGA
GCATCTATTTGAGGTGATGTTTAAAAAACTTTAACATCAAATCAAATTGTAAATTAATTTAAATATATTGCCT
TAAGGACCTACTAAAGAATGTGCCACCAGACTTTAAGTGATAGTTGCAATATCCTTGCTCAAAAAAAAAAAAAA
GTTGACTTAAACATTTTCTTTAACAGTTGTCTTTTTTTCTAAATTCAGTCTTCTCTTGCTTTTTTTTCCCTGC
TATTGAGGAAGTATTTTGCCTTCCCTACTCACTGAGAAGTATTGACTTCGTGGTACACATTCTAAAGCATTCTG
ATTTGAATATTTTGTACATTTTATCAATTATTAAACCTTCTCTCTAGTG

WO 2004/030615

PCT/US2003/028547

958/6881
FIGURE 892

MLEISNWLSILLEKAEAREREREKEEARKMKRKESAFKSMKQAAPPIELDAVWEDIRERFVKEPAFEDITLESE
RKRIFKDFMHVLEHECQHHSKNKKHSHKSKKHHRKRSRSGSDSDDDSHSKKKRQRSESRASEHSSSAESE
RSYKSKKHKKKSKKRRHKSDSPESDAEREKDKKEKDRESEKDRTRQRSESKHKSPKKKTGKDSGNWDTSGSELS
EGELEKRRRTLLEQLDDDQ

WO 2004/030615

PCT/US2003/028547

959/6881
FIGURE 893

CCAGCACGCGGCCGCTCTGGCCAGGGAAGTCCCTGTCCTTACCTTCAGCAGGAGCCGGTTCCCTGTGTGTGTGT
CCGCTCGCCCTCTGCTCCGTCTGCGGCTGCCACTGCCCTCCTACGGTCCACCATGGCCCTGCTGCACTCCGGC
CGCGTCTCCCGGGATCGCCGCCGCCCTTCCACCCGGGCTCGCCGCCGCGGCTCTGCCAGAGCCAGCTCCTGG
TGGACCCATGTGGAAATGGGACCTCCAGATCCCATTTCTGGGAGTCACTGAAGCCTTTAAGAGGGACACCAATAGC
AAAAAGATGAATCTGGGAGTTGGTGCCTACCGGATGATAACGGAAAGCCTTACGTGCTGCCTAGCGTCCGCAAG
GCAGAGGCCAGATTGCCGCAAAAAATTTGGACAAGGAATACCTGCCCATTTGGGGGACTGGCTGAATTTTGCAAG
GCATCTGCAGAACTAGCCCTGGGTGAGAACAGCGAAGTCTTGAAGAGTGGCCGGTTTGTCACTGTGCAGACCATT
TCTGGAAGTGGAGCCTTAAGGATCGGAGCCAGTTTCTGCAAGATTTTTTAAGTTTACGCCGAGATGTCTTTCTG
CCCAAACCAACCTGGGGAAACCACACACCCATCTTCAGGGATGCTGGCATGCAGCTACAAGGTTATCGGTATTAT
GACCCCAAGACTTGCGGTTTTGACTTCACAGGCGCTGTGGAGGATATTTCAAAAATACCAGAGCAGAGTGTTCTT
CTTCTGCATGCCTGCGCCACAATCCCACGGGAGTGGACCCGCGTCCGGAACAGTGGAAGGAAATAGCAACAGTG
GTGAAGAAAAGGAATCTCTTTGCGTTCTTTGACATGGCCTACCAAGGCTTTGCCAGTGGTGATGGTGATAAGGAT
GCCTGGGCTGTGCGCCACTTCATCGAACAGGGCATTAAATGTTTGTCTCTGCCAATCATATGCCAAGAACATGGGC
TTATATGGTGAGCGTGTAGGAGCCTTCACTATGGTCTGCAAGATGCGGATGAAGCCAAAAGGGTAGAGTCACAG
TTGAAGATCTTGATCCGTCCCATGTATTCCAACCTCCCTCAATGGGGCCCGGATTGCTGCTGCCATTCTGAAC
ACCCAGATTTGCGAAAACAATGGCTGCAAGAAGTGAAAGGCATGGCTGACCGCATCATTGGCATGCGGACTCAA
CTGGTCTCCAACCTCAAGAAGGAGGGTTCCACCCACAATTGGCAACACATACCGACCAAATTGGCATGTTCTGT
TTCACAGGGCTAAAGCCTGAACAGGTGGAGCGGCTGATCAAGGAGTTCTCCATCTACATGACAAAAGATGGCCGC
ATCTCTGTGGCAGGGGTCACCTCCAGCAACGTGGGCTACCTTGCCCATGCCATTACACAGGTCACCAAGTAATGT
CCCTGGTGCGAGGAAACAGAGACAACCTTTCTGTCTTCAGCCTCTGCTATTGAGAGCTTCACACAGACAATGAGA
GAGGGTGGATGGTGGTGAGTGGATCATTCTTTTCAGCCACAGTGTGTAACACTCAGCATTGTAATGTTTCTCAGA
AAAGAACATGTAGTGACACAGGGCAGAGGCATCCATGGCTGGCGTCTGGAATATTAAACCAAACCTCTCCCCGGTC
CTTTTTCTCCAACCTTTCTCAAAGAGTTTACATGTGCAAGAAAGTCATCGCACCAAAAAACCTGTCAATTATGC
CATTGCAATATTTGAGAAGCTTTAACTGAAGTGTGAGGTTCCCTCGTGAGAAACAGCACACGTTAGAGGCTTTGAG
AGAAGGCCCTAGTTCTGTCTAGTAGTCGGCCTCGTGTCTGTCTCTCCCATCTTGGAACAACCTTATCAACAGGCC
GCACTGCAGAAATGATGTTTTATGAAAACCAATGAGGCTGCTGCCACTCCAGCAAGGGAAATAATGCAGTTTCCT
GTCTTATTTAAGAAAAAGAGAAGGCTCTCTTTCTCCCTTGTCATTGCCGTTCTTTTCTTACACGCAAAGATTT
TTAACTATTGCAGATTTTCATCCCATCTACTGCTTGATTGACCATCAACTCCATCCTATCGAGATTTATTTAA
GAATGAAGAACATAATTTTCTGCTGATGCGGTACCTCACCTTTTCAGCAAAGAATAGTGGAGAGTAGGAACT
GTACTTTATCTCGGCATCCTCTTGAATGATAGTGCAAGTTTCTCCAGTTGGGATGTTGTCTCTGCCCGGTTGGAC
CTCTCCCTTTGTTGAATGTGGTGTGCAGCCTCTCATCTCACACTGTGAGTCCAGCGGCGAGGGTGGTACCAGG
AAAGAGGATATTCTAGGCTTTGCGTGCTGCTAGCTGGGTTACGGCTTCACCCACTGGAAAGAACCACCATCTGCT
CTAACCATGTAGACTTATTGCGGCCTGGTTTCTCTGTTACAATAAAATTACTGTAGACCC

WO 2004/030615

PCT/US2003/028547

960/6881
FIGURE 894

GAGTGACTCCACCGCCCGGAGCAGCGGTGCAGGACGCGCGTCTCCGCCGCCCGCGGTGACTTCTGCCTGCGCTCC
TTCTCTGAACGCTCACTTCCGAGGAGACGCCGACGATGAAGACACCGTGGAAGGTTCTTCTGGGACTGCTGGGTG
CTGCTGCGCTTGTACCATCATCACCGTGCCCGTGGTTCTGCTGAACAAAGGCACAGATGATGCTACAGCTGACA
GTCGCAAACTTACACTCTAACTGATTACTTAAAAATACTTATAGACTGAAGTTATACTCCTTAAGATGGATTT
CAGATCATGAATATCTCTACAAACAAGAAAAATAATATCTTGGTATTCAATGCTGAATATGGAACAGCTCAGTTT
TCTTGGAGAACAGTACATTTGATGAGTTTGGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTA
TTCTCTTAGAATACAACACTACGTGAAGCAATGGAGGCATTCCACACAGCTTCATATGACATTTATGATTTAAATA
AAAGGCAGCTGATTACAGAAGAGAGGATTCCAAACAACACACAGTGGGTACATGGTCACCAGTGGGTACATAAT
TGGCATATGTTTGAACAATGACATTTATGTTAAAAATTGAACCAAATTTACCAAGTTACAGAATCACATGGACGG
GGAAAGAAGATATAATATATAATGGAATAACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGCTC
TGTGGTGGTCTCCAAACGGCACTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCCTTATTGAATACT
CCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAGGCAGGAGCTGTGAATC
CAACTGTAAAGTTCTTTGTTGTAATAACAGACTCTCTCAGCTCAGTCACCAATGCAACTTCCATACAAATCACTG
CTCCTGCTTCTATGTTGATAGGGGATCACTACTTGTGTGATGTGACATGGGCAACACAAGAAAGAAATTTCTTTGC
AGTGGCTCAGGAGGATTGAGAACTATTCGGTCATGGATATTTGTGACTATGATGAATCCAGTGGAAAGATGGAAC
GCTTAGTGGCACGGCAACACATTGAAATGAGTACTACTGGCTGGGTTGGAAGATTTAGGCCTTCAGAACCTCATT
TTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAAGAAGGTTACAGACACATTTGCTATTTCCAAA
TAGATAAAAAAGACTGCACATTTATTACAAAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAAGTGATT
ATCTATACTACATTAGTAATGAATATAAAAGGAATGCCAGGAGGAAGGAATCTTTATAAAATCCAACCTTAGTGACT
ATACAAAAGTGACATGCCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTGAGTACTATTCTGTGTCTCATTGATGATA
AGGCGAAGTATTATCAGCTGAGATGTTCCGGTCTGGTCTGCCCCCTCTACTCTACACAGCAGCGTGAATGATA
AAGGGCTGAGAGTCTGGAAGACAATTCAGCTTTGGATAAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAAC
TGGACTTCATTATTTGAATGAAACAAAATTTTGGTATCAGATGATCTTGCCTCCTCATTGATAAAATCCAAGA
AATATCCTCTACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAAGCAGACACTGTCTTCAGACTGAAGTGGG
CCACTTACCTTGCAAGCACAGAAAACATTATAGTAGCTAGCTTTGATGGCAGAGGAAGTGGTTACCAAGGAGATA
AGATCATGCATGCAATCAACAGAAGACTGGGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCCAGACAATTTT
CAAAAATGGGATTTGTGGACAACAAACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATGG
TCCTGGGATCGGGAAGTGGCGTGTCAAGTGTGGAATAGCCGTGGCGCCTGTATCCCGGTGGGAGTACTATGACT
CAGTGACACAGAACGTTACATGGGTCTCCCACTCCAGAAGACAACCTTGACCATTACAGAAATTCACAGTCA
TGAGCAGAGCTGAAAATTTTAAACAAGTTGAGTACCTCCTTATTTCATGGAACAGCAGATGATAACGTTCACTTTC
AGCAGTCAGCTCAGATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGAAG
ACCATGGAATAGCTAGCAGCACAGCACACCAACATATATATACCCACATGAGCCACTTCATAAAACAATGTTTCT
CTTTACCTTAGCACCTCAAAATACCATGCCATTTAAAGCTTATTAAAACTCATTGTTTGTCTTCTTCTTCTTAA
CTGCACTGTCAAGATGATGATGATCTTTAAATAACACACTCAAATCAAGAACTTAAGGTTACCTTGTCTCCAA
ATTTACATACCTATCATCTTAAGTAGGGACTTCTGTCTTCAACACAGATTATTACCTTACAGAAGTTTGAATTATC
CGGTGCGGTTTTATTGTTTAAATCATTCTGATCAGCTGCTGAAACAACAAATAGGAATTGTTTTTATGGAGG
CTTTGCATAGATTCCCTGAGCAGGATTTTAACTCTTTTCTAACTGGACTGGTTCAAATGTTGTTCTCTTCTTAA
AGGGATGGCAAGATGTGGCAGTGATGTCACTAGGGCAGGGACAGGATAAGAGGGATTAGGGAGAGAAGATAGCA
GGGCATGGCTGGGAACCAAGTCCAAGCATACCAACACGAGCAGGCTACTGTGAGCTCCCCTCGGAGAAGAGCTG
TTCACAGCCAGACTGGCACAGTTTTCTGAGAAAGACTATTCAAACAGTCTCAGGAAATCAAATATGCAAAGCACT
GACTTCTAAGTAAAACACAGCAGTTGAAAAGACTCCAAAGAAATGTAAGGGAAACTGCCAGCAACGCAGGCCCC
CAGGTGCCAGTTATGGCTATAGGTGCTACAAAAACACAGCAAGGGTGATGGGAAAGCATTGTAAATGTGCTTTTA
AAAAAAAATACTGATGTTCTAGTGAAAGAGGCAGCTTGAAGTGAAGTGTGAACACATCAGCTTGCCCTGTAA
AAGATGAAAATATTTGTATCACAAATCTTAACCTGAAGGAGTCTTGCATCAATTTTTCTTATTTCTTTTG
AGTGTCTTAATTAAGAATATTTTAACTTCTTGGACTCATTGTTAAAAATGGAACATAAAATACAATGTTATG
TATTATTATTTCCATTCTACATACTATGGAATTTCTCCAGTCATTTAATAAATGTGCCTTCATTTTTTC

WO 2004/030615

PCT/US2003/028547

961/6881
FIGURE 895

MKTPWKVLLGLLGAAALVTIITVPVLLNKGTDATADSRKTYTLTDYLNKNTYRLKLYSLRWISDHEYLYKQENN
ILVFNAEYGNSSVFLENSTFDEFGHSINDYSISPDGQFILLEYNVVKQWRHSYTASYDIYDLNKRQLITEERIPN
NTQWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIYNGITDWVYEEEVFSAYSALWWSPNGTFLAY
AQFNDTEVPLIEYSFYSDSLQYPKTVRVPYPKAGAVNPTVKFFVNTDSLSSVTNATSIQITAPASMLIGDHYL
CDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWNCLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKII
SNEEGYRHICYFQIDKKDCTFITKGTWEVIGIEALTSDYLYYISNEYKGMPPGGRNLYKIQLSDYTKVTCLSCELN
PERCQYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFIILNETKFW
YQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASFDGRGSGYQGDKIMHAINRRLGT
FEVEDQIEAARQFSKMGFVDNKRIAIWGSYGGYVTSMVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPT
PEDNLDHYRNSTVMSRAENFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDVQAMWYTDEDHGIASSTAHQH
IYTHMSHFIKQCFSLP

WO 2004/030615

PCT/US2003/028547

962/6881
FIGURE 896

GTTTGAAATCGGAAAGTTGGCGGGGCTGCGGGAGCTGAGCCTAGAGTCCGGCTGTTGGCTAGAGTGGGCGCGGAT
CTGGTGTGGGGAAGGCGGCGGGACTCAGGCCTGCCTGCCAAGCATTGTCTACATAATGCTAGAGGACGAACTGG
CACTTTTCGATAAAAGCATAAATGAATTTTGGAATAAATTCAAAAGTACGGACACCTCCTGTGATGCGGGGAC
TAAGAGATACCTACAAGGATTCCATCAAAGCATTTCAGAGAAAAGCTGTCTGTGAAATTAAAGGAAGAAGACGAA
TGGTTGAGATGTTTCTGGAATATCAAATCAGATCAGCAGGCAAAATAAGCTCATTCAAGAAAAAAGGATAACT
TGTTAAAATTGATTGCTGAAGTAAAGGCAAAAGCAGGAATTGGAAGTACTGACTGCAAATATCCAGGATCTTA
AGGAAGAATATTCTAGGAAGAAGGAACTATTTCTACTGCTAATAAAGCGAATGCAGAGAGGTTGAAAAGGCTGC
AGAAATCTGCAGACTTGTATAAAGATCGACTTGGACTAGAAATTCGAAAAATTTATGGTGAGAAATTGCAGTTTA
TTTTCACTAATATTGACCCTAAGAATCCTGAGAGCCCATTTATGTTTTCTTACATCTCAATGAAGCAAGGGACT
ATGAAGTGTGAGATAGTCCCCCTCATCTTGAGGGCCTAGCAGAATTTCAAGAGAATGTAAGGAAGACCAACAATT
TTTCAGCTTTTCTTGCCAATGTTGCGAAAGCTTTTACTGCCACGGTTTATAATTAAACATACAAATAGTGTATATA
AAAACGGTTTATTTTCTTCTCTATTACATATCTTTTTTTTTCTTGTTTTATTATTACTATACTTTAAGTTTT
AGGGTACATGTGCACAATGTGCAGGTTTGTTACATATGTATACATGTGCCATATTGGTGTGCTGCACCCATTAAAC
TCGTCAATTCATTAGGTATATCTCCTAATGCTATCECTCCCCCTCCCCCAACCCACAACAGTCCCGTTGTGTG
ATGTTCCCTTCTGTGTCCATGTGTTCTCATTGTTCAATTTCCACCTAGGAGTGAGAATATGTGGTGTGTTGGTT
TTTTGTCCTTCGATAGTTTGCTGAGAATGATGGTTTCCAGCTTCATCCATGTTTCTTAAAGGACATGAACTCA
TCCTTTTTTATGGCTGCATAGTATCCATGGTGTATATGTGCCACATTTTCTTAATCCAGTCTATCATTGTTGGA
CATTTGGGTTGGTTCCAAGTCTTTGCTATTGTGAATAGTGCCGAAATAAACATACGTGTGCATGTGTCTCCAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

963/6881
FIGURE 897

MVEDELALFDKSINEFWNKFKSTDTSQCMAGLRDITYKDSIKAFKAEKLSVKLKEEERMVEMFLEYQNQISRQNKLI
QEKKDNLLKLIAEVKGKKQELEVLTANIQDLKEEYSRKKETISTANKANAERLKRLQKSADLYKDRLGLEIRKIY
GEKLQFIFTNIDPKNPESPFMFSLHLNEARDYEVSDSAPHLEGLAEFQENVRKTNNFSAFLANVRKAFTATVYN

WO 2004/030615

PCT/US2003/028547

964/6881
FIGURE 898

AAGCACAGGCCACCACTCTGCCCTGGTCCACACAAGCTCCGGTAGCCCCATGGAGCCCTGGCCTCTCCTCCTGCTC
TTTAGCCTTTTGCTCAGCTGGCCTCGTCCTGGGCTCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGAC
TACAGCAGCGTGGTGGGCCAGTGGAAGACCACCGCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAG
CTCATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGGGTGGATTACAAC
CTAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTACATTCTTCAGAAAAGATCTGGCGCCCAGAC
CTTGTTCTCTATAACAATGCAGATGGTGACTTTGCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGC
CACATCACGTGGACACCTCCAGCCATCTTTAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAA
CAGAACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCTGGCCATCAACCCGGAAAGCGACCAG
CCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAGTCCCGGGGCTGGAAGCACTCCGTGACC
TATTCCTGCTGCCCCGACACCCCTACCTGGACATCACTACCACTTCGTTCATGCAGCGCCTGCCCTCTACTTC
ATCGTCAACGTCATCATCCCCCTGCCTGCTCTTCTCCTTCTTAAGTGGCCTGGTATTCTACCTGCCACAGACTCA
GGGAGAAGATGACTCTGAGCATCTCTGTCTTACTGTCTTTGACTGTGTTCTTCTGGTCATCGTGGAGCTGATC
CCCTCCACGTCCAGTGCTGTGCCCTTGATTGGAAAATACATGCTGTTACCATGGTGTTCGTTCATTGCCTCCATC
ATCATCACTGTTCATCGTCATCAACACACACCACCGCTCAGCCAGCACCCATGTCATGCCCACTGGGTGCGGAAG
GTTTTTATCGACACTATCCCAAATATCATGTTTTTCTCCACAATGAAAAGACCATCCAGAGAAAAGCAAGACAAA
AAGATTTTACAGAAGACATTGATATCTCTGACATTTCTGGAAAGCCAGGGCCTCCACCCATGGGCTTCCACTCT
CCCCTGATCAAACACCCCGAGGTGAAAAGTGCCATCGAGGGCATCAAGTACATCGCAGAGACCATGAAGTCAGAC
CAGGAGTCTAACAATGCGGCGGCAGAGTGGAAGTACGTTGCAATGGTGATGGACCACATACTCCTCGGAGTCTTC
ATGCTTGTTTGCATCATCGGAACCCCTAGCCGTGTTTGCAGGTCGACTCATTGAATTAAATCAGCAAGGATGAGCA
GAAAATGAGCTGAGCTTAGCTCTGCCCTGGAACCTACCAGAGCAGAGAAGGGCAGGAGAGGAAGATTTGTCTACT
TGCTCCACTCGCACTTATCAAACGTGTTATATCCATACTTATTATTGATGATAAGATTTACCTTTATGTAAGTT
TATGGCCTTGAAGTGTTTTCATATTGCTTCTCCCTTTAGTTCTGCTGTCTCCCTGAAGAGTGAACCCTCTTTAGT
AAATGAACTAATCACT

WO 2004/030615

PCT/US2003/028547

965/6881
FIGURE 899

MEPWPLLLLFSLCSAGLVLGSEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLIQLINVDEVNQIVTTNVR
LKQQWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTPPAIFKSYCEI
IVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHF
VMQRLPLYFIVNVIIPCLLFSFLTGLVFYLPDTSGEKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGKYMFL
TMVFVIASIIITVIVINTHHRSPSTHVMPNWRKVFIDTIPNIMFFSTMKRPSREKQDKKIFTEDIDISDISGKP
GPPPMGFHSPLIKHPEVKSAIEGIKYIAETMKSDQESNNAAEWKYVAMVMDHILLGVFMLVCIIGTLAVFAGRL
IELNQQG

WO 2004/030615

PCT/US2003/028547

966/6881
FIGURE 900

GTTCGCAGCCGCCGCCGCCGCCGCTCGCTCTCCAACGCCAGCGCCGCCCTCTCGCTCGCCGAGCTCCAGCCGAAG
GAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACTGCCCCGAAATCGACCGGTGGT
AAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCT
CATCGTTACAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTTCGC
AAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTGCGCTTCCAGAGCGCAGCT
ATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTGAAGACACCAACCTGTGTGCTATCCAT
GCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGGAGAACGTGCTTAAGAATCC
ACTATGATGGGAAACATTTTCTCAAAAAAAAAAAAAAAAAATTTCTCTTCTCCTGTTATTGGTAGTTCTGAAC
GTTAGATATTTTTTTTCCATGGGGTCAAAAGGTACCTAAGTATATGATTGCGAGTGAAAAATAGGGGACAGAAA
TCAGGTATTGGCAGTTTTTCCATTTTCAATTTGTGTGTGAATTTTAAATAAATGCGGAGACGTAAAGCATTAAAT
GCAAGTTAAATGTTTCAGTGAACAAGTTTCAGCGGTTCAACTTTATAATAATTATAAATAAACCTGTTAAATTT
TTCTGGACAATGCCAGCATTGGATTTTTTAAACAAGTAAATTTCTTATTGATGGCAACTAAATGGTGTTTGT
AGCATTTTTATCATAAGTAGATTCCATCCATTCATACTTTTCTAACTGAGTTGCTTACATGCAAGTACAT
GTTTTTAATGTTGTCTGTCTTCTGTGCTGTTCTGTAAAGTTTGCTATTAAATACATTAACTAT

WO 2004/030615

PCT/US2003/028547

967/6881
FIGURE 901

CGCCGAGCTCCAGCCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACTGC
CCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGCAAGAGTGCGCCCTCTAC
TGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTC
CACTGAACTTCTGATTCGAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCT
GCGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGACAC
CAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGG
AGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTTCATTCTCTCCATGGGGTCAAAGGTACCTAAGTATAT
GATTGCGAGTGGAAA

WO 2004/030615

PCT/US2003/028547

968/6881

FIGURE 902

MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREI
AQDFKTDLRFSAAIGALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

WO 2004/030615

PCT/US2003/028547

969/6881
FIGURE 903

CAGCCGTTGAGGGGACGGGCCTGCGTTCTCTCCTCCTCCTCCCCGCCTCCAGCTGCCGGCAGGACCTTTCTCTC
GCTGCCGCTGGGACCCCGTGTCATCGCCCAGGCCGAGCACGATGCCCCCTAAAAAGGGAGGTGATGGAATTAAC
CACCCCCAATCATTGGAAGATTTGGAACCTCACTGAAAATTGGTATTGTTGGATTGCCAAATGTTGGGAAATCTA
CTTTCTTCAATGTGTTAACCAATAGTCAGGCTTCAGCAGAAAACTTCCCGTTCTGCACTATTGATCCTAATGAGA
GCAGAGTACCTGTGCCAGATGAAAGGTTTGACTTTCTTTGTCAATACCACAAACCAGCAAGCAAAATTCCTGCCT
TTCTAAATGTGGTGGATATTGCTGGCCTTGTAAGGAGCTCACAATGGGCAGGGCCTGGGGAATGCTTTTTTAT
CTCATATTAGTGCCGTGTGATGGCATCTTTTCATCTAACACGTGCTTTTGAAGATGATGATATCACGCACGTTGAAG
GAAGTGTAGATCCTATTCGAGATATAGAAAATAATACATGAAGAGCTTCAGCTTAAAGATGAGGAAATGATTGGGC
CCATTATAGATAAACTAGAAAAAGGTGGCTGTGAGAGGAGGAGATAAAAACTAAAACCTGAATATGATATAATGT
GCAAAGTAAATCCTGGGTTATAGATCAAAAAGAACCTGTTGCTTCTATCATGATTGGAATGACAAAGAGATTG
AAGTGTGAATAAACACTTATTTTTGACTTCAAAAACCAATGGTCTACTTGGTTAATCTTTCTGAAAAAGACTACA
TTAGAAAGAAAAACAAATGGTTGATAAAAAATTAAAGAGTGGGTGGACAAGTATGACCCAGGTGCTTTGGTCATT
CTTTTAGTGGGGCCTTGGAACCTCAAGTTGCAAGAATTGAGTGCTGAGGAGAGACAGAAGTATCTGGAAGCGAACA
TGACACAAAGTGCTTTGCCAAAGATCATTAAGGCTGGGTTTGCAGCACTCCAAGTAACTAGAACTTTTCACTGCAG
GCCAGATGAAGTGCGTGATGGACCATCAGGAAAGGGACTAAGGCTCCTCAGGCTGCAGGAAAGATTACACAG
ATTTTGAAAAGGGATTCAATTATGGCTGAAGTAATGAAATACGAAGATTTTAAAGAGGAAGGTTCTGAAAATGCAG
TCAAGGCTGCTGGAAAGTACAGACAACAAGGCAGAAATTATATTGTTGAAGATGGAGATATTATCTTCTTCAAAT
TTAACACACCTCAACAACCGAAGAAGAAATATAATTTAGTTATTGCTCAGATAAACATACAACCTTCCAAAAGGCA
TCTGATTTTTAAAAAATTAAAAATTTCTGAAAACCAATGCGACAAATAAAGTTGGGGAGATGGGAATCTTTGACAA
ACAAATTATTTTTATTTGTTTTAAATTAATACTGTGTACCCCCCCCCCCCCATGAAATGCAGGTTCACTAAA
TGTGAACAGCTTTGCTTTTCACGTGATTAAGACCCTACTCCAAATTGTAGAAGCTTTTCAGGAACCATATTACTC
TCATGATACTTCATTAATCTCCATCATGTATGCCAAGCCTGACACATTTGACAGTGAGGACAATGTGGCTTGCTC
CTTTTGAATCTACAGATAATGCATGTTTTACAGTACTCCAGATGTCTACACTCAATAAAACATTTGACAAAACC
AAAAAFAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

970/6881
FIGURE 904

MPPKKGGDGIKPPPIIGRFGTSLKIGIVGLPNVGKSTFFNVLTNSQASAENFPFCTIDPNESRVVPVDERFDFLC
QYHKPASKIPAFNLNVVDIAGLVKGAHNGQGLGNAFLSHISACDGIFHLTRAFEDDDITHVEGSVDPIRDIEIIHE
ELQLKDEEMIGPIIDKLEKVAVRGGDKKLKPEYD IMCKVKSWVIDQKKPVRFYHDWNDKEIEVLNKHFLFTSKPM
VYLVNLSEKDYIRKKNKWLIIKEWVDKYDPGALVIPFSGALELKLQELSAEERQKYLEANMTQSALPKIIKAGF
AALQLEYFFTAGPDEVRAWTIRKGTKAPQAAGKIHTDFEKGFI MAEVMKYEDFKEEGSENAVKAAGKYRQQGRNY
IVEDGDIIFFKFNTPPQPKKK

WO 2004/030615

PCT/US2003/028547

971/6881
FIGURE 905

CTGCCAGCCGCGCTGCTGCTGCTCCTCCTGCTGTGGGACCGCTGACCGCGCGGGCTGCTCCGCTCTCCCCGCTCCA
AGCGCCGATCTGGGCACCCGCCACCAGCATGGACGCTCGCCGCGTGCCGCAGAAAGATCTCAGAGTAAAGAAGAA
CTTAAAGAAATTAGATATGTGAAGTTGATTTCCATGGAGACCTCGTCATCCTCTGATGACAGTTGTGACAGCTT
TGCTTCTGATAATTTTGCAAAACACGAAACCTAAATTAGGTGAGATATCAGTGAAGAACTGGCAAGTGTTTTTTA
TGAGGACTCTGATAATGAATCTTTCTGCGGCTTTTCAGAAAGTGAGGTGCAAGATGTATTAGACCATTGTGGATT
TTTACAGAAACCAAGGCCAGATGTCACTAACGAACCTGGCCGGTATTTTTTCATGCCGACTCTGACGATGAATCATT
TTGCGGTTTTCTCAGAGAGTGAGATACAAGATGGAATGAGGCTGCAGTCAGTTCGGGAAGGCTGTAGGACCCGCAG
CCAGTGCAGGCACTCTGGACCTCTCAGGGTGGCGATGAAGTTTCCAGCGCGGAGTACCAGGGGAGCAACCAACAA
AAAAGCAGAGTCCCGCCAGCCCTCAGAGAATTCTGTGACTGATTCCAACCTCCGATTGAGAAGATGAAAGTGGAAT
GAATTTTTTGGAGAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAAACTCATGTCTGAATTAGA
AAGCTTCCCTGGCTCGTTCCGTGGAAGACATCCCTCCCAGGCTCCGACTCACAATCAAGGAGACCGCGAAGGCG
TACATTTCCCGGTGTTGCTTCCAGGAGAAACCTGAACGGAGAGCTCGTCTCTTACCAGGTCAAGGTCCCGGAT
CCTCGGGTCCCTTGACGCTCTACCCATGGAGGAGGAGGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAA
GACCGTGGATGGCTACATGAATGAAGATGACCTGCCCAGAAGCCGTCGCTCCAGATCATCCGTGACCCTTCCGCA
TATAATTCGCCCAGTGGAGAAATACAGAGGAGGAGTTGGAGAACGCTCTGCAGCAATTCTCGAGAGAAGATATA
TAACCGTTCACTGGGCTCTACTTGTCAATGCCGTGAGAAGACTATTGATACCAAAACAACTGCAGAAACCC
AGACTGCTGGGCGTTTCGAGGCCAGTTCTGTGGCCCTGCCTTCGAAACCGTTATGGTGAAGAGGTGAGGGATGC
TCTGCTGGATCCGAACCTGGCATTGCCCGCCTTGTGAGGAATCTGCAACTGCAGTTTCTGCCGGCAGCGAGATGG
ACGGTGTGCGACTGGGGTCTTGTGATTTAGCCAAATATCTGGAAAATTTGCTGCCTGCCTTCTACTTCTCAAATCTTTC
CCTGAAACAGGAATTTGAAATGCAAGCATAATATCTGGAAAATTTGCTGCCTGCCTTCTACTTCTCAAATCTTTC
TTGTAAAAGTTTCCAATTTTCTACTGAAACCTGAGTTAAAAATCTTGATGATCAGCCTGTTTCTATAAGAACTC
CAATCAAGTTAATCTTAGCAGACATGTGTTTCTGGAGCATCACAGAAGGTATATTGCTAGTTACACTTTGCCCTC
CTGCAGTTTCTTCTGCTCCCAACCCCATCTCATAGCATCCCCCTCTATTTCCAATGCTCCTCTCCAACCGCT
TAGTTTCTGAATTTCTTTTAAATTACAGTTTTATGAAAGCATATTTTATTTACTTGGTGTTGAAATAGCCCTCAT
AAAACCTAAGCACTTGGAACACAATAATAGTATTAATACTAAGATCTATTGAATTTAGAGAAGAGCCTTCTA
ACTTGTTTACACAAAAACGAGTATGATTTAGCATTCTACTAGTTGAAATTTTTAATAGAATCAAGGCACAAAAG
TCTTAAAACCATGTGGAAAAATTAGGTAATTATTGCAGATTGATGTCTCTCAATCCCATGTATTGCGCTTATGTT
ACAAGTTGTTGTCACAGTTGAGACTTAATTTCTCCTAATTTCTTCTGCCCGAAGGGTAAGTGGTGCGTCCAGCTT
ACACAATCATAATTCAAAGGTTGGTGGGCAATGTAATACTTAATTAATAATGATGGAAGAGCTATCTGGAGAT
TATGAGTAAGCTGATTTGAATTTTCAAGTATAAACTTTAGTATAATTGTAGTTTGCAAAGTTTATTTAGTTTAC
ATGTAAGGTATTGCAATAAAATCTTGACAATTTTGTATGGAACTTGATATTAAAACTAGTCTGTGGTTCTT
TGCAGTTTCTTGTAATTTTATAAACCAGGCACAAGGTTCAAGTTTATGATTTTAAAGCACTTTTATAACAATGATAA
GTGCCTTTTTGGAGATGTAACTTTTCAGAGTTTGTAACTGACATCTCTGCCAGTCTAGTTTCTGGGCAGGTTT
CCTGTGTCAGTATTTCCCTCCTCTTTCATTAATCAAGGTATTTGGTAGAGGTGGAATCTAAGTGTGTTGTATGT
CCAATTTACTTGATATGTAAACCATGCTGTGCTATTCAATGTTTGTATGCATAATTGGACCTTGAATCGATAAG
TGTAATAACAGCTTTTGATCTGTAATGCTTTTATACAAAAGTTTATTTTAAATAATAAAATGTTTGTCT

WO 2004/030615

PCT/US2003/028547

972/6881
FIGURE 906

MDARRVPQKDLRVKKNLKKFRYVKLISMETSSSSDDSCDSFASDNFANTKPKFRSDISEELASVFIYEDSDNESFC
GFSESEVQDVLDHCGFLQKPRPDVTNELAGIFHADSDDESFCGFSESEIQDGMRLQSVREGCRTRSQCRHSGPLR
VAMKFPARSTRGATNKKAESRQPSSENSVTDSNSDSEDESGMNFLEKRALNIKQNKAMLAKLMSELESFPGSFRGR
HPLPGSDSQSRRPRRRTFFPGVASRRNPERRARPLTRSRRIILGSLDALPMEEEEEEDKYMLVRKRKTVDGYMNED
DLPRSRRSRSSVTLPHIIRPVVEITEEELENVCSNSRREKIYNRSLGSTCHQCRQKTIDTKTNCRNPDWGVRGQF
CGPCLRNRYGEEVRDALLDPNWHCPPCRGICNCSCFCRQDGRCATGVLVYLAKYHGFGNVHAYLKSLKQEFEMQA

WO 2004/030615

PCT/US2003/028547

973/6881
FIGURE 907

GCAAGATGGCAGAAGTAGAGCAGAAGAAGAAGCGGACCTTCCGCAAGTTCACCTACCGCGGCGTGGACCTGGACC
AGCTGCTGGACATGTCTTACGAGCAGCTGGAGCAGCCGATGCAGCTGTACAGTGCGCGCCAGCGGCGGGCGGCTGA
ACCGGGGCTGCGGCGGAAGCAGCACTCCCTGCTGAAGCGCCTGCGCAAGGCCAAGAAGGAGGCGCCGCCCATGG
AGAAGCAGGAAGTGGTGAAGACGCACCTGCGGGACATGATCATCCTACCCGAGATGGTGGGCAGCATGGTGGGCG
TCTACAACGGCAAGACCTTACCTACAAGCCGTAAGCACGGCCGGCCCGGCATCGGGGCCACCCACTCCTCCC
GCTTCATCCCTCTCAAGTAATGGCTCAGCTAATAAAGGCGCACATGACTCC

WO 2004/030615

PCT/US2003/028547

974/6881
FIGURE 908

MAEVEQKKKRTFRKFTYRGVDLDQLLDMSYEQLEQPMQLYSARQRRRLNRGLRRKQHSLLKRLRKAKKEAPPMEK
QEVVKTHLRDMIILPEMVGSMVGVYNGKTFTYKPVKHGRPGIGATHSSRFIPLK

WO 2004/030615

PCT/US2003/028547

975/6881
FIGURE 909

GCTGAAATTTAAAAGTACTGAGCTTACCAAGTGTGATAAGGATGTAGAGGAACTGGAACTTTCATACACTGCTGG
TGGGAATATAAAATGGTATAACCATTTTGGAAACAACCTTGGCAGTTTATTTGTTTGTGTTTAGGTTGTTTTTACTC
ACCACTATGCTAACGAGGAACCTTGGCAGTTTCTTTAAAAGATAAACATATATCTCTGGTCCGTGCCTCCAAGATG
ACAAAGAAAAGAAGGAACAACGGTCATGCCAAAAAGGGCCGCGGCCACGTGCATCCTATTGCTGCACTAACTGT
ACCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATTCGTCATTGAAACGTAGTGGAGGCCGAGCAGTCAGG
GACATTTCTGAAGTGAGCGTCTTCAATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTATATTACTGTGTGAGT
TGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCACAAAAGACCGAACACCCCCACCCTGATTT
AGACCTGTGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGAGCTGAGTTCTTAAAGACTGAAGACAGA
CTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTT

WO 2004/030615

PCT/US2003/028547

976/6881
FIGURE 910

CTTTTATGTTAGATGAGGAAGGGGATACCCAAACAGAGGAAACCCGGCCTTCAGAAACAAAAGAAGTGGAGCCAG
AGCCAACTGAGGACAAAGATTTGGAAGCTGATGAAGAGGACACTAGGAAAAAAGATGCTTCTGATGATCTAGATG
ACTTGAACCTTCTTTAATCAAAAGAAAAAGAAGAAAAAACTAAAAAGATATTTGATATTGATGAAGCTGAAGAAG
GTGTAAAGGATCTTAAGATTGAAAGTGATGTTCAAGAACCAACTGAACCAGAGGATGACCTTGACATTATGCTTG
GCAATAAAAAGAAGAAAAAGAAGATGTTAAGTTCCCAGATGAGGATGAAGCTCTAGAAGATGAAGACAACAAAA
AAGATGATGGTATCTCATTTCAGTAATCAGACAGGCCCTGCTTGGGCAGGCTCAGAAAGAGACTACACATACGAGG
AGCTGCTGAATCGAGTGTTCAACATCATGAGGGAAAAGAATCCAGATATGGTTGCTGGGGAGAAAAGGAAATTTG
TCATGAAACCTCCACAAGTCGTCCGAGTAGGAACCAAGAAAACCTCTTTTGTCAACTTTACAGATATCTGTAAAC
TTGGTTCTATAGATGGTAATAACCAACTTGTAATCAAAGGAAGATTCCAACAGAAACAGATAGAAAATGTCTTGA
GAAGATATATCAAGGAGTATGTCACCTTGTACACATGCCGATCACC GGACACAATCCTGCAGAAGGACATGCGAC
TCTATTTCTACAGTGCGAAACTTGTCACTTCTAGATGTTCTGTTGCCATTATCAAAATGGCTTCCAGGCTGTCA
TGGGCAAGCGAGCACAGCTCCGTGCCAAAGCTAACTAATTTGCTAATCACTGATTTTGCAAAGCTTGTGTGGAG
ATGTGGCTGGACAGGTTTGCCATCAGAGTGGATATACCATTGTATTAAAAACAAGATAAAAAAGCTGCCAAGATT
TTTGGCGAGTGGTTGGTTGGTCTGAAGTCCTTGCAAGACGCTGATGCTCAAGCTGTTGACATACTCATTGCCTAC
TTTAACACCTGTCAGAGAAACGTGATATGGGGTAAGGAGGTGCTTTTTTAAATAGTTCATAGACTTCTGTAAAA
TGCAAGATAAATTAAAGTTATTATAACAGTGA

WO 2004/030615

PCT/US2003/028547

977/6881
FIGURE 911

GGTGGGAGAGGTATCGGCAGGGGCAGCGCTGCCGCCGGGGCCTGGGGCTGACCCGTCTGACTTCCCGTCCGTGCC
GAGCCCACTCGAGCCGCAGCCATGTCTGGGGACGAGATGATTTTTGATCCTACTATGAGCAAGAAGAAAAAGAAG
AAGAAGAAGCCTTTTATGTTAGATGAGGAAGGGGATACCCAAACAGAGGAAACCCGGCCTTCAGAAACAAAAGAA
GTGGAGCCAGAGCCAACTGAGGACAAAAGATTTGGAAGCTGATGAAGAGGACACTAGGAAAAAGATGCTTCTGAT
GATCTAGATGACTTGAACCTCTTTAATCAAAAGAAAAAGAAGAAAAAACTAAAAAGATATTTGATATTGATGAA
GCTGAAGAAGGTGTAAAGGATCTTAAGATTGAAAGTGATGTTCAAGAACCAACTGAACCAGAGGATGACCTTGAC
ATTATGCTTGGCAATAAAAAAGAAGAAAAAGAAGATGTTAAGTTCCCAGATGAGGATGAAGCTCTAGAAGATGAA
GACAACAAAAAGATGATGGTATCTCATTCAAGTAATCAGACAGGCCCTGCTTGGGCAGGCTCAGAAAGAGACTAC
ACATACGAGGAGCTGCTGAATCGAGTGTTCAACATCATGAGGGAAAAGAATCCAGATATGGTTGCTGGGGAGAAA
AGGAAATTTGTCATGAAACCTCCACAAGTCGTCCGAGTAGGAACCAAGAAAACTTCTTTTGTCAACTTTACAGAT
ATCTGTAAACTATTACATCGTCAACCCAAACATCTCCTTGCAATTTTTATTGGCTGAATTGGGTACAAGTGGTTCT
ATAGATGGTAATAACCAACTTGTAATCAAAGGAAGATTCCAACAGAAACAGATAGAAAATGCTTGAGAAGATAT
ATCAAGGAGTATGTCACCTGTCACACATGCCGATCACCGACACAATCCTGCAGAAGGACATGCGACTCTATTTT
CTACAGTGCAGAACTTGTCACTTAGATGTTCTGTTGCCATTATCAAAATTGGCTTCCAGGCTGTCTATGGGCAAG
CGAGCACAGCTCCGTGCCAAAGCTAACTAATTTGCTAATCACTGATTTTGCAAAGCTTGTTGTGGAGATGTGGCT
GGACAGGTTTGCCATCAGAGTGGATATACCATTGTATTAAAAACAAGATAAAAAAGCTGCCAAGATTTTTGGCGA
GTGGTTGGTTGGTCTGAAGTCCTTGCAAGACGCTGATGCTCAAGCTGTTGACATACTCATTGCCTACTTTAACAC
CTGTCAGAGAAACGTGATATGGGGTAAGGAGGTGCTTTTTTAAATAGTTCATAGACTTCTGTAAATGCAAGAT
AAATTAAAGTTATTATAACAGTGA

PCT/US2003/028547

FIGURE 912

CGAGTTTGAAGAAGGCGAGTCCGGTCTCAAATAGGAGTTAAACACCGCCGCCGGTGCGCCCCAGCCGACTCCGGC
CGTCGCCGTCGCCGCCGGGGGAGGAGGGCCATGATCCAAAGGAACAGAGCAGTTGAGAAAACCTGTTTATTGGT
GGTCTGAGCTTTGAAACTACAGATGATAGTTTACGAGAACATTTTGAGAAATGGGGCACACTCACAGATTGTGTG
GTAATGAGAGACCCCCAAACAAAACGTTCCAGGGGCTTTGGTTTTGTGACTTATTCTTGTGTTGAAGAGGTGGAT
GCAGCAATGTGTGCTCGACCACACAAGGTTGATGGGCGTGTAGTGAACCAAAGAGAGCTGTTTCTAGAGAGGA
TCTGTAAAGCCTGGTGCCCATCTAAACAGTGAAGAAAATTTTTGTTGGTGGTATTAAAGAAGATACAGAAGAATAI
AATTTGAGAGACTACTTTGAAAAGTATGGCAAGATTGAAACCATAGAAGTTATGGAAGACAGGCAGAGTGGAAAA
AAGAGAGGATTTGCTTTTGTAACTTTGTATGATCATGATACAGTTGATAAAATTGTTGTTTACAGAAATACCACT
ATTAATGGGCATAATTGTGAAGTGAAAAAGGCCCTTTCTAAACAAGAGATGCAGTCTGCTGGATCACAGAGAGGT
CGTGGAGGTGGATCTGGCAATTTTATGGGTGCGGAGGGAACCTTTGGAGGTGGTGGAGGTAATTTGGCCGTGGT
GGAACTTTGGTGGAAGAGGTAGGCTATGGTGGTGGAGGTGGTGGCAGCAGAGGTAGTTATGGAGGAGGTGATGG
TGGATATAATGGATTTGGAGGTGATGGTGGCAACTATGGCGGTGGTCTGGTTATAGTAGTAGAGGGGGCTATGG
TGGTGGTGGACCAGGATATGGAACCAAGGTGGTGGATATGGTGGAGGTGGAGGATATGATGGTTACAATGAAGG
AGGAAATTTTGGCGGTGGTAACATATGGTGGTGGTGGGAACATAATGATTTTGGAAATTATAGTGGACAACAGCA
ATCAAATTATGGACCCATGAAAGGGGGCAGTTTGGTGGAAGAAGCTCGGGCAGTCCCTATGGTGGTGGTTATGG
ATCTGGTGGTGGAAAGTGGTGGATATGGTAGCAGAAGGTTCTAAAAACAGCAGAAAAGGGCTACAGTTCTTAGCAG
GAGAGAGAGCGAGGAGTTGTCAGGAAAGCTGCAGGTTACTTTGAGACAGTCGTCCCAAATGCATTAGAGGAACTG
TAAAAATCTGCCACAGAAGGAACGATGATCCATAGTCAGAAAAGTTACTGCAGCTTAAACAGGAAACCCTTCTTG
TTCAGGACTGTCATAGCCACAGTTTGCAAAAAGTGCAGCTATTGATTAAATGCAATGTAGTGTCAATTAGATGTAC
ATTCTTGAGGTCTTTTATCTGTTGTAGCTTTGTCTTTTCTTTTTCTTTTCTTTTACATCAGGTATATTGCCCTGT
AAATTGTGGTAGTGGTACCAGGAATAAAAAATTAAGGAATTTTTAACTTTTCAATATTTGTGTAGTTTCAAGTTTT
CTACATTTTAGTACAGAACTTTAACAAAATGCAGTTTCGAAGGTGTTTCTTGTGAGTTAACAAAGTAAAGAAGA
TCATTGTTAATTACTATTTTGTATGAATTTTGCTAAAGTTAACTGTAAAGAAACACCTGCTGACTTGCAGTTTAA
GGGGAATCTATTCTCCCATTTCCAAACCATGATATGAATGGGCGCTGACATGTGGAGAGAATAGATAATTTGTG
TGTTTGCAATGTGTGTTTTAGATAAATAGGATTGGGTATTTAAATTAGCATTGTGAATTTAATAGCATTAAAGAT
TACCTTCAAATGAAAAAATCTCAAATTTCTATTTGGTTTTTGTGCATTTCTTTTAAAAATGTAATCATATGA
TTTTAGTGTGTTAGACTTGTCTGAGTCCTAGCTGTGTTTAGAACATCTCTATTCTACATTTACCTTGGTCAAATTT
GAAC TGCTGCCATAGG

WO 2004/030615

PCT/US2003/028547

979/6881
FIGURE 913

MEGHDPKEREQLRKPF IGGLSFETDDGLREHF EKWVTLTDCVVMRDPQTKCSRGFGFVTYSYIEEVDAAMCAPP
HKVDGCVVEPKRAVSREDFVKPGAHLTVKKIFVGGIKIQKNII

WO 2004/030615

PCT/US2003/028547

980/6881
FIGURE 914

CTTCATCCTGCGACTAGCACCGCGTCCGGCAGCGCCTGCCCTACACTCGCCCGTGCCATGGCCTCCGTCTCCAAG
CTCGCCTGCATCTACTCGGCCCTCATTCTGCACGACGATGAGGTGACAGTCACGGAGGATAAGATCAATGCCCTC
ATTAAAGCAGCCGGTGTAATGTTGAACCTTTTTGGCCTGGCTTGTTTGCAAAGGCCCTGGCCAACGTCAACATT
GGGAGCCTCATCTGCAATGTAGGGGCTGGTGGACCTGCTCCAGCTGAGGAGAAGAAAGTGGAAGCAAAGAAAGAA
GAATCCAAGGAGTCTGATGATGACATGGGCCTTGGTCTTTTTGACTAAACCTCTTTTATAACGTGTTCAATAAAA
AGCTGAACCTT

WO 2004/030615

PCT/US2003/028547

981/6881
FIGURE 915

MASVSKLACIYSALILHDDEVTVTEDKINALIKAAGVNVEPFWPGLFAKALANVNIGSLICNVGAGGPAPAEKK
VEAKKEESKESDDDMGLGLFD

WO 2004/030615

PCT/US2003/028547

982/6881
FIGURE 916

ACGGGGCCTGGGCGGSAGGGGCGGTGGCTGGAGCTCGGTAAAGCTCGTGGGACCCCATTTGGGGGAATTTGATCCA
AGGAAGCGGTGATTGCCGGGGGAGGAGAAGCTCCCAGATCCTTGTGTCCACTTGCAGCGGGGGAGCGGAGACGC
GGAGCGGGCCTTTTGGCGTCCACTGCGCGGTGCACCCTGCCCATCCTGCCGGGATCATGCTCTGCGGCAGCCC
GGGAGGGATGCTGCTGCTGCGGGCCGGGCTGCTTGCCCTGGCTGCTCTGCTGCTGCTCCGGGTGCCCGGGGCTCG
GGCTGCAGCCTGTGAGCCCGTCCGCATCCCCCTGTGCAAGTCCCTGCCCTGGAACATGACTAAGATGCCCCAACCA
CCTGCACCACAGCACTCAGGCCAACGCCATCCTGGCCATCGAGCAGTTCGAAGGTCTGCTGGGCACCCACTGCAG
CCCCGATCTGCTCTTCTTCTCTGTGCCATGTACGCGCCCATCTGCACCATTGACTTCCAGCACGAGCCCCATCAA
CCCCTGTAAGTCTGTGTGCGAGCGGGCCCGGCAGGGCTGTGAGCCCATACTCATCAAGTACCGCCACTCGTGGCC
GGAGAACCTGGCCTGCGAGGAGCTGCCAGTGTACGACAGGGGCGTGTGCATCTCTCCCGAGGCCATCGTTACTGC
GGACGGAGCTGATTTTCTATGGATTCTAGTAACGGAACTGTAGAGGGGCAAGCAGTGAACGCTGTAAATGTAA
GCCTATTAGAGCTACACAGAAGACCTATTTCCGGAACAATTACAACATATGTCATTTCGGGCTAAAGTTAAAGAGAT
AAAGACTAAGTGCCATGATGTGACTGCAGTAGTGGAGGTGAAGGAGATTCTAAAGTCCCTCTCTGGTAAACATTCC
ACGGGACACTGTCAACCTCTATACCAGCTCTGGCTGCCTCTGCCCTCCACTTAATGTTAATGAGGAATATATCAT
CATGGGCTATGAAGATGAGGAACGTTCCAGATTACTCTTGGTGGAAAGGCTCTATAGCTGAGAAAGTGAAGGATCG
ACTCGGTAAAAAAGTTAAGCGCTGGGATATGAAGCTTCGTATCTTGGACTCAGTAAAGTGATTCTAGCAATAG
TGATTCCACTCAGAGTCAGAAGTCTGGCAGGAACCTCGAACCCCCGGCAAGCACGCAACTAAATCCCCGAAATACAA
AAAGTAACACAGTGGACTTCTTATTAAGACTTACTTGCAATTGCTGGACTAGCAAAGGAAAATTGCACTATTGCAC
ATCATATTCTATTGTTTACTATAAAAATCATGTGATACTGATTATTACTTCTGTTTCTCTTTTGGTTTCTGCTT
CTCTCTTCTCTCAACCCCTTTGTAATGGTTTGGGGGCAGACTCTTAAGTATATTGTGAGTTTCTATTTCACTAA
TCATGAGAAAACTGTTCTTTTGCAATAATAATAAATTAAACATGCTGTTA

WO 2004/030615

PCT/US2003/028547

983/6881
FIGURE 917

MVCGSPGGMLLLRAGLLALAALCLLRVPGARAAACEPVRIPLCKSLPWNMTKMPNHLHHSTQANAILAIEQFEG
LGTHCSPDLLFFLCAMYAPICTIDFQHEPINPCKSV CERARQGCEPILIKYRHSWPENLACEELPVYDRGVCISP
EAIVTADGADFPMDSNGNCRGASSERCKCKPIRATQKTYFRNNYNYVIRAKVKEIKTKCHDVTAVVEVKEILKS
SLVNIPRDTVNLYTSSGCLCPPLNVNEEYIIMGYEDEERSRLLLVEGSIAEKWKDRLGKKVKRWDMKLRHLGLSK
SDSSNSDSTQSQKSGRNSNPRQARN

WO 2004/030615

PCT/US2003/028547

984/6881
FIGURE 918

ATGTCCATCAGGACGACCCAGAAGTCCTACAGGGTGTCCACTTCTGGCCCCGGGCCTTCAGCAGCCATTTCTAC
ACAAGTGGGCCTGGTGCCTCCATCAGCTCCTCGAGCTTCTCCCAAGTGGGCAGCAGCAGCTTCCGGGGTGGCCTG
GGAGGAGGCTACGGTGGGGCCAGTGGCATGGGAGGCATCACCACCGTCACTGTCAACCAGAGCCTGCTGAGCCCC
CTTAACCTGGAGGTGGACCCACACATCCAGGCAGTGCACACTCAGAAGAAGGAGCAGATCAAGACCCTCAACACT
AAGTTTGCCACCTTCATATACAAGAGTTACATCAACAACCTTAGGCAGCAGCTGGAGACTCTGGGCCAGGAAAAG
CTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGGGGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATGAGATC
AATAAGCGTACAGAGATGGAGAATGAATTTGTCCTCATCAAGAAGGATGTGGATGAAGCTTACCTGAACAAGGTA
GAGCTGGAGTCTCGCCTGGAAGGGCTGACTGACGAAATCAACTTCCTCAGGCAGCTGTATGAAGAGGATATCCCG
GAGCTGCAGTCCCAGATCTCAGACACGTCTGTGGTGTGCCCATGGACAACAGCCACTCCCTGGACATGGACAGC
ATCATCAATGAGGTCAAGCGCAGTACGAGATCACCAACCGCAGCCAGCTGGCTCCAGGCAGAGATTGAGGGTCTC
AAAGGCCAGAGGGCTTCCCTGGAGGCCGCCATCGCAGATGCGGAGCAGCGCGGGGAGTTGGCCGTTAAGGATGCC
AGCGCCAAGCTGTCTGAGCTGGAGGCCGCCCTGCAGCAAACCAAGCAGGACGTGGAGCTGATGAACGACAAGCTG
GCCCTGGACATTGAGATCGCCACCTACAGGCAGCTGCTGGAGGGCGAGGAGAGCTGGCTGGAGTCTGGGATGCAG
AGCATGAGTATCCATACAAAGACCATCAGCAGCTATGCAGGTGGTCTGAGCTCGGCCTATGGGGGCCTCACAAAGC
CCCGGCCTCAGCTGTGGACTGGGCTCCAGCTTTGGCTCTGGCGCGGGCTCCAGTTCCTTCAGCTGCATCAGCTAC
ACCAGGGCCGTGGTTGTGAAGAAGATTGAGACCCGTGATGGGACGCTGGTGTGAGAGTTCTCTGACGTCCTGCCC
AAGTGA

WO 2004/030615

PCT/US2003/028547

985/6881
FIGURE 919

MSIRTTQKSYRVSTSGPRAFSSHFYTSGPGASISSSSFSQVGSSSFRRGGLGGGYGGASGMGGITTVTVNQSLLSF
LNLEVDPHIQAVHTQKKEQIKTLNFKFATFIYKSYINNLRQQLTLGQEKLEAELGNMQGLVEDFKNKYEDEI
NKRTEMENEFVLIKKDVDEAYLNKVELESRLGLTDEINFLRQLYEEDIPELQSQISDTSVVLPMDNSHSLDMDS
IINEVKRSTRSPTAASWLQAEIEGLKGQRASLEAAIADAEQRGELAVKDASAKLSELEAALQQTQDVELMNDKL
ALDIEIATYRQLLEGEESWLESGMQSMSIHTKTISSYAGGLSSAYGGLTSPGLSCGLGSSFGSGAGSSSFSCISY
TRAVVVKKIETRDGTLVSEFSDVLPK

WO 2004/030615

PCT/US2003/028547

986/6881
FIGURE 920

ACGCAACCCCATAGGTAGCACGCCGTTACCCGTGGGGAGCGTTTCCGCCATTTTTGAAAATTAATTGGGAAGGT
ACTGGTTTTAAGTGTAGTTGCCGACGCAATGGCAGCCTTTGCAGTGGAACCTCAGGGGCCCGCTTAGGATCTGA
ACCAATGATGCTGGGTTACCCACATCTCCAAAGCCAGGAGTTAATGCCAGTTCTTACCTGGATTTTTAATGGG
GGATTTGCCAGCTCCGGTGACTCCACAACCTCGATCAATTAGTGGCCCTTCAGTAGGAGTAATGGAAATGAGATC
ACCTTTACTTGCAGGTGGGTCAACCACCACAACCAGTTGTACAGCTCATAAAGATAAAAGTGGCGCTCCACCAGT
TAGAAGTATATATGATGACATTTCTAGCCCAGGACTTGGATCAACACCTTTAACTTCAAGAAGACAGCCAAACAT
TTCAGTAATGCAGAGTCCTCTTGTGGAGTTACATCTACTCCTGGAACAGGGCAAAGTATGTTTAGTCCAGCAAG
TATCGGTCAGCCACGAAAGACGACATTATCTCCTGCCAGTTGGATCCTTTTTTATACTCAAGGAGATTCTTTGAC
TTCAGAAGATCACCTCGATGACTCTTGGGTGACTGTATTTGGGTTTCTCAAGCATCTGCTTCTACATATTACT
ACAATTTGCACAGTATGGGAATATCTTAAACATGTGATGTCTAATACAGGAAATTGGATGCATATTCGTTATCA
ATCTAAACTGCAGGCTCGGAAAGCCTTAAGCAAAGATGGGAGGATTTTTGGAGAATCCATCATGATTGGTGTA
ACCATGTATTGACAAAAGTGTTATGGAAAGCAGTGACAGATGTGCTTTATCATCTCCATCTTTAGCCTTTACACC
ACCAATCAAACTCTAGGTACACCAACACAACCTGGAAGTACTCCTAGGATTTCTACCATGAGACCTCTTGCTAC
AGCATACAAAGCCTCTACTAGTGATTATCAGGTTATTTCTGACAGACAAACGCCAAAAAAGATGAAAGTCTTGT
ATCCAAAGCAATGGAGTACATGTTTGGCTGGTAGTAGAACACCAAGAAGGAGGTTGCTACACTAAAACAGAGTTA
GCAGAGTGCTGCTGGTTCCCTTCGGTTAGTTATATAACTGTTCTGAGTATTGGATAGCTATCTCATACTTCTTT
TAGAAAGAGCCTTTTTTATTAAAGGATACAACCTATTTGTAGCTCGCACTTTAAAGATGCTTGAGATACATTTT
AAAGAAAACAAAAATCCCTGTAAATAGGATTTTGTGCTTTCTGTAACAGTGCATGCTTCAGCACAGAAAACCTCA
GCATTGATTATTGTAAATTAATAACTGAAATTGTGGTGAGACGTCATAGTCTTCATGAGAACGTGGGGGTGAAT
TTCATGAAGGGGAACATAGTTATTTCTACCGACACAAATATTATAATTAGCAATTTGAATTATGGTCTTTTAAT
TTAGATAGTATTTAATAATTTAATTATCCTTGTTTGTATATGTCCTGTCACAGAGTGTCTCTTGGTGTATTCTA
AAACGAGCATTCTTTAAAAAACCTAAAGTTTCTTGATAATAAACATTGTCAATGAT

WO 2004/030615

PCT/US2003/028547

987/6881
FIGURE 921A

GGCTGAGTTTTATGACGGGCCCCGGTGCTGAAGGGCAGGGAACAACCTTGATGGTGCTACTTTGAACTGCTTTTCTT
TTCTCCTTTTTTGACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCAAAAGGGGAGCTGGCTA
CTTCTCGCTCTGCTTCATCCCACTATTATTTTGGCACAACAGGAAGCTGTTGAAGGAGGATGTTCCCATCTTGGT
CAGTCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGTGACTCAGGATCCGTTCTC
TGCGATGACATAATAATGTGACGATCAAGAATTAGACTGCCCAACCCAGAAATTCCATTTGGAGAATGTTGTGCA
GTTTGCCACAGCCTCCAACCTGCTCCTACTCGCCCTCCTAATGGTCAAGGACCTCAAGGCCCAAGGGAGATCCA
GGCCCTCCTGGTATTCTGGGAGAAATGGTGACCCTGGTATTCCAGGACAACCAGGGTCCCCTGGTTCTCCTGGC
CCCCCTGGAATCTGTGAATCATGCCCTACTGGTCTCAGAACTATTCTCCCCAGTATGATTTCATATGATGTCAAG
TCTGGAGTAGCAGTAGGAGGACTCGCAGGCTATCCTGGACCAGCTGGCCCCCAGGCCCTCCCGGTCCCCCTGGT
ACATCTGGTTCCTGGTTCCCCCTGGATCTCCAGGATACCAAGGACCCCCCTGGTGAACCTGGGCAAGCTGGTCCT
TCAGGCCCTCCAGGACCTCCTGGTGCTATAGGTCCATCTGGTCTGCTGGAAAAGATGGAGAATCAGGTAGACCC
GGACGACCTGGAGAGCGAGGATTGCCTGGACCTCCAGGTATCAAAGGTCCAGCTGGGATACCTGGATTCCCTGGT
ATGAAAGGACACAGAGGCTTCGATGGACGAAATGGAGAAAAGGGTGAAACAGGTGCTCCTGGATTAAAGGGTGAA
AATGGTCTTCCAGGCGAAAATGGAGCTCCTGGACCCATGGGTCCAAGAGGGGCTCCTGGTGAGCGAGGACGGCCA
GGACTTCTGGGGCTGCAGGTGCTCGGGGTAAATGACGGTGCTCGAGGCAGTGATGGTCAACCAGGCCCTCCTGGT
CCTCCTGGAACGCCGATTCCCTGGATCCCCCTGGTGCTAAGGGTGAAAGTTGGACCTGCAGGGTCTCCTGGTTCA
AATGGTGCCCCTGACAAAAGAGGAGAACCTGGACCTCAGGGACACGCTGGTGCTCAAGGTCTCCTGGCCCTCCT
GGGATTAATGGTAGTCTGGTGGTAAAGGCGAAATGGGTCCCGCTGGCATTCTCCTGGAGCTCCTGGACTGATGGGA
GCCCGGGGTCTCCAGGACCAGCCGGTGCTAATGGTGCTCCTGGACTGCGAGGTGGTGACGTGAGCCTGGTAAAG
AATGGTGCCAAAGGAGAGCCCGGACCACGTGGTGAAACGCGGTGAGGCTGGTATTCCAGGTGTTCCAGGAGTAAA
GGCGAAGATGGCAAGGATGGATCACCTGGAGAACCTGGTGCAAATGGGCTTCCAGGAGCTGCAGGAGAAAGGGGT
GCCCCCTGGGTTCAGAGGACCTGCTGGACCAAATGGCATCCCAGGAGAAAAGGGTCTGCTGGAGAGCGTGGTGCT
CCAGGCCCTGCAGGGCCAGAGGAGCTGCTGGAGAACCTGGCAGAGATGGCGTCCCTGGAGGTCCAGGAATGAGG
GGCATGCCCGGAAGTCCAGGAGGACCAGGAAGTGATGGGAAACCAGGGCCTCCCGGAAGTCAAGGAGAAAGTGGT
CGACCAGGTCTCCTGGGCCATCTGGTCCCCGAGGTACGCTGGTGTGCTATGGGCTTCCCCGGTCTTAAAGGAAAT
GATGGTGCTCCTGGTAAGAATGGAGAACGAGGTGGCCCTGGAGGACCTGGCCCTCAGGGTCTCCTGGAAAGAAT
GGTGAACCTGGACCTCAAGGACCCCCAGGGCCTACTGGGCCTGGTGACAAAGGAGACACAGGACCCCCCTGGT
CCACAAGGATTACAAGGCTTGCTGGTACAGGTGGTCTCCTCAGGAGAAAATGGAAAACCTGGGGAACCAGGTCCA
AAGGGTGATGCCGGTGACCTGGAGCTCCAGGAGGCAAGGGTGATGCTGGTGCCCCCTGGTGAACGTGGACCTCCT
GGATTGGCAGGGGCCCAGGACTTAGAGGTGGAGCTGGTCCCCCTGGTCCCGAAGGAGGAAAGGGTGCTGCTGGT
CCTCCTGGGCCACCTGGTGCTGCTGGTACTCCTGGTCTGCAAGGAATGCCTGGAGAAAGAGGAGGTCTTGGAAGT
CCTGGTCCAAAGGGTGACAAGGGTGAACCGCGGCCAGGTGCTGATGGTGCTCCAGGGAAAGATGGCCCAAGG
GGTCTACTGGTCTATTGGTCTCCTGGCCAGCTGGCCAGCCTGGAGATAAGGGTGAAAGGTGGTGCCCCCGGA
CTTCCAGGTATAGCTGGACCTCGTGGTAGCCCTGGTGAGAGAGGTGAAACTGGCCCTCCAGGACCTGCTGGTTTC
CCTGGTGCTCCTGGACAGAAATGGTGAACCTGGTGGTAAAGGAGAAAAGAGGGGCTCCGGGTGAGAAAGGTGAAGGA
GGCCCTCCTGGAGTTGACAGGACCCCTGGAGGTTCTGGACCTGCTGGTCTCCTGGTCCCCAAGGTGTCAAAGGT
GAACGTGGCAGTCTTGGTGGACCTGGTGCTGCTGGCTTCCCTGGTGCTCGTGGTCTTCTGGTCTCCTGGTAGT
AATGGTAACCCAGGACCCCCAGGTCCAGCGGTTCTCCAGGCAAGGATGGGCCCCAGGTCTGCGGGTAACACT
GGTGCTCCTGGCAGCCCTGGAGTGCTGGACCAAAAGGTGATGCTGGCCAACCAGGAGAGAAGGGATCGCCTGGT
GCCAGGGCCACCAGGAGCTCCAGGCCCACTTGGGATTGCTGGGATCACTGGAGCACGGGGTCTTGAGGACCA
CCAGGCATGCCAGGTCTAGGGGAAGCCCTGGCCCTCAGGGTGTAAGGGTGAAAGTGGGAAACCAGGAGCTAAC
GGTCTCAGTGGAGAACGTGGTCCCCCTGGACCCAGGGTCTTCTGGTCTGGCTGGTACAGCTGGTGAACCTGGA
AGAGATGGAACCCCTGGATCAGATGGTCTTCCAGGCCAGATGGATCTCCTGGTGGCAAGGGTGATCGTGGTGAA
AATGGTCTCCTGGTGCCCCCTGGCGCTCCTGGTTCATCCAGGCCACCTGGTCTGCTGGTCCAGCTGGAAAGAGT
GGTGACAGAGGAGAAAGTGGCCCTGCTGGCCCTGCTGGTGCTCCCGGTCTGCTGGTTCCCGAGGTGCTCCTGGT
CCTCAAGGCCACGTGGTGACAAAGGTGAAACAGGTGAACGTGGAGCTGCTGGCATCAAAGGACATCGAGGATTTC
CCTGGTAATCCAGGTGCCCCAGGTTCTCCAGGCCCTGCTGGTCAGCAGGGTGCAATCGGCAGTCCAGGACCTGCA
GGCCCCAGAGGACCTGTTGGACCCAGTGGACCTCCTGGCAAAGATGGAACAGTGGACATCCAGGTCCCATTGGA

WO 2004/030615

PCT/US2003/028547

988/6881
FIGURE 921B

CCACCAGGGCCTCGAGGTAACAGAGGTGAAAGAGGATCTGAGGGCTCCCCAGGCCACCCAGGGCAACCAGGCCCT
CCTGGACCTCCTGGTGCCCCCTGGTCCTTGCTGTGGTGGTGTGGAGCCGCTGCCATTGCTGGGATTGGAGGTGAA
AAAGCTGGCGGTTTTGCCCCGTATTATGGAGATGAACCAATGGATTTCAAAATCAACACCGATGAGATTATGACT
TCACTCAAGTCTGTTAATGGACAAATAGAAAGCCTCATTAGTCCTGATGGTTCTCGTAAAAACCCCGCTAGAAAC
TGCAGAGACCTGAAATTCTGCCATCCTGAACTCAAGAGTGGAGAATACTGGGTTGACCCTAACCAAGGATGCAAA
TTGGATGCTATCAAGGTATTCTGTAATATGGAACTGGGGAAACATGCATAAGTGCCAATCCTTTGAATGTTCCA
CGGAAACACTGGTGGACAGATTCTAGTGCTGAGAAGAAACACGTTTGGTTTGGAGAGTCCATGGATGGTGGTTTT
CAGTTTAGCTACGGCAATCCTGAACTTCCTGAAGATGTCCTTGATGTGCAGCTGGCATTCTTCGACTTCTCTCC
AGCCGAGCTTCCCAGAACATCACATACACTGCAAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAAATGTA
AAGAAGGCCCTGAAGCTGATGGGGTCAAATGAAGGTGAATTCAAGGCTGAAGGAAATAGCAAATTCACCTACACA
GTTCTGGAGGATGGTTGCACGAAACACACTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCT
GTGAGACTACCTATTGTAGATATTGCACCCATGACATTGGTGGTCCTGATCAAGAATTTGGTGTGGACGTTGGC
CCTGTTTGCTTTTTTATAAACCAAACCTCTATCTGAAATCCCAACAAAAAAATTTAACTCCATATGTGTTCCTCTT
GTTCTAATCTTGTCAACCAGTGCAAGTGACCGACAAAATTCAGTTATTTATTTCCAAAATGTTTGGAAACAGTA
TAATTTGACAAAGAAAAATGATACTTCTCTTTTTTGTCTGTCCACCAAATACAATTCAAATGCTTTTTGTTTTA
TTTTTTTACCAATTCCAATTTCAAATGTCTCAATGGTGCTATAATAAATAAACTTCAACACTCTTTATGATAAC
AACACTGTGTTATATTCTTTGAATCCTAGCCCATCTGCAGAGCAATGACTGTGCTCACCAGTAAAAGATAACCTT
TCTTTCTGAAATAGTCAAATACGAAATTAGAAAAGCCCTCCCTATTTTAACTACCTCAACTGGTCAGAAACACAG
ATTGTATTCTATGAGTCCCAGAAGATGAAAAAATTTTATACGTTGATAAAACTTATAAATTTTATTGATTAATC
TCCTGGAAGATTGGTTTAAAAAGAAAAGTGTAATGCAAGAATTTAAAGAAATATTTTTTAAAGCCACAATTATTTT
AATATTGGATATCAACTGCTTGTAAGGTGCTCCTCTTTTTTCTTGTCATTGCTGGTCAAGATTACTAATATTTG
GGAAGGCTTTAAAGACGCATGTTATGGTGCTAATGTACTTTCACTTTTAACTCTAGATCAGAATTGTTGACTTG
CATTGAGAACATAAATGCACAAAATCTGTACATGTCTCCATCAGAAAGATTGATTGGCATGCCACAGGGATTCT
CCTCCTTCATCCTGTAAAGGTCAACAATAAAAACCAAATTATGGGGCTGCTTTTGTCACTAGCATAGAGAATG
TGTTGAAATTTAACTTTGTAAGCTTGTAATGTGGTTGTTGATCTTTTTTTTCTTACAGACACCCATAATAAATA
TCATATTAAATTC

WO 2004/030615

PCT/US2003/028547

989/6881
FIGURE 922

MMSFVQKGSWLLALLHPTIILAQQEAVEGGCSHLGQSYADRDVWKPEPCQICVCDSGSVLCDDIICDDQELDCP
NPEIPFGECCA VCPQPP TAPTRPPNGQGPQGP KGDPPGPIGRNGDPGIPGQPGSPGSPGPPGICESCPTGPQN
YSPQYDSYDVKSGVAVGGLAGYF GPAGPPGPPGPPGTSGHPGSPGSPGYQGPPEGQAGPSGPPGPPGAIGPSG
PAGKDGESGRPGRP GERGLPGPPGIKGPAGIPGFPGMKGHRGFDGRNGEKGETGAPGLKGENGLPGENGAPGPMG
PRGAPGERGRPGLP GAAGARGNDGARGSDGQGP PP GPPGTAGFP GSPGAKGEVGPAGSPGSNGAPGQRGEPGPQG
HAGAQQPPGPPGINGSPPGKGEMGPAGIPGAPGLMGARGPPGPAGANGAPGLRGGAGEPGKNGAKGEPGPRGERG
EAGIPGVPGAKGEDGKDGSPPGEPGANGLPGAAGERGAPGFRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPG
RDGVPGGPGMRGMFGSPGGPGSDGKPGPPGSGGESGRPPGPPGSPGPRGQPGVMGFP GPKGNDGAPGKNGERGGPG
GPGPQGP PGKNGETGFPQGP PGTPGPGDKGDTGPPPGQLQGLPGTGGPPGENGKPGEPGPKGDAGAPGAPGGKG
DAGAPGERGPPGLAGAPGLRGGAGPPGPEEGGKGAAGPPGPPGAAGTPGLQGMPPGERGGLGSPGPKDKGEPGGPG
ADGVPGKDGPRGPTGPIGPFGPAGQPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGPAGFPAGPQNGEPGGKG
ERGAPGEKGE GPPGVAGPPGGSGPAGPPGPQGVKGERGSPGGPGAAGFP GARGLP GPPGSNGNPGPPGPSGSPG
KDGPPGPAGNTGAPGSPGVSGPKGDAGQPGGEKGSPPGAQGGPPGAPGLGIAGITGARGLAGPPGMPGPRGSPGPQG
VKGESGKPGANGLSGERGPPGPQGLPGLAGTAGEPGRDGNPGSDGLPGRDGSPGGKGDRENGSPGAPGAPGHPG
PPGPVGPAGKSGDRGESGPAGPAGAPGPAGSRGAPGPQGPRGDKGETGERGAAGIKGHRGFPGNPGAPGSPGPAG
QQGAIGSPGPAGPRGPVGPSPGPPGKDGTS GHPGPIGPPGPRGNRGERGSEGSPPGHPGQPGPPGPPGAPGPCCGV
GAAAIAIGIGGEKAGGFAPYYGDEPMDFKINTDEIMTSLKSVNGQIESLISPDGSRKNPARNCRDLKFCHPELKSG
EYWVDPNQCKLDAIKVFCNMETGETCISANPLNVPRKHWWTDSSAEKKHVWFGESMDGGFQFSYGNPELPEDVL
DVQLAFLRLSSRASQNIYHCKNSIAYMDQASGNVKKALKLMSNEGEFKAEGNSKFTYTVLEDGCTKHTGEWS
KTVFEYRTRKAVRLPIVDIAPYDIGGPDQEF GVDVGPVCFLL

WO 2004/030615

PCT/US2003/028547

990/6881
FIGURE 923

ACGCGTCCGAGCTGGCTCAGGGCGTCCGCTAGGCTCGGACGACCTGCTGAGCCTCCCAAACCGCTTCCATAAGGC
TTTGCCTTTCCAACCTTCAGCTACAGTGTTAGCTAAGTTTGGAAAGAAGGAAAAAGAAAATCCCTGGGCCCTTT
TCTTTTGTTCTTTGCCAAAGTCGTCGTTGTAGTCTTTTTGCCCAAGGCTGTTGTGTTTTTAGAGGTGCTATCTCC
AGTTCCTTGCACTCCTGTTAACAAGCACCTCAGCGAGAGCAGCAGCAGCGATAGCAGCCGAGAAGAGCCAGCGG
GGTCGCCTAGTGTCATGACCAGGGCGGGAGATCACAAACCGCCAGAGAGGATGCTGTGGATCCTTGGCCGACTACC
TGACCTCTGCAAAATTCCTTCTCTACCTTGGTCATTCTCTCTACTTGGGGAGATCGGATGTGGCACTTTGCGG
TGCTGTGTTTTCTGGTAGAGCTCTATGGAACAGCCTCCTTTTGACAGCAGTCTACGGGCTGGTGGTGGCAGGGT
CTGTTCTGGTCCTGGGAGCCATCATCGGTGACTGGGTGGACAAGAATGCTAGACTTAAAGTGGCCAGACCTCGC
TGGTGGTACAGAAATGTTTCAGTCATCCTGTGTGGAATCATCCTGATGATGGTTTTCTTACATAAACATGAGCTTC
TGACCATGTACCATGGATGGGTTCTCACTTCCGTGCTATATCCTGATCATCACTATTGCAATATTGCAAAATTTGG
CCAGTACTGCTACTGCAATCACAAATCCAAAGGGATTGGATTGTTGTTGTTGTCAGGAGAAGACAGAAGCAAACCTAG
CAAATATGAATGCCACAATACGAAGGATTGACCAGTTAACCAACATCTTAGCCCCATGGCTGTTGGCCAGATTA
TGACATTTGGCTCCCCAGTCATCGGCTGTGGCTTTATTTGCGGATGGAACCTGGTATCCATGTGCGTGGAGTACG
TCCTGCTCTGGAAGTTTACCAGAAAACCCAGCTCTAGCTGTGAAAGCTGGTCTTAAAGAAGAGGAAACTGAAT
TGAAACAGCTGAATTTACACAAAGATACTGAGCCAAAACCCCTGGAGGGAACCTCATCTAATGGGTGTGAAAGACT
CTAACATCCATGAGCTTGAACATGAGCAAGAGCCTACTTGTGCCTCCAGATGGCTGAGCCCTTCCGTACCTTCC
GAGATGGATGGGTCTCCTACTACAACCAGCCTGTGTTTCTGGCTGGCATGGGTCTTGCTTTCTTTTATATGACTG
TCCTGGGCTTTGACTGCATCACCACAGGGTACGCCTACACTCAGGGACTGAGTGGTTCATCCTCAGTATTTTGA
TGGGAGCATCAGCTATAACTGGAATAATGGGAACCTGTAGCTTTTACTTGGCTACGTCGAAAATGTGGTTTGGTTC
GGACAGGTCTGATCTCAGGATTGGCACAGCTTTCCTGTTTGATCTTGTGTGTGATCTCTGTATTTCATGCCTGGAA
GCCCCCTGGACTTGTCCGTTTCTCCTTTTGAAGATATCCGATCAAGGTTTCAATCAAGGAGAGTCAATTACACCTA
CCAAGATACCTGAAATTACAACCTGAAATATACATGTCTAATGGGTCTAATTCTGCTAATATTGTCCCGGAGACAA
GTCCTGAATCTGTGCCATAATCTCTGTCACTGTCTGTTTGCAGGCGTCATTGCTGCTAGAAATCGGTCTTTGGT
CCTTTGATTAACTGTGACACAGTTGCTGCAAGAAAATGTAATTGAATCTGAAAGAGGCATTATAAATGGTGTAC
AGAACTCCATGAATATCTTCTGATCTTCTGCATTTTCATCATGGTCATCCTGGCTCCAAATCCTGAAGCTTTTG
GCTTGCTCGTATTGATTTCAGTCTCCTTTGTGGCAATGGGCCACATTATGTATTTCCGATTTGCCAAAATACTC
TGGGAAACAAGCTCTTTGCTTGCGGTCTGATGCAAAAGAAGTTAGGAAGGAAAATCAAGCAAATACATCTGTTG
TTTGAGACAGTTTAACTGTTGCTATCCTGTTACTAGATTATATAGAGCACATGTGCTTATTTTGTACTGCAGAAT
TCCAATAAATGGCTGGGTGTTTGTCTGTTTTTACCAGAGCTGTGCCTTGAGAACTAAAGCTGTTTAGGAAAC
CTAAGTCAGCAGAAATTAACCTGATTAATTTCCCTTATGTTGAGGCATGGAAAAAAATTTGGAAAAGAAAAACTCA
GTTTAAATACGGAGACTATAATGATAACACTGAATTTCCCTATTTCTCATGAGTAGATACAATCTTACGTAAAAG
AGTGGTTAGTCACGTGAATTCAGTTATCATTGACAGATTCTTATCTGTACTAGAATTCAGATATGTCAGTTTTT
TGCAAAACTCACTCTTGTTCAGACTAGCTAATTTATTTTTTGCATCTTAGTTATTTTTTAAAAACAAATCTTTC
AAGTATGAAGACTAAATTTTGATAACTAATATTATCCTTATTGATCCTATTGATCTTAAGGTATTTACATGTATG
TGGAACAAACAAACACTTAACTAGAATTCTCTAATAAGGTTTATGGTTTAGCTTAAAGAGCACCTTTGTATTTT
ATTATCAGATGGGGCAACATATTGTATGAAGCATATGTAGCACTTCACAGCATGGTTATCATGTAAGCTGCAGGT
AGAAGCAAAGCTGTAAAGTAGATTTATCACACAATGACTGCATACAGACTTCAAATATGTCAATAGTTTGGTCAT
AGAACCTAGAAGCCAAAAGCCACACAGAAGGGCAAGAATCCCAATTTAACTCATGTTATCATCATTAGTGATCTG
TGTTGTAGAACATGAGGGTGTAAAGCCTTCAGCCTGGCAAGTTACATGTAGAAAGCCACACTTGTGAAGGTTTTG
TTTTACAAATCACTTGATTTAACACACTCAGGTAGAATATTTTTTATTTTTTACTGTTTTATACCCAGAAGTTATTT
CTACATTGTTCTACAGCAAGAATATTCTATAAAGTATCCCTTTCAAATGCCTTTGAGAAGAATAGAAGAAAAAA
GTTTGTATATATTTTAAAAAATTGTTTTAAAAGTCAGTTTGCAACATGTCTGTACCAAGATGGTACTTTGCCTTA
ACGTTTTATATGCACTTTTCATGGAGACTGCAATACGTTGCTATGAGCACTTTCTTTATCCTTGGAGTTTAATCCT
TTGCTTCATCTTTCTACAGTATGACATAATGATTGCTATGTTGTAAATCTTTGTAAAAAATTTCTATATAAAA
ATATTTTGAATCTTAAAAAATAAAAAA

WO 2004/030615

PCT/US2003/028547

991/6881
FIGURE 924

MTRAGDHNRRQGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELYGNLLLLTAVYGLVVAGSVLVL
GAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIIITIANIANLASTAT
AITIQRDWIVVAGEDRSKLANMNATIRRIDQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWK
VYQKTPALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGVV
SYYNQPVFLAGMGLAFLYMTVLGFDCITTGYAYTQGLSGSILSILMGASAITGIMGTVAFTWLRKCGLVRTGLI
SGLAQLSCLILCVISVFMPGSPDLDSVSPFEDIRSREIQGESITPTKIPETITEIYMSNGSNSANIVPETSPEV
PIISVSLLFAGVIAARIGLWSFDLTVTQLLQENVIESERGIINGVQNSMNYLLDLLHFIMVILAPNPEAFGLLVL
ISVSFVAMGHIMYFRFAQNTLGKLFACGPDAKEVRKENQANTSVV

WO 2004/030615

PCT/US2003/028547

992/6881
FIGURE 925

TTTTGTGAAGAGACGAAGACTGAGCGGTTGCGGCCGCGTTGCCGACCTCCAGCAGCAGTCCGGCTTCTCTACGCAG
AACCCGGGAGTAGGAGACTCAGAATCGAATCTCTTCTCCCTCCCTTCTTGTTTTCGGCTTTGTGAGAAACCTTA
CCATCAAACACAATGGCCAGCAACGTTACCAACAAGACAGATCCTCGTTCCATGAACCTCCCGTGTATTCAATTGGG
AATCTCAACACTCTTGTGGTCAAGAAATCTGATGTGGAGGCAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGC
TCTGTTTCATAAGGGCTTTGCCTTCTTTCAGTATGTTAATGAGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGAT
GGCAGAAATGATTGCTGGCCAGGTTTATAGATATTAACCTGGCTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGT
GTGAAACGATCTGCAGCGGAGATGTACGGCTCCTCTTTTGACTTGGATTGTGACTTTCAACGGGACTATTATGAT
AGGATGTACAGTTACCCAGCACGTGTACCTCCTCCTCCTCTATTGCTCGGGCTGTAGTGCCCTCGAAACGTCAG
CGTGTATCAGGAAACACTTCACAAAGGGGCATAAGTGGCTTCAATTCTAAGAGTGGACAGCGGGGATCTTCCAAG
TCTGGAAAGTTGAAAGGAGATGACCTTCAGGCCATTAAGAGGGAGCTGACCCAGATAAAACAAAAGTGGATTCT
TTCTTGGAAAACCTGGAAAAAATTGAAAAGGAACAGAGCAAACAAGCAGTAGAGATGAACAATGTTAAGTCAGAA
GAGGAGCAGAGCAGCAGCTCCGTGAAGAAAGATGAGACTAATGTGAAGATGGAGTCTGAGGGGGGTGCAGATGAC
TCTGCTGAGGAGGGGGACCTACTGGATGATGATGATAATGAAGATGGGGGGATGACCAGCTGGAGTTGATCAAGG
ATGATGAAAAAGAGGCTGAGGAAGGAGAGGATGACAGAGACAGCGCCAATGGCGAGGATGACTCTTAAGCACATA
GTGGGGTTTTAGAAATCTTATCCCATTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTACCAGATCCT
CTCCCTTAGTATCTTCAGCACATGCTCACTGTTTTTCCCCATCCTTGTCCTTCCCATGTTTCATTAATTAATTCATA
TTGCCCCGCGCCTAGTCCCATTTTCACTTCTTTGACGCTCCTAGTAGTTTTGTGAAGTCTTACCCTGTAATTTT
TGCTTTTAATTTTGATACCTCTTTATGACTTAACAATAAAAATGATGTATGGTTTTTATCAACTGTCTCCAAAAT
AATCTCTTGTTATGCAGGGAGTACAGTTCTTTTCATTCATACATAAGTTCAGTAGTTGCTTCCCTAACTGCAAAG
GCAATCTCATTTAGTTGAGTAGCTCTTGAAAGCAGCTTTGAGTTAGAAGTATGTGTGTTACACCCCCACATTAGT
GTGCTGTGTGGGCGAGTTCAACACAAATGTAACAATGTATTTTTGTGAATGAGAGTTGGCATGTCAAATGCATCC
TCTAGAAAAATAATTAGTGTATAGTCTTAAGATTTGTTTTCTAAAGTTGATACTGTGGGTTATTTTTGTGAACA
GCCTGATGTTTGGGACCTTTTTTCTCAAATAAACAAGTCCTTATTAAACCAGG

WO 2004/030615

PCT/US2003/028547

993/6881
FIGURE 926

GCCGACCTCCAGCAGCAGTCGGCTTCTCTACGCAGAACCCGGGAGTAGGAGACTCAGAATCGAATCTCTTCTCCC
TCCCCCTTCTTGTTTTTCGGCTTTGTGAGAAACCTTACCATCAAACACAATGGCCAGCAACGTTACCAACAAGACAG
ATCCTCGTTCCATGAACCTCCCGTGATTTCATTGGGAATCTCAACACTCTTGTTGGTCAAGAAATCTGATGTGGAGG
CAATCTTTTCGAAGTATGGCAAATTTGTGGGCTGCTCTGTTTCATAAGGGCTTTGCCTTCTTTCAGTATGTTAATG
AGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGATGGCAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGG
CTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGTGTGAAACGATCTGCAGCGGAGATGACCTTCAGGCCATTAA
GAGGGAGCTGACCCAGATAAAACAAAAAGTGGATTCTTTCTGGAAAACCTGGAAAAAATTGAAAAGGAACAGAG
CAAACAAGCAGTAGAGATGAACAATGTTAAGTCAGAAGAGGAGCAGAGCAGCAGCTCCGTGAAGAAAGATGAGAC
TAATGTGAAGATGGAGTCTGAGGGGGGTGCAGATGACTCTGCTGAGGAGGGGGACCTACTGGATGATGATGATAA
TGAAGATGGGGGGATGACCAGCTGGAGTTGATCAAGGATGAGGATGACTCTTAAGCACATAGTGGGGTTTAGAAA
TCTTATCCCATTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTTACCAGATCCTCTCCCCTAGTATCT
TCAGCACATGCTCACTGTTTTCCCATCCTTGTCTTCCCATGTTTATTAAATTCATATTGCCCCGCGCCTA
GTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTTGTAAAGT

WO 2004/030615

PCT/US2003/028547

994/6881
FIGURE 927

GAGACGAAGACTGAGCGGTTGCGGCCGCGTTGCCGACCTCCCCTTCTTGTTTTTCGGCTTTGTGAGAAACCTTACC
ATCAAACACAATGGCCAGCAACGTTACCAACAAGACAGATCCTCGTTCCATGAACCTCCCGTGTATTTCATTGGGAA
TCTCAACACTCTTGTTGGTCAAGAAATCTGATGTGGAGGCAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGCTC
TGTTTCATAAGGGCTTTGCCTTCTTTTCAGTATGTTAATGAGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGATGG
CAGAAATGATTGCTGGCCAGGTTTTAGATATTAACCTGGCTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGTGT
GAAACGATCTGCAGCGGAGATGTACGGCTCCTCTTTTGACTTGGATTGTGACTTTCAACGGGACTATTATGATAG
GATGTACAGTTACCCAGCACGTGTACCTCCTCCTCCTATTGCTCGGGCTGTAGTGCCCTCGAAACGTCAGCG
TGTATCAGGAAACACTTCACAAAGGGGCATAAGTGGCTTCAATTCTAAGAGTGGACAGCGGGGATCTTCCAAGTC
TGGAAGTTGAAAGGAGATGACCTTCAGGCCATTAAGAGGGAGCTGACCCAGATAAAACAAAAAGTGGATTCTTT
CCTGAAAAACCTGAAAAAAATTGAAAAGGAACAGAGCAAACAAGCACTGGAGTTGATCAAGGATGATGAAAAAGA
GGCTGAGGAAGGAGAGGATGACAGAGACAGCGCCAATGGCGAGGATGACTCTTAAGCACATAGTGGGGTTTAGAA
ATCTTATCCCATTTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTTCACCAGATCCTCTCCCCTAGTATC
TTCAGCACATGCTCACTGTTTTCCCCATCCTTGTCTTCCCATGTTCAATTAATTAATTCATATTGCCCCGCGCCT
AGTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTT

WO 2004/030615

PCT/US2003/028547

995/6881
FIGURE 928

ATCTTTTAGAGAAATCTCGGGTTGTAAACAGCCAAGAGGTGAAAGAAACTTCCATGTGTTCTATCAGCTGCTCT
CTGGTGCCCTCTGAAGAGCTCCTCAATAAACTTAAGCTTGAGAGGGATTTTACGAGGTATAACTACCTGAGTCTGG
ATTCGGCCAAAGTGAATGGAGTGGATGATGCAGCAAATTTTAGAACCGTGCGGAATGCCATGCAGATTGTGGGCT
TTATGGATCATGAAGCTGAGTCTGTCTTGGCGGTGGTGGCAGCAGTGTGAAACTGGGGAACATTGAGTTCAAGC
CCGAATCTCGAGTGAATGGTCTAGATGAAAGCAAAATCAAAGATAAAAATGAGTTAAAAGAAATTTGTGAATTGA
CCGGCATTGATCAATCAGTTCTAGAACGAGCATTAGTTTCCGAACAGTTGAGGCCAAACAGGAGAAAGTTTCAA
CTACACTGAATGTGGCTCAGGCTTATTATGCCCCGTGATGCTCTGGCTAAAAACCTCTACAGCAGGTTGTTTTCAT
GGTTGGTAAATCGAATCAATGAAAGCATTAAAGGCACAAACAAAAGTGAGAAAGAAGGTCATGGGTGTTCTGGACA
TTTATGGCTTTGAGATTTTCGAGGACAACAGCTTTGAGCAGTTTATTATTAATTATTGTAACGAAAAGCTGCAAC
AAATCTTCATTGAACTTACTCTTAAAGAAGAGCAGGAGGAGTATATACGGGAGGATATAGAATGGACTCACATTG
ACTACTTCAATAATGCTATCATTTGTGACCTAATAGAAAATAACACAAATGGAATCCTGGCCATGCTGGATGAAG
AGTGCCCTCAGACCTGGCACAGTCACTGATGAGACCTTCTTAGAAAAGCTGAACCAAGTATGTGCCACCCACCAGC
ATTTTGAGAGCAGGATGAGCAAGTGCTCTCGGTTTCTCAATGACACGTCTCTGCCTCACAGCTGCTTCAGGATCC
AGCATTATGCTGGAAGGTTGCTGTACCAGGTGGAAGGATTGCTTGACAAAACAATGACCTTCTCTATCGAGACC
TGTCCCAAGCCATGTGGAAGGCCAGCCATGCCCTCATCAAGTCTTTGTTCCCCGAAGGGAATCCCGCCAAGATCA
ACCTGAAAAGGCCCTCTACAGCAGGCTCACAGTTCAAGGCATCCGTGGCCACTCTGATGAAAACCTACAGACCA
AGAACCCAAACTATATTAGGTGTATCAAACCGAATGATAAAAAAGCAGCACACATCTTCAACGAGGCTCTAGTGT
GTCATCAGATCAGGTACCTGGGGCTTTTGGAAGCGTCCGAGTGCGGAGGGCAGGCTACGCCTTCAGGCAGGCCT
ATGAACCTTGCCCTAGAAAGATACAAAATGCTTTGTAAACAAACATGGCCTCATTGGAAAGGACCAGCCAGGTCTG
GTGTGGAGGTCTATTTAATGAATTAGAAATTCCCGTGGAAGAATACTCCTTTGGTAGATCAAAGATATTCATCC
GAAACCCAAGAACATTATTCAAATTAGAAGACCTGAGGAAGCAACGCCTGGAGGACTTGGCCACTCTCATTGAGA
AGATATATCGGGGGTGGAAATGCCGCACACACTTCTGCTAATGAAAAAAGCCAAATTGTGATTGCCGCTGGT
ACAGGAGATATGCGCAACAAAAGAGGTACCAGCAGACAAAGAGTTCCGCCTTAGTAATTCAGTCTTATATCCGGG
GTTGGAAGGCTCGAAAAATTCTGCGGGAAGTGAAGCATCAAAGCGCTGTAAGGAAGCAGTCACGACCATTGCTG
CATATTGGCATGGGACCCAGGCTCGAAGGGAATTGAAACGCTTGAAGGAGGAGGCTAGGCGTAAGCATGCAGTTG
CTGTCAATTTGGGCTTACTGGCTTGGACTGAAGGTACGTAGAGAATACAGGAAATCTTCAGAGCCAATGCTGGAA
AGAAAATCTATGAGTTTACGCTTCAGAGAATTGTGCAAAAATACTTCTTGGAATGAAAAATAAGATGCCTTCCT
TATCTCCAATAGACAAGAATTGGCCCTCAAGACCTTACTTATTCTTGGATTCTACTACAAGGAGCTAAAAAGGA
TTTTCCACTTGTGGAGGTGTAAAAAATACAGGGACCAATTACAGACCAGCAGAACTTATTTATGAAGAGAAAC
TAGAAGCCAGTGAACCTCTCAAAGACAAGAAGGCTTTATACCCATCTAGTGTGGGCAACCATTCGAAGGGGCTT
ACCTGGAAATCAACAAGAACCCCAAGTATAAGAACTCAAAGATGCCATTGAAGAAAAGATCATCATTGCTGAAG
TCGTGAACAAAATTAACCGTGCTAATGGGAAGAGTACATCTCGGATTTTCTTAAACAAACAATAATCTCCTTC
TTGCTGACCAAAAGTCTGGACAAATCAAGTCAGAGGTTCCATTGGTGGATGTGACCAAGGTATCAATGAGCTCAC
AAAATGATGGCTTCTTCGCCGTCCACCTCAAAGAGGGGCTCAGAAGCAGCTAGTAAAGGAGACTTCTCTTCAGCA
GTGATCACCTGATTGAAATGGCCACCAAGCTCTATCGCACAACTCTCAGCCAAACCAACAGAAGCTCAATATTG
AGATTTCCGATGAGTTCTTGGTACAGTTTACAGAGGACAAAGTATGTGTGAAGTTTATTAGGAACCTGTAGTAT
GATATTTAACAATATAGGCTTCAAAGAAGGGCTGGTCTTAAGAGGGGCAGAAATGAATGACCAGGTTAAATCCCT
CTACATGTGGTTTCTGTTTG

WO 2004/030615

PCT/US2003/028547

996/6881
FIGURE 929

AGGTCAGAAATGTGAATTCCAGGATGCCTATGTTCTGTTGAGTGAAAAGAAAATTTCTAGTATCCAGTCCATTGT
ACCTGCTCTTGAAATTGCCAATGCTCACCGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCT
AAGTACACTCGTCTTGAAATAGGCTAAAGGTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCCAGGGTTTGGTGACAA
TAGAAAGAACCAGCTTAAAGATATGGCTATTGCTACTGGTGGTGCAGTGTGGAGAAGAGGGATTGACCCTGAA
TCTTGAAGACGTTAGCCTCATGACTTAGGAAAAGTTGGAGAGGTCATTGTGACCAAAGACGATGCCATGCTCTT
AAAAGGAAAAGGTGACAAGGCTCAAATTGAAAAACGTATTCAAGAAATCATTGAGCAGTTAGATGTCACAACTAG
TGAATATGAAAAGGAAAACTGAATGAACGGCTTGCAAACTTTTCAGATGGAGTGGCTGTGCTGAAGGTTGGTGG
GACAAGTGATGTTGAAGTGAATGAAAAGAAAGACAGAGTTACAGATGCCCTTAATGCTACAAGAGCTGCTGTTGA
AGAAGGCATTGTTTTGGGAGGGGGTTGTGCCCTCCTTCGATGCATTCCAGCCTTGGACTCATTGACTCCAGCTAA
TGAAGATCAAAAAATTGGTATAGAAATTATTAAGAAGAACTCAAAATTCAGCAATGACCATTGCTAAGAATGC
AGGTGTTGAAGGATCTTTGATAGTTGAGAAAAATTATGCAAAGTTCCTCAGAAAGTTGGTTATGATGCTATGGCTGG
AGATTTTGTGAATATGGTGGAAAAAGGAATCATTGACCCAACAAAGGTTGTGAGAACTGCTTTATTGGATGCTGC
TGGTGTGGCCTCTCTGTTAACTACAGCAGAAAGTTGTAGTCACAGAAATTCCTAAAGAAGAGAAGGACCTTGAAT
GGGTGCAATGGGTGGAATGGGAGGTGGTATGGGAGGTGGCATGTTCTAACTCCTAGACTAGTGCTTTACCTTTAT
TAATGAAGTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCAATAACTTCAGAGAAGTCAGTTGGAGAAAATGAA
GAAAAAGGCTGGCTGAAAATCACTATAACCATCAGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGC
TGTATTGTCCATGCCTACAGATAATTTATTTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG
TACAAGAGCCATGTACCAGTGTACTGCTTCAACTTAAATCACTGAGGCATTTTACTACTATTCTGTTAAATC
AGGATTTTAGTGCTTGCCACCACCAGATGAGAAGTTAAGCAGCCTTCTGTGGAGAGTGAGAATAATTGTGTACA
AAGTAGAGAAGTATCCAATTATGTGACAACCTTTGTGTAATAAAAAATTTGTTTAA

WO 2004/030615

PCT/US2003/028547

997/6881
FIGURE 930

GCTACACTAGAGCAGAGTACGAGTCTGAGGCGGAGGGAGTAATGGCAGGACAAGCGTTTAGAAAGTTTCTTCCAC
TCTTTGACCGAGTATTGGTTGAAAGGAGTGCTGCTGAAACTGTAACCAAAGGAGGCATTATGCTTCCAGAAAAAT
CTCAAGGAAAAGTATTGCAAGCAACAGTAGTCGCTGTTGGATCGGGTTCTAAAGGAAAGGGTGGAGAGATTCAAC
CAGTTAGCGTGAAAGTTGGAGATAAAGTTCTTCTCCCAGAATATGGAGGCACCAAAGTAGTTCTAGATGACAAGG
ATTATTTCCCTATTTAGAGATGGTGACATTCTTGGAAAGTACGTAGACTGAAATAAGTCACTATTGAAATGGCATC
AACATGATGCTGCCCATTCCTGAAGTTCTGAAATCTTTCGTCATGTAAATAATTTCCATATTTCTCTTTTATA
ATAAACTAATGATAACTAATGACATCCAGTGTCTCCAAAATTGTTTCCTTGACTGATATAAACTTCCAAATA
AAAATATGTAAAT

WO 2004/030615

PCT/US2003/028547

998/6881
FIGURE 931

MAGQA FRKFLPLFDRVLVERSAAETVIKGGIMLPEKSQ GKVLQATVVAVGSGSKGKGGEIQPVSVKVGDKVLLPE
YGGTKVVLDDKDYFLFRDGDILGKYVD

WO 2004/030615

PCT/US2003/028547

999/6881

FIGURE 932

GATTTGACCCTTGAGCCGTAGGGAGCGCGGCATTTTCTGGAAAGTTCTGGAACCGAGCGAGGCCCGGGAAC TAGA
CTAAGCCGGCCGGAGAGGGCTGAGCGCGCTAGCACACCCTGCGCGGAAATGCTTCGGTTACCCACAGTCTTTCGC
CAGATGAGACCGGTGTCCAGGGTACTGGCTCCTCATCTCACTCGGGCTTATGCCAAAGATGTAAAATTTGGTGCA
GATGCCCCGAGCCTTAATGCTTCAAGGTGTAGACCTTTTAGCCGATGCTGTGGCCGTTACAATGGGGCCAAAGGGA
AGAACAGTGATTATTGAGCAGAGTTGGGGAAGTCCCAAAGTAACAAAAGATGGTGTGACTGTTGCAAAGTCAATT
GACTTAAAAGATAAATACAAAAACATTGGAGCTAAACTTGTTCAAGATGTTGCCAATAACACAAATGAAGAAGCT
GGGGATGGCACTACCACTGCTACTGTACTGGCACGCTCTATAGCCAAGGAAGGCTTCGAGAAGATTAGCAAAGGT
GCTAATCCAGTGGAAATCAGGAGAGGTAGGAATGTCTGTTGTCACCACAGTGTTCTAAACTTCAGTGTGCTTTAA
GGCATTGATTCCTTGGACCTAAGGAAAGTGTTAACTTGAGGAAATTAATCCTTCTCTCATTCTCCTCCTTGGCCT
GGAGAAATCTTAAACTGGGTTTTCTTTAGCAAGCTTGGCTGT

WO 2004/030615

PCT/US2003/028547

1000/6881
FIGURE 933

TGGAAAGAGTGGAAACGAGAAAAACCTTTCAGACTATTGTGTTCTGGGCCAGCGTCCAATGCATTACCAAATATGA
ACCAGCTGGCATCCCTGGGGAAAACCAACGAACAGTCTCCTCAAGCCAAATTCACCACAGTACTCCAATCCGAA
ACCAAGTGCCCGCATTACAGCCCATCATGAGCCCTGGTCTTCTTTCTCCCCAGCTTAGTCCACAACCTTGTAAGGC
AACAAATAGCCATGGCCCATCTGATAAACCAACAGATTGCCGTTAGCCGGCTCCTGGCTCACCAGCATCCTCAAG
CCATCAACCAGCAGTTTCTGAACCATCCACCCATCCCCAGAGCAGTTAAGCCAGAGCCAACCAACTCTTCCGTGG
AAGTCTCTCCAGATATCTACCAGCAAGTCAGAGATGAGCTGAAGAGGGGCCAGTGTGTCCCAAGCTGTCTTTGCAA
GAGTGGCATTCAACCGCACACAGGTACAATTAGCATTAAACACTGTAATTAACAGTAATACTGGGGACAGAATTG
AGATAGGTTATAATTATTTTATCTCTTTAAAAAGCTTTATGGATCTCAGGACATAGAATTAGATTAATTAATAA
TCCTTAGTTAATGAAACGCTATTACCATTGATCCATGCATGACCATGATTAATTAATAATTGATTAATTTTGAT
GAGGTAATGGACATCTTTGAACCCAACATGCAACTCAGGACCCCAAATGTTACTAATGACTTGGGTATGTACTCT
CTCATCTCTCCATTTACTGTTTGCAGATGTAACCCCTGATCTTGAATTTTGTGATTATCAGTCTCTTGCCATTTT
TAAAAACAAATTATAAACTATGCATGCCAGACAATCTATTTTTTTCCCTTGGTTTTGAACGTTATAAAAGAAA
TAAATTTATGTTTTATAATTTTATAAGTAAAGTTTTATTTAAAAATTTATAAAATCCTTCAAAACATAAAAGTT
AGATTTAAGATATTGATAAAATGATAATGGATAGTTTACTTTTTATTTTAAATGTTTGAGAGAATTATATGCCAAT
TATAACACTAAATGTTGAAAAATGTAACAGTTAATTCACACGTCTTATTTTTATTGAGGGTGCTTATATGTAAGA
CATTCTTTTCTGCTAGTAGTTCTTAAACTGGAGTGTGCATCAGAATCACCTGGAGGGCTGTGAAACACAGACTGC
TGGGCCTCATCCCATAGTTTCTGATTGAGTAAGTCTGAGGTTGGACTCAGAAATGGACATTTCTAACAAGATCCC
AGGTGATTATGATGGTACTGATCCGGGGCCGCATGTTGAGAAAACTTACCTAGCCCTTATATGAGTAAGAACAA
AGCAGATGTGCATAATCTCGGGGAGCTAACGATCTAGTGGTGAAAACAGGTAACCAGATAATTAGAGTAAATG
TGAAGTGTTATGAGTAATGTTGGAGAGTGTAAGCAATAGTTGTGGTGGAGGTTTCATGGTGAGCTGGAGGTGAGGA
ATACTTCCAGGAGAATGAATATGGTAAGCCTTCAAGAAAACAGTAGATTAAATTTTACGACCCCTCGTAAATGCA
AGGCAGGAAGCTAAGCTCTATGTGGGTGCAAAGAGGAAAAAGATAATGGGCAAGCACATATGTAAACAACACTCT
AGAGTATTAGGTTGTCAATGGGTTAGACCTTGAAGGATTAATAAAGTACAGCAGGCAAAGATGATGAAGAAGPAG
ATTATTATTTTAAGGTAAAGACATTCATAGGAAAGATGTTGAGTTAAAAATGCAGGAATAATTTGAAGACATAA
AACAACTGATTTCTGAGAAAAACCTGTGAACGTACAGAATGTAGGAATGCTTTCATTTATCTGATACCTGTTCA
GAGACACATGATAACACACGCTGTAGATGGACCTTACAAATGAAAGAAAGCATGCTGGATTGAAACCTCAATAAT
TTGGAATAACAGGAATGTTTCCAAATTTAATGATTACTTCAGAAGTTAAGGGCTGGGCACAGTGGCTCATGTC
TGATGCTTAGCACTTTGGGAGGCCAAGGTGGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGGCAAG
ATGGTAAAAACCATCTCTACTAAAACAGAACAAAACAAAAAATTAGCTGGGCGTGGTGATGCGTGCCTGTAGT
CTCAGCTACTCAGGAGGCTGAGGCAGAAGAATCCCTTGAACCCAGGAGGCGGAGGCTGCAGTGAGCCGAGATCAT
GCCACTGCACTCCAGCCTGAGTGAGAGTGAACTCCATCTCAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1001/6881
FIGURE 934

GAGAGGAGACACCGCCGAGTTGCCGGTACATCGGGGATTCTGGCTCTTTCTCTTTCGCCTTAAATTCGGGTGT
CTTTTATGAATAATCAAAAGCAGCAAAAGCCAACGCTATCAGGCCAGCGTTTTAAACTAGAAAAAGAGATGAAA
AAGAGAGGTTTGACCCTACTCAGTTTCAAGACTGTATTATTCAAGGCTTAAGTGAACCGGTACTGATTTGGAAG
CAGTAGCTAAGTTTCTTGATGCTTCTGGAGCAAACTTGATTACCGTCGATATGCAGAAACACTCTTTGACATTC
TGGTGGCTGGTGGAAATGCTGGCCCCAGGTGGTACACTGGCAGATGACATGATGCGTACAGATGTCTGCGTGTTTG
CAGCCCAAGAAGATCTAGAGACCATGCAAGCATTGCTCAGGTTTTTAACAAGTTAATCAGGCGCTACAAATACC
TGGAGAAAGGTTTTGAAGATGAAGTAAAAAGCTGCTGCTGTTCTTGAAGGGTTTTTCAGAGTCGGAGAGGAACA
AGCTAGCTATGTTGACTGGTGTTCTTCTGGCTAATGGAACACTTAATGCATCCATTCTTAATAGCCTTTATAATG
AAAATTTGGTTAAAGAAGGAGTTTCAGCAGCTTTTGCTGTGAAGCTCTTTAAATCATGGATAAATGAAAAAGATA
TCAATGCAGTAGCTGCAAGTCTTCGGAAAGTCAGCATGGATAACAGACTGATGGAACCTTTTCTGCCAATAAGC
AAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAAGAGCTTTCAGAATATGTTCCGAATCAGC
AAACCATCGGAGCTCGTAAGGAGCTCCAGAAAGAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATA
TAATTTTATATGTCAAGGAGGAGATGAAAAAACAACATCCAGAGCCAGTTGTATCGGAATAGTCTGGTCAA
GTGTAATGAGCACTGTGGAATGGAACAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAGCACTTGAAGCAAT
ACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTGACTCTGTTACTGAAGATTCAGGAGTATT
GCTATGACAACATTCATTTTCATGAAAGCCTTCAGAAAATAGTGGTGCTTTTTTATAAAGCTGAAGTCCTGAGCG
AGGAGCCCATTTTGAAGTGCTATAAAGATGCACATGTTGCAAAGGGGAAGAGTGTTTTCTTGAGCAAATGAAAA
AGTTTGTAGAATGGCTCAAAAATGCTGAAGAAGAACTGTAATCTGAAGCTGAAGAAGGTGACTGAAATTTTGAAC
TACACCCTCAGTAAAGCAAACAGGAGTTGTAGATAAAATGTCATGTCTCATGTGTCCTGGTTCTTACATCTTCTCT
ACCTCCCTGTATCAAGCATGATATAAGGGCTTCATGGCAAATTTTATTTTAACTGTTTCTATGGTTGCTGGA
TGTTGGGTTTAGTTTCTAAAACCATGTTTTAAGTAGCTACAGGAGCTATAGATTGAATCTAATGTTGCATTAGT
CTTTTCAGTTATCTTCTACCTCCTGTATTTTCTACTGTAATAATGTAATTTAAGGCCTTCCACAATGAACAGTTC
ACTTTATTCCCTGGGTTTTCTATAAACAGTTTTAAGGATATGATTGGTTAAAAATAATTTGTTATAAAAAATTC
TGTTTGCAAATTAACTGGAAAAGTATCCAGAGTCTCAAAGGCAATGATTTGTGAGATAATATGGCATGCCCGG
AGCCCTGCTCATCAATGAAAAACCCATATGTAATAATCGAATTCATTTAACATGAATCTTGAGTACGTGGACCAT
TGCTTGCAATGTTAACTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGCATTTTTTAACTCCAGATATCCTAAAGCTC
AATTGTTTGGTCTCTGGTTTTTCATCCTTAGAGAAGCCATGGAGAACAGACTTGAAAAGTTTAGGAAATCATAATG
TGGCAGAGGTGGTGGGAAGAAGAAAGTTGAGCTTTTCCCCTTGAGAACTTCTGCATTTAGTTTCTATCTTTCC
AGGCAAAACAAATGGGTATTCTTTTCATACAACCATTTTCAAATGAACCTTAGAAAAGTCTTAACATTTAAGGTA
TTTTATGCACAGAATACACTTAGATTGATAGGAAAGAACTCGTAATGGAGTTTGAGTAAAGAAATGACTGATGT
ACTAAACCCAGTAAAAATGTTGAAAATGTTAAAGGTCAGCATGTTCTAATTGGGAATCTAGATATAGCTTAGAT
TTCTATTGGCTTAGAGTATTTGCTATAACAAATGAAGTGCAATGACAATTATATATTCTACTCGGTCATACTG
GACTGGCTTCGTTCTCTTAATATACTCAGTAATGACTCAAGCCTCTGGCTATTAACATACCCTAGTTGCCGTTTT
TTAATTGCCATGAGCCAAATACTTCTTGGTATACAATTGATCCATTTATTTTAAATGGCTGCCTTTTCATTTTCAT
CTTTTCTTGCTGCTACCCATCTATGTATGTAGTCAATTGGGGGAAATGTAGCCACATTTTTTATGGGAAGACTT
TGTGTTAAAAGTGAACATTTTGAAGGTTTTTAAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA
GAAATCGCCCTTTTGAAGGTGCCATTCTTATGAGCCAAAAGTTTGTCAATTTAAAAGTTCATTTTGAGGGAATAA
CATGTAATATAATTTGAAATAAAGGTATAGTAACCTTAAAAAGAACATTATACTGATTGTTGTGAATGGGGTGA
ATTTGTTAAAATGAGTAACTTTGATAAAGTTTTTCATGCACAGGCAAAATGTATTCAGTAGATTTCTACGTAGTG
ATCTGCTTTTACTTTGTAATTTGTAGTTCTCAAAAGACTTTTTTTTTAAAAAATAAAGTCCATACTTACACTT

WO 2004/030615

PCT/US2003/028547

1002/6881
FIGURE 935

MNNQKQQKPTLSGQRFKTRKRDEKERFDPTQFQDCIIQGLTETGTDLEAVAKFLDASGAKLDYRRYAETLFDILV
AGGMLAPGGTLADDMMRTDVCVFAAQEDLETMQAFAQVFNKLIRRYKYLEKGFEDVKKLLFLKGFSESERNKL
AMLTGVLLANGTLNASILNSLYNENLVKEGVSAFAVKLFKSWINEKDINAVAASLRKVSMDNRLMELFPANKQS
VEHFTKYFTEAGLKELSEYVRNQQTIGARKELQKELQEQMSRGDPFKDIILYVKEEMKKNNIPEPVVIGIVWSSV
MSTVEWNKKEELVAEQAIKHLKQYSPLLAFTTQGGQSELTLLKIQEYCYDNIHFMKAFQKIVVLFYKAEVLSEE
PILKWKDAHVAKGKSVFLEQMKKFVEWLKNAEESESEAEEGD

WO 2004/030615

PCT/US2003/028547

1003/6881
FIGURE 936

ACGCAGAGAAGTTTCCGGGACTGAACTTTGAACTTTACCTGATTTCTGTATGTTTGTCATCTTGCGTACGCCCAGT
CCCCACGACAGTCCGGTTTGTAGATTCCCTGATCTGCAATTCTTCCCGTTTCCTTCATGGATTTGAAGGCTCTCCT
TTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAGAGTTGGGACAATGTTGGATTACTGGTGGAACCAAG
CCCACCACATACTGTAAATACACTCTTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAA
GAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACATGGAA
GGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCC
CCAGGGCGTCAACAACCTGGTTGGCTAAAGGGCTTGGAGCTTGACCTCCAGGCCCATAACATCCTTCCAAAGCTCC
CAACTACCCTACAGAGGGAAACCACCGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTC
TGCAGTGAAAGGAATTGACGGTGTCTGTCACTTCTTTTCTGCTAGGACTGGTAATGAGGAACAAACACGGAT
TAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGGAACAAACAACCTTTATCAGAA
GACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACATACTGGAATGGGACGGTTATGCACACTGGATGAATC
TGTCTCCCTGGCAACCATGATTGATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGT
GGGGAGAACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAGGGTGT
TGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCTGCTTCCCAAGGAATAAATGT
CATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGA
GAATAAGATAAATATTATCCTATCAGAGACTGACAGGGACCTCTTCAGGTGGTATAATTGCAGAAACATCAGGA
TAACACATTCTACAAATCAGCTGGATGCCAACTTAAATTTGTAACATGAGTCAGTGGGACTGGTGTGCTTCCAGA
GAGTGTCTTCGAGGGTATCATCATTTCCGGTTTGTTAATCTTATTCACCAAATGTTCTATCGCTCGTAAGGTAAA
ACTGTAATATAACTACCATATTAAATAACAAATGTTTATTATAAACTCTAGGAAAGATTGAATAAAATCTGTTTA
CTTAACATTC

WO 2004/030615

PCT/US2003/028547

1004/6881
FIGURE 937

MLSSCVRPVPTTVRFVDSLICNSSRSFMDLKALLSSLNDFASLSFAESWDNVGLLVEPSPPHTVNTLFLTNDLTE
EVMEEVLQKKADLILSYHPPIFRPMKRITWNTWKERLVIRALENRVGIYSPHTAYDAAPQGVNNWLAKGLGACTS
RPIHPSKAPNYPTTEGNHRVEFNVNYTQDLQVMSAVKGIDGVSVTSFSARTGNEEQTRINLNCTQKALMQVVDFL
SRNKQLYQKTEILSLEKPLLLHTGMGRCLTLDSESVSLATMIDRIKRHLKLSHIRLALGVGRTLESQVKVVALCAG
SGSSVLQGVEADLYLTGEMSHHDTLDAASQGINVILCEHSNTERGF₁LSDLRDMLD₂SHLENKINIILSETDRDPLQ
VV

WO 2004/030615

PCT/US2003/028547

1005/6881
FIGURE 938

CTCCTTTCTGCCCCTGGACGCCGCCGAAGAAGCATCGTTAAAGTCTCTCTTCACCCTGCCGTCATGTCTAAGTCA
GAGTCTCCTAAAGAGCCCCGAACAGCTGAGGAAGCTCTTCATTGGAGGGTTGAGCTTTGAAACAACCGATGAGAGC
CTGAGGAGCCATTTTGAGCAACGGGGAACGCTCACAGACTGTGTGGTAATGAGAGATCCAAACACCAAGTGCTCC
ACGGGCTTTGGGTTTGTGCATATGCCACTGTGAAGGAGGTGGAGGCAGCTATGAATGCAAGGCCACAGAAGGTG
GATGGAAGAGTCGTGGAACCAAGAGAGCTGTCTCGAGAGAAGATTCTCAAAGACCAGGTGCCCACTTAAGTGTG
AAAAAGATATTTGTTGGTGGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATTATTTGAACAGTATGGA
AAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGGAAGAAAAGGGGCTTTGCCTTTGTAACCTTTGAT
GACCATGACTCCGTGGATAAGATTGTCAATTCAGAAAATACCACACTGTGAATGGCCACAAGTGTGAAGTTAGAAAA
GCCCTGTCAAAGCAAGAGATGACTAGTGCTTCATCTAGCCAAAGAGGTGGAAGTGGTCTGGAACCTTTGGTGGT
GGTCGTGGAGGTGGTTTCAGTGGGAATGACAACTTTGGTTCATGGAAGAACTTCAGTGGTTCATGGTGGCTTTGGT
GGCAGCCGTGGTGGTGGTGGATATGATGGCAGTGGGGATGGCTATAATGGATTGGTAATGATGGAAGCCATTTT
GGAGGTGGTGGGAAGCTACAATGATTTTGGCAATTACAAAATCAGTCTTCAAATTTGGACCCGTGAAGGGAGGA
AATTTTGGAGGCAGAAGCTCTGGCCCCATGGCGGTGGAGGCCAATACTTTGCAAAACCACGAACTAAGGTGGC
TATGGCGGTTCCAGCAGTAGCAGTAGCTATGGCAGTGGCAGAAGATTTTAATTAGGAAACAAAGCTTAGCAGGAG
AGGAGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAAGTTCAGCCAAGCACAGTGGTGGCA
GGGCCTAGCTGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAACCTCGAGGACTGTAT
TTGTGACTAATTGTATAACAGGTTATTTTAGTTTTCTGTCTGTGGAAAGTGTAAGCATTCCAACAAAGGGTTT
AATGTAGATTTTTTTTTTTTGCACCCATGCTGTTGATTGCTAAATGTAATAGTCTGATCGTGACGCTGAATAAATG
TCTTTTTTTTTTAATGTGCTGTGTAAAGTTAGTCTACTCTGAAGCCATCTTGGTAAATTTCCCCAACAGTGTGAAG
TTAGAATTCCTTCAGGGTGATGCCAGGTTCTATTTGGAATTTATATACAACCTGCTTGGGTGGAGAAGCTATTGT
CTTCGGAAACCTTGGTGTAGTTGAACTGATAGTTACTGTTGTGACCTGAAGTTCACCATTAAGGGATTACCCA
AGCAAAATCATGGAATTATTGGTTATAAAAGTGATTGTTGGCACATCCTATGCAATATATCTAAATTGAATAATG
GTACCAGATAAAATTATAGATGGGAATGAAGCTTGTSTATCATCCATTATCATGTGTAATCAATAAACGATTAA
TTCTCTGGAA

WO 2004/030615

PCT/US2003/028547

1006/6881
FIGURE 939

MSKSESPKEPEQLRKLF IGGLSFETTDESLSHFQRTLTDCVVMRDPNTKCS TGFGFVTYATVKEVEAAMNAR
PQKVDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAF
VTFDDHDSVDKIVIQKYHTVNGHNCEVRKALSKQEMTSASSSQRGRSGSGNFGGGRGGGFSGNDNFGHGRNFSGH
GGFGGSRGGGGYDGS GDGYNGFGNDGSHFGGGGSYNDFGNYKNQSSNFGPVGKGNFGGRSSGPYGGGGQYFAKPR
NRWLWRFQQVAVAMAVAEDF

WO 2004/030615

PCT/US2003/028547

1007/6881
FIGURE 940

GAGGCGTAGCGGAAGTTACTGCAGCCGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTTGTAAACCCCGGAGCG
AGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCGGGTGAAGCCACCGTCATCATGTCTGACCAGGAG
GCAAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGGTGAATATATTAACTCAAAGTCATTGGACAGGAT
AGCAGTGAGATTCACCTCAAAGTGAAAATGACAACACATCTCAAGAACTCAAAGAATCATACTGTCAAAGACAG
GGTGTTCGAATGAATTCACCTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCCAAAAGAACTG
GGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAACGGGGGGTCATTCAACAGTTTAGATATTCTTT
TTATTTTTTTTCTTTCCCTCAATCCTTTTTTATTTTTTAAAAATAGTTCTTTTGTAATGTGGTGTTCAAAACGGA
ATTGTTATTCATTATTGTTTGTTCATTGTGCTGATTTTTGTTGATCAAGCCTCAGTCCCCTTCATATTACC

WO 2004/030615

PCT/US2003/028547

1008/6881
FIGURE 941

ATGTTGGTGCTGTTTGAAACGTCTGTGGGTTACGCCATCTTTAAGGTTCTAAATGAGAAGAACTTCAAGAGGTT
GATAGTTTATGGAAAGAATTTGAAACTCCAGAGAAAGCAAACAAAATAGTAAAGCTAAAACATTTTGAGAAATTT
CAGGATACAGCAGAAGCATTAGCAGCATTACAGCTCTGATGGAGGGCAAATCAATAAGCAGCTGAAAAAGTT
CTGAAGAAAATAGTAAAGAAGCCCATGAACCGCTGGCAGTAGCTGATGCTAAACTAGGAGGGGTCATAAAGGAA
AAGCTGAATCTCAGTTGTATCCATAGTCCTGTTGTTAATGAACTTATGAGAGGAATTCGTTACAAAATGGATGGA
TTAATCCCTGGGGTAGAACCACGTGAAATGGCAGCTATGTGTCTTGGATTGGCTCACAGCCTGTCTCGATATAGA
TTGAAGTTTAGCGCTGATAAAGTAGACACAATGATTGTTTCAGGCAATTTCCCTGTTAGATGACTTGGATAAAGAA
CTAAACAACACTACATTATGCGATGTAGAGAATGGTATGGCTGGCATTTCCTGAATTAGGAAAAATTATTTTCAGAT
AATTTAACATACTGCAAGTGTTTACAGAAAGTTGGCGATAGGAAGAACTATGCCTCTGCCAAGCTTTCTGAGTTG
CTGCCAGAAGAAGTTGAAGCAGAAGTGAAAGCAGCTGCAGAGATATCAATGGGAACAGAGGTTTCAGAAGAAGAT
ATTTGCAATATTCTGCATCTTTGCACCCAGGTGATTGAAATCTCTGAATATCGAACCAGCTCTATGAATATCTA
CAAAATCGAATGATGGCCATTGCACCCAATGTTACAGTCATGGTTGGGGAATTAGTTGGAGCACGGCTTATTGCT
CATGCAGGTTCTCTTTTAAATTTGGCCAAGCATGCAGCTTCTACCGTTCAGATTCTTGGAGCTGAAAAGGCACTT
TTCAGAGCCCTCAAATCTAGACGGGATACCCCTAAGTATGGTCTCATTATCATGCTTCACTCGTGGGCCAGACA
AGTCCCAAACACAAAGGAAAGATTTCTCGAATGCTGGCAGCCAAAACCGTTTTGGCTATCCGTTATGATGCTTTT
GGTGAGGATTCAAGTTCTGCAATGGGAGTTGAGAACAGAGCCAAATTAGAGGCCAGGTTGAGAACTTTGGAAGAC
AGAGGGATAAGAAAAATAAGTGGAACAGGAAAAGCATTAGCAAAAACAGAAAAATATGAACACAAAAGTGAAGTG
AAGACTTACGATCCTTCTGGTGACTCCACACTTCCAACCTGCTCTAAAAACGCAAAATAGAACAGGTAGATAAA
GAGGATGAAATTACTGAAAAGAAAGCCAAAAAGCCAAGATTAAAGTTAAAGTTGAAGAAGAGGAAGAAGAAAA
GTGGCAGAAGAAGAAGAAACATCTGTGAAGAAGAAGAAGAAAGGGGTAAAAAGAAACACATTAAGGAAGAACCA
CTTTCTGAGGAAGAACCATGTACCAGCACAGCAATTGCTAGTCCAGAGAAAAAGAAGAAAAAGAAAAAAGAGA
GAGAACGAGGATTAA

WO 2004/030615

PCT/US2003/028547

1009/6881
FIGURE 942

GGAGGCCAAGGTGCAACTTTCTTCGGTCGTCCCGAATCCGGGTTTCATCCAACACCAGCCGCTCCACCATGCCGC
CGAAGTTCGACGGTGCCACTTCTGCCCTGGCCCCCAAGATCGGCCCCCTGGGTCTGTCTCCAAAAAAGGTTGGTG
ATGACATTGCCAAGGCAACGGGTGACTGGAAGGGCCTGAGGATTACAGTGAACTGACCATTGAGAACAGACAGG
CCCAGATTGAGGTGGTGCCTTCTGCCTCTGCCCTGATCATCAAAGCCCTCAAGGAACCACCAAGAGACAGAAAGA
AACAGAAAAACATTAAACACAGTGGGAATATCACTTTTGATGAGATCGTCAACATTGTTGACAGATGCGGCACC
GATCCTTAGCCAGAGAACTCTCTGGAACCATTAAAGAGATCCTGGGGACTGCCCAGTCTGTGGGCTGTAATGTTG
ATGGCCGCCATCCTCATGACATCATCGATGACATCAACAGTGGTGCTGTGGAATGCCAGCCAGTTAAGCACAAA
GGAAAATATTTCAATAAAGGATCATTTGACAACCTG

WO 2004/030615

PCT/US2003/028547

1010/6881
FIGURE 943

MPPKFDGATSALAPKIGPLGLSPKKVGDDIAKATGDWKGLRITVKLTIQNRQAQIEVVPSASALIIKALKEPPRD
RKKQKNIKHSGNITFDEIVNIVRQMRHRSLARELSGTIKEILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS

WO 2004/030615

PCT/US2003/028547

1011/6881
FIGURE 944

ATGGGAAGATTTGATGGACATGGACATGAGCCTCCTGAGGCCCCAGAACTATCTTTTCGGTTGTGAACTAAAGGCC
GACAAAGATGATCACTTTAAGGTGGATAATGATGAAAATGAGACCATCAGTTTAGGGGCTGGTGCAAGGGATGAA
TTGCACATTGTTGAAGCAGAGGCCATGAATGATGAAGGCAGTCCAATTAAAGTCACACTGGCAACTTTGAAAATG
TCTGTACAGCCAACTGCTTCCCTTGGGGGCTTTGAAATCACACCACCAGTGGTCTTACAGTTGAAGTGTGGTTCA
GGGCCAGTGCATATTAGTAGACAGTGCTTAGTAGCTGTGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAG
GATGTGAACCTCTTAAGCATATCTGGAAAGCGGTCTGCCTCTGGAGGTGGTAGCAAGGCGCCCAGCTACCGCGCC
CACTGGTCAGAAGTGTGGCCAGCGTCTATGCAGGCCCTGGGAGCTCAGGGTGGCTTGGGGTCCAGGAGCATGGCC
GCAGGTATGGCCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAAGGAGACCATGCAAAGCCTGAATGAC
CGCCTGGCCTCCTACCTGGACAGAGTGAGGAGCCTGGAGATGGGAACTGGAAGCTGGAGAGCAAAATCTGGGAG
CACCTGGAGAAGAAGGGACCCAGGTGAGAGACTGGGGCCACTACTTCAAGACCATCGAGGAGGACCTGACTCAG
ATCTTCACAAGTACTGTGGACAATACCTGCATCATTCTGCAGATCGACAATGCCCATCTTGCTGCTGATGACTTT
AGAGTCAAGTATGAGACAGAGCCGGCCACGTGCCAGTCTGTGGAGAACGACATCCATGGGCTCCACAAGGTCATT
GATGACACCAGTGTCACTCAGCTGCAGCTAGAGACAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCCTGAAG
AAGAACCACGAAGAGGAAGTAAAAGGCCTACAAGCCCAGATTGCCAGCTCTGTTGACCATGGAGGCCTTGGAGAT
CGACCTGGACTGGATGAAAAATCTGGAGGCCAGCTTGGAGAACAGCCTGAAGGGGGGGTGGAGGCCTGTACACC
CTGCAGATGGAACAACCTCAATGGGATCCTGCTGCACCTGGAGTCAGAGCTGGCACAGACCTGGGCAGAGGGACAG
GGCCAGGCCAGGAGTACCAGGCCCTGCCAAACATCAAGCAGCAACTCCACGCAAACCATCCAAAAGACTCCCCAC
CTGCCAACAGTGGATGGCAAAGTGGTGTCTGAGACCAATGACACCAAAGTTCTGAGACATTAA

WO 2004/030615

PCT/US2003/028547

1012/6881
FIGURE 945

MEDLMDMDMSLLRPQNYLFGCELKADKDDHFKVDNDENETISLGAGARDELHIVEAEAMNDEGSPIKVTLATLKM
SVQPTASLGGFEITPPVVLQLKCGSGPVHISRQCLVAVEEDAESSEDEEEEDVNLLSISGKRSASGGGSKAPSYRA
HWSEVWPASMQUALGAQGGLGSRSMAGMAGGLAGMGGIQNEKETMQSLNDRLASYLDRVRSLEMGNWKLESKIWE
HLEKKGPQVRDWGHYFKTIEEDLTQIFTSTVDNTCIIILQIDNAHLAADD FRVKYETEPATCQSVENDIHGLHKVI
DDTSVTQLQLETEIEALKEELLFLKKNHEEEVKGLQAQIASSVDHGGLGDRPGLDEKSGGQLGEQPEGGVEACYT
LQMEQLNGIILLHLESELAQTWAEQGQQAQEQALPNIKQQLHANHPKDSHLPTVDGKVVSETNDTKVLRH

WO 2004/030615

PCT/US2003/028547

1013/6881
FIGURE 946

GACAGTTTAGCAGAACAGCCTCCGCGGCTCCGGGGAGAAGCAATATGTTAAGGATACCTGTAAGAAAGGCCTTAG
TAGGCCTTTCTAAGTCTCCTAAAGGATGTGTTTGAACAACCTGCCACAGCAGCAAGCAACTTGATTGAAGTATTTG
TTGATGGTCAGTCTGTCTATGGTGAACCGGGAACGACCGTCTCCAAGCTTGTGAGAAGGTTGGCATGCAGATCC
CTCGATTCTGTTATCATGAAAGGTTGTCTGTTGCTGGAACTGCAGGATGTGCCTTGTGAAATTGAGAAAGCCC
CTAAGGTTGTAGCTGCTTGTGCCATGCCAGTAATGAAGGGTTGGAATATCCTAACAACTCAGAAAAATCCAAAA
AAGCCAGGGAAGGTGTGATGGAGTTCTTATTAGCAAATCACCCATTGGACTGTCCTATTTGTGACCAGGGAGGTG
AATGTGATCTGCAGGACCAGTCCATGATGTTTGGAAATGATAGGAGCCGATTTTTAGAGGGGAAGCGTGCTGTGG
AAGACAAGAACATTGGGCCATTGGTAAAGACCATCATGACAAGATGTATACAGTGTACTCGCTGCATCAGGTTTG
CAAGTGAGATTGCAGGAGTAGATGATTTGGGAACAACAGGCAGAGGAAATGATATGCAAGTTGGCACATACATTG
AAAAGATGTTTCATGTCTGAACGTCTGCGGAATATCATTGATATCTGCCCTGTAGGTGCCCTAACCTCTAAGCCCT
ATGCCTTTACTGCCCGGCTTGGGAAACAAGAAAGACAGAATCCATTGATGTAATGGATGCGGTTGGAAGTAATA
TTGTGGTTAGCACAGAAGTGGAGAAAGTATGAGGATTTTGCCACGTATGCATGAGGACATCAATGAAGAGTGGA
TCTCTGATAAAACCAGATTTGCCATGATGGGCTAAACGTCAAAGACTTACCGAGCCAATGGTCAGAAATGAAA
AAGGGCTTTTAACCTATACTTCTTGGGAGGATGCGCTCTCTCGCGTAGCTGGAATGTTGCAGAGTTTCAAGGCA
AAGATGTGGCAGCAATTGCAGGTGGCTTGGTGGATGCTGAAGCCCTGGTAGCTCTCAAAGATTGCTTAATAGAG
TGGACTCTGACACCTTATGCACTGAAGAGGTCTTCCCCACTGCAGGAGCTGGCACAGATTTGCGTTCCAATTATC
TTCTTAATACTACAATTGCTGGTGTGGAAGAGGCAGATGTTGTTCTTCTGGTTGGTACAAACCCAGGTTTTGAGG
CACCCTGTTTTAATGCTAGAAATTCGAAAGAGCTGGCTGCATAATGACTTAAAAGTGGCCCTTATAGGCAGTCCAG
TGGACCTCATTACACATATGACCACCTGGGAGACTCCCCAAAATTCTTCAAGACATTGCTTCGGGAAGCCATC
CATTTAGCCAGGTCTTAAAGGAAGCTAAAAAACCAATGGTGGTTTTAGGCAGTTCTGCACTCCAAAGAAATGATG
GAGCAGCAATTCCTGAGCTGTTTTCTAGCATTGCACAAAAGATTCCGGATGACTAGTGGTGTACTGGTGATTGGA
AAGTTATGAATATCCTTCATAGGATTGCAAGTCAAGTAGCTGCTTGGACCTTGGCTATAAGCCTGGGGTGAAG
CAATTCGGAAGAACCCTCCCAAGGTGCTGTTTCTCCTGGGAGCAGATGGAGGTTGTATCACACGACAGGATTGTC
CAAAGGATTGTTTTATTATTTATCAAGGACATCATGGTGTGTTGGGGCTCCCATAGCTGATGTTATTCTCCAG
GAGCTGCTTACACAGAGAAGTCTGCTACATATGTCAACACTGAGGGTAGAGCTCAGCAGACTAAGGTAGCAGTGA
CACCTCCTGGCTTGGCAAGAGAAGACTGGAATAATTATAAGAGCACTCTCTGAGATTGCTGGAATGACTCTTCCAT
ATGATACTCTGGATCAAGTAAGGAACAGATTGGAAGAAGTCTCTCCTAATCTTGTTCGATATGATGATATTGAAG
GGGCTAATTACTTCCAGCAAGCAAATGAGCTCTCAAAGCTAGTGAACCAGCAGCTTCTTGCTGACCCACTTGTTT
CACCTCAGCTAACTATAAAAGACTTCTACATGACAGATTCAATTAGCAGAGCCTCACAGACAATGGCCAAATGTG
TCAAAGCTGTCACAGAGGGTGGCCAGGCAGTAGAGGAACCATCCATATGCTGAAGCTTCTACTAGGATCCAGTT
TTGCCGCAGATAATTAATGGACAACCTGTAGTGCAGTGATCCTTTACAGGTTTATTTCTTTGTAAAAAAAATAAT
ATAAATTTGAATCATGTAATATTTAAGGTTATACTATGCCATTTTGAAAATGATATTAGTTATCAACTTTGCAGT
TTGAAAAACATGTATTGTGTGTAAAGGTTAAATAACAAAACCTATGCAGATGCTCTTAAAGCATTGATAACCTTT
GTGACGAACATAAAGAGATCCTTAAATT

WO 2004/030615

PCT/US2003/028547

1014/6881
FIGURE 947

MLRIPVRKALVGLSKSPKGCVRTTATAASNLIIEVFVDGQSVMEVPGTTVLQACEKVGMQIPRFCYHERLSVAGNC
RMCLVEIEKAPKVVAACAMPVMKGWNILTNSEKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMFNGDR
SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDDLGTTRGNDMQVGTYIEKMFMSSELSGNIIDI
CPVGALTSPYAFTARPWETRKTESIDVMDAVGSNIVVSTRIGEVMRILPRMHEDINEEWISDKTRFAYDGLKRQ
RLTEPMVRNEKGLTYTTSWEDALSRVAGMLQSFQKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEEVFPTA
GAGTDLRSNYLLNTTIAGVEEADVLLVGTNPRFEAPLFNARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPK
ILQDIASGSHPFSQLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRMTSGVTGDWKVMNHLRIASQVAA
LDLGYKPGVEAIRKNPPKVLFLLGADGGCITRQDLPKDCFIYQGHGVDVGAPIADVILPGAAYTEKSATYVNT
GRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTLPYDTLDQVRNRLEEVSFNLVRYDDIEGANYFQQANELSKLV
NQQLLADPLVPPQLTIKDFYMTDSISRASQTMKCVKAVTEGAQAVEEPSIC

WO 2004/030615

PCT/US2003/028547

1015/6881
FIGURE 948

GCCTCGAGGCGGGCGTCTTCGGTCATCTCCGGCGCTTCTAGGGCTGGTTCCCGTCATCTTCGGGAGCCGTGGAGC
TCTCGGATACAGCCGACACCAATGGGTTTCGGAGACCTGAAAAGCCCTGCCGGCCTCCAGGTGCTCAACGATTACC
TGGCGGACAAGAGCTACATCGAGGGGTATGTGCCATCACAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCC
CACCGCCTGCCGACTTGTGTCATGCCCTACGTTGGTATAATCACATCAAGTCTTACGAAAAGGAAAAGGCCAGCC
TGCCAGGAGTGAAGAAAGCTTTGGGCAAATATGGTCCTGCCGATGTGGAAGACACTACAGGAAGTGGAGCTACAG
ATAGTAAAGATGATGATGACATTGACCTCTTTGGATCTGATGATGAGGAGGAAAGTGAAGAAGCAAAGAGGCTAA
GGGAAGAACGTCTTGCAACAATATGAATCAAAGAAAGCCAAAAAACCTGCACTTGTTGCCAAGTCTTCCATCTTAC
TAGATGTGAAACCTTGGGATGATGAGACAGATATGGCGAAATTAGAGGAGTGCCTCAGAAGCATTCAAGCAGACG
GCTTAGTCTGGGGCTCATCTAACTAGTTCCAGTGGGATACGGAATTAAGAAACTTCAAATACAGTGTGTAGTTG
AAGATGATAAAGTTGGAACAGATATGCTGGAGGAGCAGATCACTGCTTTTGAGGACTATGTGCAGTCCATGGATG
TGGCTGCTTTCAACAAGATCTTAAAATCCATCCTGGATCATGGCATTTAAATAAAAGATTGAAAGATTAAAA

WO 2004/030615

PCT/US2003/028547

1016/6881
FIGURE 949

MGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAVSSPPPADLCHALRWYNHIKSYEKEKASLPGVKKA
LGKYGPADVEDTTGSGATDSKDDDDIDLFGSDDEEESEEAKRLREERLAQYESKKAKKPALVAKSSILLDVKPWD
DETDMAKLEECVRSIQADGLVWGSSKLVFVGYGIKKLQIQCVVEDDKVGTDMLLEEQITAFEDYVQSM DVAAFNKI

WO 2004/030615

PCT/US2003/028547

1017/6881
FIGURE 950

GGACAATTTGTGGGCCATTTAATTCAGGGCCCCCAATTCGTACGTGGAGAAGTGGGAATGCAAAAGTACTTTGAC
CTTTAACCTTCGGTCCGGCGCGGTGGAGGGAAACGCCTCCGTCTCTATATAAGGAATTTTCCGGTCTCTTCGGGT
CCTTTTTCCTCTCTTCAGCGTGGGGCGCCACAAATTTGCGCGCTCTCTTTCTGCTGCTCCCCAGCTCTCGGATAC
AGCCGACACCAATGGGTTTCGGAGACCTGAAAAGCCCTGCCGGCCTCCAGGTGCTCAACGATTACCTGGCGGACAA
GAGCTACATCGAGGGGTATGTGCCATCACAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCCCACCGCCTGC
CGACTTGTCATGCCCTACGTTGGTATAATCACATCAAGTCTTACGAAAAGGAAAAGGCCAGCCTGCCAGGAGT
GAAGAAAGCTTTGGGCAAATATGGTCCTGCCGATGTGGAAGACACTACAGGAAGTGGAGCTACAGATAGTAAAGA
TGATGATGACATTGACCTCTTTGGATCTGATGATGAGGAGGAAAGTGAAGAAGCAAAGAGGCTAAGGGAAGAACG
TCTTGACAATATGAATCAAAGAAAGCCAAAAAACCTGCACTTGTTGCCAAGTCTTCCATCTTACTAGATGTGAA
ACCTTGGGATGATGAGACAGATATGGCGAAATTAGAGGAGTGCCTCAGAAGCATTCAAGCAGACGGCTTAGTCTG
GGGCTCATCTAAACTAGTTCCAGTGGGATACGGAATTAAGAACTTCAAATACAGTGTGTAGTTGAAGATGATAA
AGTTGGAACAGATATGCTGGAGGAGCAGATCACTGCTTTTGAGGACTATGTGCAGTCCATGGATGTGGCTGCTTT
CAACAAGATCTTAAAATCCATCCTGGATCATGGCATTTAAATAAAAGATTGAAAGATTAAAA

WO 2004/030615

PCT/US2003/028547

1018/6881
FIGURE 951

MGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAVSSPPPADLCHALRWYNHIKSYEKEKASLPGVKKA
LGKYGPADVEDTTGSGATDSKDDDDIDLFGSDDEEESEEAKRLREERLAQYESKKAKKPALVAKSSILLDVKPWD
DETDMAKLEECVRSIQADGLVWGSSKLVPGYGIKKLQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI

WO 2004/030615

PCT/US2003/028547

1019/6881
FIGURE 952

GAAGGGGCGGGGCCAAAACCTGCGCGCCCAATCGGGGTGACGCTCTAGCCTTGCCGGGGACTCGTGGGTAACCTTGC
TTTTGGGAGCCAGCGGTATGGCGTCGGGCTGCAAGATTGGCCCGTCCATCCTCAACAGCGACCTGGCCAATTTAG
GGGCCGAGTGCTCCGGATGCTAGACTCTGGGGCCGATTATCTGCACCTGGACGTAATGGACGGGCATTTTGTTC
CAACATCACCTTTGGTCACCTGTGGTAGAAAGCCTTCGAAAGCAGCTAGGCCAGGACCCTTTCTTTGACATGCA
CATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTAGCAGGAGCCAATCAGTACACCTTTTCATCT
CGAGGCTACTGAGAACCCAGGGGCTTTGATTAAAGACATTCGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAA
ACCAGGAACCTCAGTTGAGTATTTGGCACCATGGGCTAATCAGATAGATATGGCCTTGTTTATGACAGTGAAC
GGGTTTGGAGGGCAGAAATTCATGGAAGATATGATGCCAAAGGTTCACTGGTTGAGGACCCAGTTCCCATCTTT
GGATATAGAGGTCGATGGTGGAGTAGGTCTTGACACTGTCCATAAATGTGCAGAGGCAGGAGCTAACATGATTGT
GTCTGGCAGTGCTATTATGAGGAGTGAAGACCCAGATCTGTGATCAATCTATTAAGAAATGTTTGCTCAGAAGC
TGCTCAGAAACGTTCTCTTGATCGGTGAACCATAAGGAGCCAGTGTTCTGTTCATGAAATCTCCCTTTTACT
GGAAACAGGAATATTGACTACCAATCACAATGCAATTGAAGCCGTACTGCTTTTTTGAGCAGTTATTTCATTCC
AGTGATTAAACGATTGTGTCAGAATATTCTAAGAGGTCAGAAATTGGTGTGTATAACTACATTTTTAGTGATGC
AATTTATTGATTAGTGAGTAAGATACTGTTTTTATTGAGAGATTTGATTTTTATAAAGTAAAAATACGGCTGCAT
TAGGGTTACAAACAGAAAAGTGCTTAATGTCTAAGGAGGGCATATTAGCTACACTACAAAACAAATTTTGTCT
GTACTTCTGAAAAGATTTTGTGTTTCTCAGCTGTTTTCCAAAAGCAAAGGAAGTCTTTATGGTTTTTTTCTAT
TTCATGTTATTGTGATTTGTTTATAAGTTTGGGTGGGGTGCAACCATATTCTTGGTCTTAAATCTATCACCT
TTCACCTTACACTTGATGTGTGAAAACATATAAAAACATGTGTGAAACCCAGGGGTTCTAAAATACAAGCATAGA
TTTTATCAGGGTGTTTTGTCAAAGCAGGTTATTCAGTGATTCCTCCCCACCATTCTTAAGAACGTTAAATAATGC
TGTTGTGTTAGCTCTGAGTAGAAAGGAAAAAGTAAACCTCTGTTTGGAGGTAATATTGGGTTGAATTCGACTG
CCCCTTTCTAGCTGGACCTTTAACAAATCACCCAATCTTTTTTGTGTTTCTCTAAAGTCATTTATACATTAAATG
TAATTATAGCAACTGTGGGGTCTGTTGAGAATTAAGAGCTAACACTATATATGTAAAGTTTCCAGTACTAGTCC
CAGAATTTAGAATATGCTCAACACAAAGTAAACAGCATTATATAAGTTTATATTTTGTGAGTTATAAAGTACTT
TGATATATTCTCATTAATCTGTAAATCACCTCTATAAGTAAGTGGTAATAATAAAGCAGATATTTTGTCCCCA
TTTAAAAATGAAGAAATTAATGCTTAATAGGGTGGTACCCTGGAAAGGATCTGGGAAGTGGTAGAATTTCTGGT
CTGTACTTTTACAAATGGAGCCCTTGGGAGGTGGGTAGGTAAAAGAAGCTTTTACTTAACGTTGTCTTATTTT
CAGTCTAATTTTACGCTGTAGCAGAACCAGATGGCTGAGAAAATTCGGAACCTATGGATCTTGACCCCAAGGATA
TATTATTTTATTCCAAGAAAGATCAGGTAGGCGAAAAGATGACAGGATACAGAGTCAATCCATAAACTAAATATT
TATAACTGTTCTGAATTATACAGAGTCTAAAAATATGTGTCAGCTACTTCATTCCTGTAAATACTCTTGCTGTGT
TATAAATATGGCAAGAAATAAACATGACCAATATCAATAGACTTCTTGAGGCTACTATAAGTTTTGAGAAATAAG
GTTCAAAAATAAGAATGCTAACACTTAAGCACAGACTAGAGCTTGCTTGGGTTTCTTCTGCAATTACAAGGTAA
AAATTTGTTAATGTTTGTGTTTTTATTGAGCTTGGGAAAGCTTTGTGCCATGAATACGTCGCATTTAATAACAAGCA
ACACACGGCATATAGAAATAACTTTAATTAAAAACTTACATAGAAGATTATAATATCAGACGTGACAAAGATTT
GAGTTTATTTGCCTGGACAACCTTGGGTTTGTCTGGCTTTTGTGTTTTCTTTTCTTTAAAAATAAATGTACAGTAA
ACTAC

WO 2004/030615

PCT/US2003/028547

1020/6881
FIGURE 953

MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEATEN
PGALIKDIRENGMKVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMMPKVHWLRTQFPSLDIEVD
GGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLRNVCEAAQKRSLDR

WO 2004/030615

PCT/US2003/028547

1021/6881
FIGURE 954A

GAAGAGCAAGAGGCAGGCTCAGCAAAATGGTTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCCGGTTG
TTATGACAATGGAAAACACTATCAGATAAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTTGGTTTGTAC
TTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACAC
TGGAACACTTACCGAGTGGGTGACACTTATGAGCGTCTTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG
GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCTTACAAGATTGGTGA
CACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAAAGGAGAATG
GACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTTCGGAGAAACGTGGGA
GAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACCTTC
TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCG
AGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGCA
GACCACATCGAGCGGATCTGGCCCCCTTACCGATGTTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCC
TCTTCCCTATGGCCACTGTGTGCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG
AAATAAGCAAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGG
TGGAACCTCAAAATGGAGAGCCATGTGTCTTACCATTACCTACAATGGCAGGACGTTCTACTCCTGCACCACAGA
AGGGCGACAGGACGGACATCTTTGGTGCAGCACAACCTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCAC
AGACCACACTGTTTTGGTTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCCTTCTTATACAA
CAACCACAAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAATA
TGATGCCGACCAGAAAGTTTGGGTTCTGCCCCATGGCTGCCACGAGGAAATCTGCACAACCAATGAAGGGGTCTAT
GTACCGCATTTGGAGATCAGTGGGATAAGCAGCATGACATGGGTACATGATGAGGTGCACGTGTGTTGGGAATGG
TCGTGGGGAAATGGACATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT
GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACGTACATGCTTCGGTCAGGGTCGGGGCAG
GTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTACAGAGACTGGGACGTTTTATCAAATTGGAGATTTCATGGGA
GAAGTATGTGCATGGTGTGATACCAAGTGTCTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTT
ACAGACCTATCCAAGCTCAAGTGGTCTGTGCAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC
CATCCAGTGGAAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGG
CCGTTGGAAGGAAGCTACCATAACAGGCCACTTAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATA
CGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGAAGTGCCTTTGACTTCACCACCACAGCAC
CAGCACACCTGTGACCAGCAACACCGTGACAGAGAGACGACTCCCTTTTTCTCCTCTTGTGGCCACTTCTGAATC
TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTGCGGATTCCGGGT
GGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACAT
CCCTGACCTGCTTCTTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGAT
CCTGTCTACTTCACAAACAACAGCGCCTGATGCCCTCCTGACACGACTGTGGACCAAGTTGATGACACCTCAAT
TGTTGTTTCGTGGAGCAGACCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTTCGCCATCAGTAGAAGGTAG
CAGCACAGAACTCAACCTTCTGAACTGCAAACTCCGTCAACCTCAGTGAAGTGTGCAACCTGGTGTTCAGTATAA
CATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCAATTCAACAAGAAACCACTGGCACCCC
ACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTACCATCATGTG
GACACCGCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCGTCAACCTGCCTGGCGAGCACGGGCA
GAGGCTGCCCATCAGCAGGAACACCTTTCAGAAAGTCAACGGGCTGTCCCTGGGGTCACCTATTACTTCAAAGT
CTTTGCAAGTGAAGCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAA
CCTCCAGTTTGTCAATGAACTGATTCTACTGTCTGGTGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA
CCGACTGACCGTGGGCCCTTACCCGAAGAGGACAGCCAGGAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCC
ACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAA
AGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCAC
CATTGTGATCAGATGGACGCTGTCCAAGAAATGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC
ACCACGAGAAGTGAAGTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGAAGTCCAGGAGTAGAATACGTCTACAC
CATCCAAGTCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTTGTCTCCACC
AACAACTTGCATCTGGAGGCAACCCCTGACACTGGAGTGTCTCAGTCTCCTGGGAGAGGAGCACCACCCACAGA
CATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCAGGGAAATCTTTGGAAGAAGTGGTCCATGC

WO 2004/030615

PCT/US2003/028547

1022/6881
FIGURE 954B

TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGA
TGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCCTCCTCCCACTGACCTGCGATTACCAA
CATTGGTCCAGACACCATGCGTGTACCTGGGCTCCACCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTA
CTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA
TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGG
AAGACAGAAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTTTACTGTGCA
CTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCG
AGAAGATCGGGTGCCCCACTCTCGGAATTCCATCACCTCACCACCTCACTCCAGGCACAGAGTATGTGGTCAG
CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAG
GGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTACAGTGAGATA
TTACAGGATCACTTACGGAGAGACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTAC
AGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG
CCCCGCAAGCAGCAAGCCAATTTCCATTAAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGA
TGTTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCTGTTACTGGTTACAGAGTAACCACCAC
TCCCCAAAATGGACCAGGACCAACAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTT
GCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTTCAGAC
TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTGCGATTCCATCAAAATTGCTTG
GGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCATGAGCTATT
CCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACCGGGTCTGAGTACACAGTCAGTGT
GGTTGCCTTGACGATGATATGGAGAGCCAGCCCCCTGATTGGAACCCAGTCCACAGCTATTCTCGCACCACCACTGA
CCTGAAGTTCACTCAGGTCAACCCACAAGCCTGAGCGCCAGTGGACACCACCAATGTTTCAGTCACTGGATA
TCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGT
GGTTGTATCAGGACTTATGGTGGCCACCAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAG
ACCAGCTCAGGGAGTTGTCAACCACTCTGGAGAATGTGAGCCCAACGAAGGGCTCGTGTGACAGATGCTACTGA
GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAA
TGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTGAGAGCTACACCATCACAGGTTTACAACCAGGCAC
TGACTACAAGATCTACCTGTACACCTGAATGACAATGCTCGGAGCTCCCCTGTGGTATCGACGCCTCCACTGC
CATTGATGCACCATCCAACCTGCGTTTCTGGCCACCACACCAATTCCTTGCTGGTATCATGGCAGCCGCCACG
TGCCAGGATTACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCGG
CCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCAATTGCCCTGAA
GAATAATCAGAAGAGCGAGCCCCGTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACA
CCCCAATCTTCATGGACCAGAGATCTTGGATGTTCCCTTCCACAGTTCAAAGACCCCTTTTCGTACCCACCCTGG
GTATGACACTGGAATGGTATTGAGCTTCTGGCACTTCTGGTTCAGCAACCCAGTGTGGGCAACAAATGATCTT
TGAGGAACATGGTTTATAGGCGGACCACACCGCCACAACGGCCACCCCCATAAGGCATAGGCCAAGACCATAACC
GCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACAT
CATTTCATGTCACTCCTGTTGGCACTGATGAAGAACCCTTACAGTTTCAGGGTTCCTGGAACCTTACCAGTGCCAC
TCTGACAGGCCTCACCAGAGGTGCCACCTACAACGTCATAGTGAGGCACTGAAAGACCAGCAGAGGCATAAGGT
TCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTCGTGCTTTGA
CCCCACACAGTTTCCCATTTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTG
CCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCATGACAATGGTGTGAACATA
CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGAAA
AGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTATGATGATGGGAAGACATAACCACGTAGGAGAACAGTG
GCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCAGCGGGCTGGCGCTGTGACAACCTG
CCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCACTACTGGCCAGTCTTACAACAGTATTCTCAGAGATACCA
TCAGAGAACAAAACATAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGA
TTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCGCAAGATCCATCTAAACTGGAGT
GATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCA
GCTCAACTCACAGCTTCTCCAAGCATCACCTGGGAGTTTCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT

WO 2004/030615

PCT/US2003/028547

1023/6881
FIGURE 954C

GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCA
ATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAATTTTAAGTAGGAAAGTC
ACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGA
TATTTTAAATATCCACAGTACTCACTTTTTCCAAATGATCCTAGTAATTGCCTAGAAATATCTTTCTCTTACCTG
TTATTTATCAATTTTTCCAGTATTTTTATACGGAAAAAATTGTATTGAAAACACTTAGTATGCAGTTGATAAGA
GGAATTTGGTATAATTATGGTGGGTGATTATTTTTTATACTGTATGTGCCAAAGCTTTACTACTGTGGAAAGACA
ACTGTTTTAATAAAAGATTTACATTCC

WO 2004/030615

PCT/US2003/028547

1024/6881
FIGURE 955

CGGCAGCCCTCCTACCTGCGCACGTGGTGCCGCTGCTGCTGCCTCCCGCTCGCCCTGAACCCAGTGCCTGCAGCC
ATGGCTCCCGGCCAGCTCGCCTTATTTAGTGTCTCTGACAAAACCGGCCTTGTGGAATTTGCAAGAAACCTGACC
 GCTCTTGGTTTGAATCTGGTCGCTTCCGGAGGGACTGCAAAAGCTCTCAGGGATGCTGGTCTGGCAGTCAGAGAT
 GTCTCTGAGTTGACGGGATTTCTTGAATGTTGGGGGGACGTGTGAAAACCTTGCATCCTGCAGTCCATGCTGGA
 ATCCTAGCTCGTAATATTCCAGAAGATAATGCTGACATGGCCAGACTTGATTTCATCTTATAAGAGTTGTTGCC
 TGCAATCTCTATCCCTTTGTAAAGACAGTGGCTTCTCCAGGTGTAACCTGTTGAGGAGGCTGTGGAGCAAATTGAC
 ATTGGTGGAGTAACCTTACTGAGAGCTGCAGCCAAAAACACGCTCGAGTGACAGTGGTGTGTGAACAGAGGAC
 TATGTGGTGGTGTCCACGGAGATGCAGAGCTCCGAGAGTAAGGACACCTCCTTGGAGACTAGACGCCAGTTAGCC
 TTGAAGGCATTCACTCATACGGCACAATATGATGAAGCAATTTTCAAGATTATTTTCAAGAAACAGTACAGCAAAGGC
 GTATCTCAGATGCCCTTGAGATATGGAATGAACCCACATCAGACCCCTGCCAGCTGTACACACTGCAGCCCAAG
 CTTCCCATCACAGTTCTAAATGGAGCCCCCTGGATTTATAAACTTGTGCGATGCTTTGAACGCCTGGCAGCTGGTG
 AAGGAACTCAAGGAGGCTTTAGGTATTCCAGCCGCTGCCTCTTTCAAACATGTCAGCCCAGCAGGTGCTGCTGTT
 GGAATTCCACTCAGTGAAGATGAGGCCAAAGTCTGCATGGTTTATGATCTCTATAAAACCCTCACACCCATCTCA
 GCGGCATATGCAAGAGCAAGAGGGGCTGATAGGATGTCTTCATTTGGTGATTTTGTGTCATTGTCCGATGTTTGT
 GATGTACCAACTGCAAAAATATTTCCAGAGAAGTATCTGATGGTATAATTGCCCCAGGATATGAAGAAGAAGCC
 TTGACAATACTTTCCAAAAAGAAAAATGGAACTATTGTGTCCTTCAGATGGACCAATCTTACAAACCAGATGAA
 AATGAAGTTCGAACCTCTCTTTGGTCTTCATTTAAGCCAGAAGAGAAATAATGGTGTCGTCGACAAGTCATTATTT
 AGCAATGTTGTTACCAAAAAATAAAGATTTGCCAGAGTCTGCCCTCCGAGACCTCATCGTAGCCACCATTGCTGTC
 AAGTACACTCAGTCTAACTCTGTGTGCTACGCCAAGAACGGGCAGGTATCGGCATTGGAGCAGGACAGCAGTCT
 CGTATACACTGCACTCGCCTTGCAAGGAGATAAGGCCAACTATTGGTGGCTTAGACACCATCCACAAGTGCTTTTCG
 ATGAAGTTTAAACAGGAGTGAAGAGAGCAGAAATCTCCAATGCCATCGATCAATATGTGACTGGAACCATTTGGC
 GAGGATGAAGATTTGATAAAGTGGAAAGGCACTGTTTGAGGAAGTCCCTGAGTTACTCACTGAGGCAGAGAAGAAG
 GAATGGGTTGAGAACTGACTGAAGTTTCTATCAGCTCTGATGCCTTCTTCCCTTTCCGAGATAACGTAGACAGA
 GCTAAAAGGAGTGGTGTGGCGTACATTGCGGCTCCCTCCGGTTCTGCTGCTGACAAAAGTTGTGATTGAGGCCTGC
 GACGAACCTGGGAATCATCCTCGCTCATACGAACCTTCGGCTCTTCCACCACTGATTTTTACCACACACTGTTTTTT
 GGCTTGCTTATGTGTAGGTGAACAGTCACGCCTGAACTTTGAGGATAACTTTTTAAAAAATAAAACAGTATCT
 CTTAAACAATGTTTTGATCTACATAAACATTGTAAAAATTTTCAATCACGCTTTTTAACTTTCTTACCACAAAA
 AAATGATAAGTGGGTGAAGTGATGGTTATGTTAATTAGCGTGC

WO 2004/030615

PCT/US2003/028547

1025/6881
FIGURE 956

MAPGQLALFSVSDKTGLVEFARNLTALGLNLVASGGTAKALRDAGLAVRDVSELTGFPEMLGGRVKTLPVAVHAG
ILARNIPEDNADMARLDFNLIRVVACNLYPFVKTVASPGVTVEEAVEQIDIGGVTLLRAAAKNHARVTVVCEPED
YVVVSTEMQSSESKDTSLETRRQLALKAFTHTAQYDEAISDYFRKQYSKGVSQMPLRYGMNPHQTPAQLYTLQPK
LPITVLNGAPGFINLCDALNAWQLVKELKEALGIPAAASFKHVSPAGAAVGIPLSEDEAKVCMVYDLYKTLTPIS
AAYARARGADRMSSFGDFVALSDVCDVPTAKIISREVSDGIIAPGYEEEALTILSKKKNGNYCVLQMDQSYKPDE
NEVRTLFGHLHSQKRNGVVDKSLFSNVVTKNKDLPEALRDLIVATIAVKYTQSNVVCYAKNGQVIGIGAGQQS
RIHCTRLAGDKANYWWLRHHPQVLSMKFKTGVKRAEISNAIDQYVTGTIGEDEDLIKWKALFEEVPELLTEAEKK
EWVEKLTEVSISSDAFFPFRDNVDRAKRSGVAYIAAPSGSAADKVVEACDELGIILAHTNLRRLFHH

WO 2004/030615

PCT/US2003/028547

1026/6881
FIGURE 957

GCAGCCAATTAAGCCAAGTGAAGTTTCCTTTTCCTTGTGGGGGCCAGTGTGCAATGGCTGCACACAGCAGCTTCCTT
GGTAGTGACACAGCCTGTTGGTTGTATGGGTTGCTCTGAGGGACCTTGGAGACAGGCCTTTCCAATGGATGTTT
ATGTTTCTGACCTTGCCTACCCCAATGTAGGCTCCAAACAGGCATGCGAGGTGCCTTTGGAATGCCCCAGGGCA
CTGTGGCCAGGGTTCACATTGGCCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTG
AGGCCCTGCGCAGGGCCAAGTTCAAGCTTCCTGGCCACCAGAAGATCCACATCTCAAAGAAGTGGGGCTTCACCA
AGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAGAAGTGGCTCATCCCAGATGGCTGTGGGGTCAAGTACA
TCCCCAATCGTGGCCCTCTGGACAAGTGGCGGGCCCTGCACTCATGAGGGCTTCCAATGTGCTGCCCCCTCTTA
ATACTACCAATAAATTCTACTTCCTGTCAAAAAATGTCACTAATGTACCCTAAATTTTCTTTTTTATTTTTAT
TTTTTATTTATTTATTTATTTTTTTTGGATGGTGTCTTGCTCTTTTGCCAGACTGGAGTGAAGTAGCATGATCT
TGGCTTACTGCAACCTCCACCCCCAG

PCT/US2003/028547

1027/6881

GGCGGGCGACCAAAGCCCTGAGGACCGGCAACATGGTGCGGTGCGGGAAATAAGGCAGCTGTTGTGCTGTGTATG
GACGTGGGCTTTACCATTGAGTAACCTCCATTCTGGTATAGAATCCCCATTTGAACAAGCAAAGAAGGTGATAACC
ATGTTTGTACAGCGACAGGTGTTTGTCTGAGAACAAGGATGAGATTGCTTTAGTCCTGTTTGGTACAGATGGCACT
GACAATCCCCTTTCTGGTGGGGATCAGTATCAGAACATCACAGTGCACAGACATCTGATGCTACCAGATTTTGAT
TTGCTGGAGGACATTGAAAGCAAAATCCAACCAGGTTCCTCAACAGGCTGACTTCCTGGATGCACTAATCGTGAGC
ATGGATGTGATTCAACATGAAACAATAGGAAAGAAGTTTGAGAAGAGGCATATTGAAATATTCAGTGACCTCAGC
AGCCGATTACAGCAAAAGTCAGCTGGATAATTATAATTTCATAGCTTGAAGAAATGTGACATCTCCCTGCAATTCTTC
TTGCCCTTCTCACTTGGCAAGGAAGATGGAAGTGGGGACAGAGGAGATGGCCCCCTTCGCTTAGGTGGCCATGG
CCTTCCTTTCCACTAAAAGGAATTACCGAACAGCAAAAAGAAGGTCTTGAGATAGTGAAAATGGTGATGATATCT
TTAGAAGGTGAAGATGGGTGGATGAAATTTATTTCATTTCAGTGAGAGTCTGAGAAAACCTGTGCGTCTTCAAGAAA
ATTGAGAGGCATTCATTTCAGTGGCCCTGCCGACTGACCATTGGCTCCAATTTGTCTATAAGGATTGCAGCCTAT
AAATCGATTCTACAGGAGAGAGTTAAAAAGACTTGGACAGTTGTGGATGCAAAAACCTTAAAAAAGAAGATATA
CAAAAAGAAACAGTTTATTGCTTAAATGATGATGATGAAACTGAAGTTTTTAAAGAGGATATTATTCAAGGGTTC
CGCTATGGAAGTGATATAGTTCTTTCTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGC
TTCTCTGTTTTGGGATTTTGTAAATCTTCTCAGGTTTCAGAGAAGATTCTTCATGGGAAATCAAGTTCTAAAGGTC
TTTGCAGCAAGAGATGATGAGGCAGCTGCAGTTGCACCTTTCCTCCCTGATTCAIGCTTTGGATGACTTAGACATG
GTGGCCATAGTTTCGATATGCTTATGACAAAAGAGCTAATCCTCAAGTCGGCGTGGCTTTTCTCATATCAAGCAT
AACTATGAGTGTTTTAGTGATGTGTCAGCTGCCTTTTCATGGAAGACTTGGCGCAATACATGTTTTTCATCCTTGAAA
AACAGTAAGAAATATGCTCCCACCGAGGCACAGTTGAATGCTGTTGATGCTTTGATTGACTCCATGAGCTTGGCA
AAGAAAGATGAGAAGACAGACACCCTTGAAGACTTGTTTTCCAACCACCAAAATCCCAATCCTCGATTTTCAGAGA
TTATTTTCAGTGCTGCTGTCACAGAGCTTTACATCCCCGGGAGCCTCTACCCCCAATTCAGCAGCATATTTGGAAT
ATGCTGAATCCTCCCGCTGAGGTGACAACAAAAGTCAGATTTCCTCTCTCTAAATATAAGACCCTTTTCTCTG
ATTGAAGCCAAGAAAAAGGATCAAGTGACTGCTCAGGAAATTTTCCAAGACAACCATGAAGATGGACCTACAGCT
AAAAAATTAAGACTGAGCAAGGGGGAGCCCACTTCAGCGTCTCCAGTCTGGCTGAAGGCAGTGTACCTCTGTT
GGAAGTGTAATCCTGCTGAAAACCTTCCGTGTTCTAGTGAAACAGAAGAAGGCCAGCTTTGAGGAAGCGAGTAAC
CAGCTCATAAATCACATCGAACAGTTTTTGGATACTAATGAAACACCGTATTTTATGAAGAGCATAGACTGCATC
CGAGCCTTCCGGGAAGAAGCCATTAAGTTTTTGAAGAGCAGCGCTTTAACAACCTTCTGAAAGCCCTTCAAGAG
AAAGTGGAATTAACAATTAATTCATTTCTGGGAAATTTGTTGTCCAGGATGGAATTACTCTGATACCAAAGAG
GAAGCCTCTGGAAGTTCTGTACAGCTGAGGAAGCCAAAAAGTTTTCTGGCCCCCAAGACAAACCAAGTGGAGAC
ACAGCAGCTGTATTTGAAGAAGGTGGTGATGTGGACGATTTATTGGACATGATATAGTTCGTGGATGTATGGGGA
ATCTAAGAGAGCTGCCATCGCTGTGATGCTGGGAGTTCTAACAACAAAGTTGGATGCGGCCATTCAAGGGGAGC
CAAAATCTCAAGAAATTCACAGCAGGTTACCTGGAGGCGGATCATCTAATTCTCTGTGGAATGAATACACACATA
TATATTACAAGGGATAAATTTAGACCCCATACAAGTTTATAAAGAGTCATTGTTATTTTCTGGTTGGTGATTATT
TTTTCTGTGGTCTTACTGATCTTTGTATATTACATACATGCTTTGAAGTTTCTGGAAAGTAGATCTTTTCTTGAC
CTAGTATATCAGTGACAGTTGCAGCCCTTGTGATGTGATTAGTGTCTCATGTGGAACCATGGCATGGTTATTGAT
GAGTTTCTTAACCCTTTCCAGAGTCTCTCTTTGCTGATCCTCCAACAGCTGTCACAACTTGTGTTGAGCAAGCA
GTAGCATTTGCTTCTCTCCAACAAGCAGCTGGGTAGGAAAACCATGGGTAAGGACGGACTCACTTCTCTTTTTA
GTTGAGGCCTTCTAGTTACCACATTACTCTGCCTCTGTATATAGGTGGTTTTCTTTAAGTGGGGTGGGAAGGGGA
GCACAATTTCCCTTCATACTCCTTTTAAAGCAGTGAGTTATGGTGGTGGTCTCATGAAGAAAAGACCTTTTGGCCC
AATCTCTGCCATATCAGTGAACCTTTAGAAACTCAAAAACCTGAGAAATTTACTTCAGTAGTTAGAATTATATCAC
TTCAGTGTTCTCTACTTGCAAGCCTCAAGAGAGAAAGTTTTCGTTATATTAAACACTTAGGTAACCTTTTCGGTC
TTTCCATTTCTACCTAAGTCAGCTTTTCATCTTTGTGGATGGTGTCTCCTTTACTAAATAAGAAAATAACAAAGC
CCTTATTCTCTTTTTTTTCTTGCTCTATTCTTGCTTGAGTTCCAGTTCTCTTTGGTGTACAGACTTCTTGGA
CCCAGTCACCTCTGTCTTCAGCACCCCTCATAAGTCGTCATAATACACAGTTTTGTACATGTAACATTAAAGGCA
TAAATGACTC

WO 2004/030615

PCT/US2003/028547

1028/6881
FIGURE 959

MVRSGNKAADVLCMDVGFTMSNSIPGIESPFQAKKVITMFVQRQVFAENKDEIALVLFGTGTDNPLSGGDQYQ
NITVHRHMLPDLLEDIESKIQPGSQADFLDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDII
IHSLKKCDISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGSPFPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIY
SFSESLRKLCVFKKIERHSIHWPCLRTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD
DETEVLKEDIIQGFRYGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCKSSQVQRFFMGNQVLKVFAARDDEAAAV
ALSSLIHALDDLDMAIVRYAYDKRANPQVGVAFFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ
LNAVDALIDSMSLAKKDEKTDLTLEDLPPTTKIPNPRFQRLFQCLLHRALHPREPLPPIQQHIWNMLNPPAEVTTK
SQIPLSKIKTFLPLIEAKKQDVTAQEIFQDNHEDGPTAKKLKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFRV
LVKQKKASFEEASNQLINHIEQFLDTNETPYFMKSIDCIRAFREEAIKFSEEQRFNFLKALQEKVEIKQLNHF
EIVVQDGITLITKEEASGSSVTAEAEAKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI

PCT/US2003/028547

CTTTTGTAGGCAAGTGTGGATTGAACACAGAGAAGGGAAGAGAGGAAGAACAGAGAGGAAGAGAAGGGAAGGAAGTGTTT
GTGTATAGAGAGAGAGAAAGACGAATAGAGTTAGGAAAAGGAAGACAAGCAGGTGGGCAGGAAGGACATGCACCGA
GACCAGGCAGGGGCCCAACTTTACGTCCAGCCCTGGCCTGGGGTCGGGAGAGGTGGGCGCTAGAAGATGCAGCC
CAGGATGTGGCAATCAATGACACTATTGGGGTTTCCCAGGATGGATTGGTCAGGGGGAGAAAGGAAAAGGCAAAA
CACTCCAGGACCTCTCCCGGATCTGTCTCCTCCTCTAGCCAGCAGTATGGACAGCTGGACCCCTGAACCTCTCTCT
CCTCTTACCTGGGCAGAGTGTGTCTCTCCCCAAATTTATAAAACTAAAATGCATTCCATTCTCTGAAAGCAA
AACAAATTCATAATTGAGTGATATTAAATAGAGAGGTTTTTCGGAAGCAGATCTGTGAATATGAAATACATGTGCA
TATTTTCATTCCCCAGGCAGACATTTTTTAGAAATCAATACATGCCCAATATTGGAAAGACTTGTCTCTCCACGG
TGACTACAGTACATGCTGAAGCGTGCCGTTTCAGCCCTCATTTAATTCAATTTGTAAGTAGCGCAGCAGCCTCT
TGGGGGAGGATAGGCTGAAAAAAAAAAGTGGGCTCGTATTTATCTACAGGACTCCATATAGTCATATATAGGCAT
ATAAATCTATTCTTTTTCTTTGTTTTTTTTCTTTCTTCTTTCTTTCAAAGGTTTGCAATTAACCTTTCAAAGTAGT
TCCTATAGGGGCATTGAGGAGCTTCTCATTTCTGGGAAAACCTGAGAAAACCCATATTCTCCTAATACAACCCGTA
ATAGCATTTTTTGCTGCTCGAGGCAGAGTTTCCCGTGAGCAATAAACTCAGCTTTTTTGTTGGGGCAGAGTACTG
GATTTGACAGTGATTCCCCACGTGTGTTTCATCTGCACCCACCGAGCCAGGCAGAGGCCAGCCCTCCGTGGTGCAC
ACAGCACGCGCCTCAGTCCATCCCATTTTAGTCTTTAAACCCTCAGGAAGTCACAGTCTCCGGACACCACACCAC
ATGAGCCCAACAGGTCCACGATGGATCCACAGTCCCACCCAGCCTTTTCTTTTCATCTGAACAGAATGTGCAT
TTTTGGAAGCCTCCCTCACTCTCCATGCTGGCAGAGCAGGAGGGAGACTGAAGTAAGAGATGGCAGAGGGAGATG
GTGGCAAAAAGGTTTAGATGCAGGAGAACAGTAAGATGGATGGTTCCGGCCAGAGTCGATGTGGGGAGGAACAGA
GGGCTGAAGGGAGAGGGGGCTGACTGTTCCATTCTAGCTTTGGCACAAAGCAGCAGAAAGGGGGAAAAGCCAATA
GAAATTTCTTAGCTTCCCCACCATATGTATTTCTAGGATTTGAGAGGAAAGAGAGGAAAATGGGGGAATGGGT
TGCAAAATAGAAATGAGCTTAATCCAGGCCGAGAGCCAGGGAAGGTGAGTAACCTTTAGGAGGGTGCTAGACTTT
AGAAGCCAGATAGGAAGAATCAGTCTAAACTGGCCATGCTTTGGAAGGGACAAGACTATGTGCTCCGCTGCCAC
CTTCAGCCTGCAATGAGGGACTGAGGCCACAGAGTCTTTCAGCTCTTCTCCTCATTCTGGCCAGTCCCTGCATCC
TCCCTGGGGTGGAGGATGGAAGGAAAGCTGGGACAAGCAGGGAACGCATGATTAGGGATGCTGTCTACTCGGCAG
CCAGATTCGAAACTCCCATTTCTCCAATGACTTCTCTCAACCAATGGGTGGCCTTGTGACTGTTCTTTAAGGCTGA
AGATATCCAGGAAAGGGGGCTTGGACACTGGCCAAGGAGACCCCTTCGTGCTGTGGACACAGCTCTCTTCACTCT
TTGCTCATGGCATGACACAGCGGAGACCGCTCCAACAACGAATTTGGGGCTACGAAGAGGAATAGCGAAAAAGC
AAATCTGTTTCAACTGATGGGAACCTTATAGCTATAGAACTTGGGGGCTATCTCCTATGCCCTTGGACAGGACAG
TTGGCTGGGGACAGGAGAAGTGCTCAATCTTCATGAGACAAAGGGGCCCGATAGGGCCAGCAGCCACAAGGCCTT
GACCTGCCGAGTCAGCATGCCCCATCTCTCTGCACAGCTGTCCCCATAAACCAACTCACGTTTCTGTATGTCTTA
GGCCAGTATCCCAAACCTCTTCCACGTCACTGTTCTTTCCACCCATTCTCCCTTTGCATCTTGAGCAGTTATCCA
ACTAGGATCTGCCAAGTGGATACTGGGGTGCCACTCCCCTGAGAAAAGACTGAGCCAGGAACCTACAAGCTCCCC
CACATTCTCCAGCCTGGACCTAATCTTTGAGAGGGGCTCTCTCTTACGGACTGTGTCTGGACTTTGAGCAGG
CTTCTGCCCCTTGCGTTGGCTCTTTGCTGCCAGCCATCAGGTGGGGGATTAGAGCCTGGTGTAAGTGCCGCAGAG
TCTTCCGGTTTCCAAAGTTCTGTGCTGCGAACCCTCAACCTGTGAGTCTCTTCTGCATGCAGGAGTTTCTCCTGGG
CAGCTGGTCACTCCCCAGAGAAGCTGGGCCTTCATGGACACATGGAACCTAAGCCTCCCAATGGGAGGTTCTGGCT
GAGCCCAGGGTGGGGAGATCTTGGGAAGGGAGGCACCTGGAGGAAGACGGCACCTCTTCCCCATGGCAGGGTGTG
AGGGAGGCAGGTTTGGAAATGGTGCGAGTATGGCAATCTAAGCAGGGGTCTGGTCTCTTTGACTCCAGGCTGGCCT
TTGGCCGACTGTCTGCTCACCAGAGACCTTGGACTCCGACTATCCATGGCTCCGAATCTAAGTGCTGCCACT
CCCATGCTCACACCACAGAAGGTCTTCCATCCCCCTTAGATTCTGTGCTCACTCCACCACTGAGGAAGATGCC
TCTGTCTTTCCACGACTGCCAGGATAGGGAAGCCAGCCAGGACTGACCCTCCTTCTCCTCCAGCCTGCCCTGA
CCCACCTGGCAAAGCAGGGCACATGAGGGGAGGAAGGCAGGCGCACGAGGTCCAGGGAGGCCCTTTTCTGATCATGCC
CCTTGGGACACTGGCCCCATGAGGGGAGGAAGGCAGGCGCACGAGGTCCAGGGAGGCCCTTTTCTGATCATGCC
GTTCTCTCCACCCCCATCTCCCCACCACCACCTCTGTGGCCTCCATGGTACCCCCACAGGGCTGGCCTCCCCTA
GAGGTTGGGCTCAACCACCTGCTCCCGCCACGCACCGGTTAGTGAGACAGGGCTGCCACGGCAACCGCCAAGCC
CCCCCTCAAGGTGGGACAGTACCCCGGACCATCTCACTCACTCTGAGAGGGCTCCGGCCAGAAATGGGAACCTCA
GAGAAGAGCTCTAAGGAGAAGAAACCCCATAGCGTCAGAGAGGATATGTCTGGCTTCCAAGAGAAGGAGGCTCC
GTTTTGCAAGTGGAGGAGGGACGAGGGACAGGGGTTTACCAGCCAGCAACCTGGGCCTTGTACTGTCTGTGT

WO 2004/030615

PCT/US2003/028547

1030/6881
FIGURE 960B

TTTAAAACCACTAAAGTGCAAGAATTACATTGCACTGTTTCTCCACTTTTTATTTTCTCTTAGGCTTTTGTTTCT
ATTTCAAACATACTTTCTTGGTTTTCTAATGGAGTATATAGTTTAGTCATTTACAGACTCTGGCCTCCTCTCCT
GAAATCCTTTTGGATGGGGAAAGGGAAGGTGGGGAGGGTCCGAGGGGAAGGGGACCCAGCTTCCCTGTGCCCGC
TCACCCCACTCCACCAGTCCCCGGTCGCCAGCCGGAGTCTCCTCTCTACCGCCACTGTCACACCGTAGCCACAT
GGATAGCACAGTTGTCAGACAAGATTCCTTCAGATTCCGAGTTGCCTACCGGTTGTTTTCGTTGTTGTTGTTGTT
GTTTTCTTTTTCTTTTTTTTTTTGAAGACAGCAATAACCACAGTACATATTACTGTAGTTCTCTATAGTTTTAC
ATACATTCATACCATAACTCTGTTCTCTCCTCTTTTTTGTGTTTCAACTTTAAAAACAAAAATAAACGATGATAAT
CTTTACTGGTGAAAAGGATGAAAAATAAATCAACAAATGCAACCAGTTTGTGAG

WO 2004/030615

PCT/US2003/028547

1031/6881
FIGURE 961

MLWKGQDYVLRCPPSACNEGLRPTSLSSSSSILASPCILPGVEDGRKAGTSRERMIQGCCHSAARFRNSHSPMTS
STNGWPCDCSLRLKISRKGGLDTGQGDFVLWTQLSSLFAHGMTQRRPPPTTNLGLRRGIAKKQICFN

WO 2004/030615

PCT/US2003/028547

1032/6881
FIGURE 962

CCTCTGTGGCCTCCATGGTACCCCCACAGGGCTGGCCTCCCCTAGAGGGTGGGCCTCAACCACCTGCTCCCGCCA
CGCACCGGTTAGTGAGACAGGGCTGCCACGGCAACCGCCAAGCCCCCTCAAGGTGGGACAGTACCCCGGACCCA
TCCACTCACTCCTGAGAGGGCTCCGGCCCAGAATGGGAACCTCAGAGAAGAGCTCTAAGGAGAAGAAACCCATA
GCGTCAGAGAGGATATGTCTGGCTTCCAAGAGAAAGGAGGCTCCGTTTTGCAAAGTGGAGGAGGGACGAGGGACA
GGGGTTTTACCAGCCAGCAACCTGGGCCTTGTAAGTGTCTGTGTTTTTAAACCACTAAAGTGCAAGAATTACATT
GCACTGTTTTCTCCACTTTTTATTTTCTCTTAGGCTTTTGTTTTCTATTTCAAACATACTTTCTTGGTTTTCTAATG
GAGTATATAGTTTAGTCATTTACAGACTCTGGCCTCCTCTCCTGAAATCCTTTTGGATGGGGAAAGGGAAGGTG
GGGAGGGTCCGAGGGGAAGGGGACCCAGCTTCCCTGTGCCCCGCTCACCCCACTCCACCAGTCCCCGGTCGCCAG
CCGGAGTCTCCTCTCTACCGCCACTGTACACCGTAGCCACATGGATAGCACAGTTGTCAGACAAGATTCCCTC
AGATTCCGAGTTGCCTACCGGTTGTTTTCGTTGTTGTTGTTGTTGTTTTCTTTTCTTTTTTTTTTTGAAGACA
GCAATAACCACAGTACATATTACTGTAGTTCTCTATAGTTTTACATACATTCATACCATAACTCTGTTCTCTCCT
CTTTTTTGTTTTCAACTTTAAAAACAAAAATAAACGATGATAATCTTTACTGGTGAAAAGGATGGAAAAATAAAT
CAACAAATGCAACCAGTTTGTGAGAAAAAAGCCGAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1033/6881
FIGURE 963

MVFPQGWPFPLEGGPQPPAPATHRLVRQGCHGNRQAPLKVGQYPGPIHSLLRGLRPRMGTSEKSSKEKKPHSVRED
MSGFQEKGGSVLQSGGGTRDRGFTSQQPGPCTVCVFKTTKVQELHCTVSPLFIFS

WO 2004/030615

PCT/US2003/028547

1034/6881
FIGURE 964

GGCGAGGGAGGAGGAAGAAGCGGAGGAGCGGCTCCCGCGCTCGCAGGGCCGTGCCACCTGCCCCGCCCGCCGCT
CGCTCGCTCGCCCCGCCGCGCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCCGCGCTGCCGCTG
CCGCCGCCGCGCTGCTGCCGCTGCTGCTGCTACTGGGCGCGAGTGGCGGCGGCGGGGGCGCGCGCGGAG
GTGCTGTTCCGCTGCCCCGCCCTGCACACCCGAGCGCCTGGCCGCGCTGCCGGCCCCCGCCGGTTGCGCGCGCCGCC
GCGGTGGCCGCGAGTGGCCGGAGGCGCCCGCATGCCATGCGCGGAGCTCGTCCGGGAGCCGGGCTGCGGCTGCTGC
TCGGTGTGCGCCCCGGCTGGAGGGCGAGGCGTGCGGCGTCTACACCCCGCGCTGCCGGCCAGGGGCTGCGCTGCTAT
CCCCACCCGGGCTCCGAGCTGCCCCTGAGGCGCTGGTTCATGGGCGAGGGCACTTGTGAGAAGCGCCGGGACGCC
GAGTATGGCGCCAGCCCGGAGCAGGTTGCAGACAATGGCGATGACCACTCAGAAGGAGGCCTGGTGGAGAACCAC
GTGGACAGCACCATGAACATGTTGGGCGGGGAGGCGAGTGGTGGCCGGAAGCCCCCTCAAGTCGGGTATGAAGGAG
CTGGCCGTGTTCCGGGAGAAGGTCAGTGAAGCAGCACCAGGAGTGGGCAAGGGTGGCAAGCATCACCTTGGCCTG
GAGGAGCCCAAGAAGCTGCGACCAACCCCTGCCAGGACTCCCTGCCAACAGGAAGTGGACAGGTCTTGGAGCGG
ATCTCCACCATGCGCCTTCCGGATGAGCGGGGCCCTCTGGAGCACCTCTACTCCCTGCACATCCCCAACTGTGAC
AAGCATGGCCTGTACAACCTCAAACAGTGCAAGATGTCTCTGAACGGGCAGCGTGGGGAGTGGTGGTGTGAAC
CCCAACACCGGGAAGCTGATCCAGGGAGCCCCACCATCCGGGGGGACCCGAGTGTATCTCTTCTACAATGAG
CAGCAGGAGGCTCGCGGGGTGCACACCCAGCGGATGCAGTAGACCGCAGCCAGCCGGTGCCTGGCGCCCCCTGCC
CCCGCCCCCTCTCAAACACCGGCAGAAAACGGAGAGTGCTTGGGTGGTGGGTGCTGGAGGATTTCCAGTTCTGA
CACACGTATTTATATTTGAAAAGAGACCAGCACCAGCTCGGCACCTCCCCGGCCTCTCTCTCCAGCTGCAGA
TGCCACACCTGCTCCTTCTTGCTTTCCCGGGGGAGGAAGGGGGTGTGGTCGGGGAGCTGGGGTACAGGTTTGG
GGAGGGGGAAGAGAAATTTTATTTTGAACCCCTGTGTCCCTTTTGCATAAGATTAAAGGAAGGAAAAGT

WO 2004/030615

PCT/US2003/028547

1035/6881

FIGURE 965

AGCGGATCTCCACCATGCGCCTTCCGGATGAGCGGGGCCCTCTGGAGCACCTCTACTCCCTGCACATCCCCAACT
GTGACAAGCATGGCCTGTACAACCTCAAACAGTGCTGGTGTGTGAACCCCAACACCGGGAAGCTGATCCAGGGAG
CCCCCACCATCCGGGGGGGACCCCGAGTGTCATCTCTTCTACAATGAGCAGCAGGAGGCTCGCGGGGTGCACACCC
AGCGGATGCAGTAGACCGCAGCCAGCCGGTGCCTGGCGCCCCCTGCCCCCGCCCCCTCTCCAAACACCGGCAGAAA
ACGGAGAGTGCTTGGGTGGTGGGTGCTGGAGGATTTTCCAGTTCTGACACACGTATTTATATTTGGAAAGAGACC
AGCACCGAGCTCGGCACCTCCCCGGCCTCTCTCTTCCCAGCTGCAGATGCCACACCTGCTCCTTCTTGCTTTCCC
CGGGGGAGGAAGGGGGTTGTGGTTCGGGGAGCTGGGGTACAGGTTTGGGGAGGGGGAAGAGAAATTTTATTTTGTG
AACCCCTGTGTCCCTTTTGCATAAGATTAAAGGAAGG

WO 2004/030615

PCT/US2003/028547

1036/6881
FIGURE 966

CTTCCTTTCTGGGCTCGGACCTAGGTCGCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAAT
ACGGGACCCGCTATGGGGCCTCCCTCCGGAAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTACACTT
GCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGTGGTTCCTGCATGAAGACAG
TGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTACAGGTAAAGTCCGCCATCAGAAGACTGAAGGAGT
TGAAAGACCAGTAGACGCTCCTCTACTCTTTGAGACATCACTGGCCTATAATAAATGGGTAAATTTATGTAACAA
AAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1037/6881
FIGURE 967

MAKRTKKVGIVGKYGTRYGASLRKMOVKKIEISQHKYTCSEFCGKTKMKRRVGIWHCGSCMKTVAGGAWTYNTTS
AVTVKSAIRRLKELKDQ

WO 2004/030615

PCT/US2003/028547

1038/6881
FIGURE 968

CCCCCGCCACCTCACACACCCCCATCCGGGAGACCCACGTGCAGCTGGGCCCCGGGCTGGCGCCGCACCTCGGGG
TCTGCGCGTCTCCCCGGCGCGTTCGGGGCGCAGCCCCACGACACGGACCCCTGGCGGGGGCGGCATCCGAGAAGTC
GCAGGCGGAGAGGGGGCGTCTGGAGGCCGGGGCGGGGACGCTGCGGCCCGCGGCCACACAAAGGAGGCGGGCGG
GAAGGCGGGGCAAGGCGGGCCGGGGCGGGGGCGGCAGGAAGGGGGCGGGGGCCCGCGCGGCGCCGCCGATAAAGC
CCCCGCGCGCGCGGCAGCCAGCTTGCGCTGTGGGGCTGCCCGGGCTGCGCGGCGTCTGCAGGCGCCACCGCTGCC
TCTTTCCGGCTGTGACCCCTCCTCGCCGCCCGCGCTTGGCTGCGTCCCTCCGACTCCCCGCGCCGCCGAGACCAGGC
TCCCGCTCCGGTTGCGGCCGCACCGCCCTCCGCGGGCGCCCCCTGGGGATCCAGCGAGCGCGGTCTGCTCTTGGTG
GAAGGAACCATGAACTGGCATCTCCCCCTCTTCTCTTGGCCTCTGTGACGCTGCCTTCCATCTGCTCCCACTTC
AATCCTCTGTCTCTCGAGGAAGTGGCTCCAACACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCCCT
CATGACAACATCGTGATCTCTCCCATGGGATTGCGTCCGTCTGGGGATGCTTCAGCTGGGGGCGGACGGCAGG
ACCAAGAAGCAGCTCGCCATGGTGATGAGATACGGCGTAAATGGAGTTGGTAAATATTAAAGAAGATCAACAAG
GCCATCGTCTCCAAGAAGAATAAAGACATTGTGACAGTGGCTAACGCCGTGTTTGTAAAGATGCCTCTGAAATT
GAAGTGCCTTTTGTACAAAGGAACAAAGATGTGTTCCAGTGTGAGGTCCGGAATGTGAACTTTGAGGATCCAGCC
TCTGCCTGTGATTCCATCAATGCATGGGTTAAAAATGAAACCAGGGATATGATTGACAATCTGCTGTCCCCAGAT
CTTATTGATGGTGTGCTCACCAGACTGGTCTCGTCAACGCAGTGTATTTCAAGGGTCTGTGGAAATCACGGTTC
CAACCCGAGAACACAAAGAAACGCACTTTCGTGGCAGCCGACGGGAAATCCTATCAAGTGCCAATGCTGGCCAG
CTCTCCGTGTTCCGGTGTGGGTGACAAAGTGCCCCAATGATTTATGGTACAACCTTATTGAAGTGCCTACCA
GGGGAAAGCATCAGCATGCTGATTGCACTGCCGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATC
AGCACCAAGACCATAGACAGCTGGATGAGCATCATGGTGCCCAAGAGGGTGCAGGTGATCCTGCCCAAGTTCACA
GCTGTAGCACAAACAGATTTGAAGGAGCCGCTGAAAGTTCTTGGCATTACTGACATGTTTGATTATCAAAGGCA
AATTTTGCAAAATAACAAGGTCAGAAAACCTCCATGTTTCTCATATCTTGCAAAAAGCAAAATTTGAAGTCAGT
GAAGATGGAACCAAGCTTCAGCAGCAACAACCTGCAATTCATTGCAAGATCATCGCCTCCCTGGTTTATAGTA
GACAGACCTTTTCTGTTTTTTCATCCGACATAATCCTACAGGTGCTGTGTTATTCATGGGGCAGATAAAACAAACCC
TGAAGAGTATACAAAGAAACCATGCAAGCAACGACTACTTTGCTACGAAGAAAGACTCCTTTCCTGCACTTTT
CATAGTTCTGTTAAATATTTTTGTACATCGCTTCTTTTCAAACCTAGTTCTTAGGAACAGACTCGATGCAAGTG
TTTCTGTTCTGGGAGGTATTGGAGGGAAAAACAAGCAGGATGGCTGGAACACTGTACTGAGGAATGAATAGAAA
GGCTTCCAGATGTCTAAAAGATTCTTTAACTACTGAACTGTTACCTAGGTAAACAACCCTGTTGAGTATTGCT
GTTTGTCCAGTTCAGGAATTTTGTGTTTGTGTTTGTCTATATGTGCGGCTTTTCAGAAGAAATTTAATCAGTGTGA
CAGAAAAAAAATGTTTTATGGTAGCTTTTACTTTTTATGAAAAAAAATTTATTTGCCTTTTAAATCTTTTCCC
CCATCCCCCTCCAAAGTCTTGATAGCAAGCGTTATTTTGGTGGTAGAAACGGTGAAATCTCTAGCCTCTTTGTGT
TTTTGTTGTTGTTGTTGTTGTTTATATAATGCATGTATTCACTAAAAATAAAATTTAAAAAACTCCTGTCTT
GCTAGACAAGGTTGCTGTTGTGCAGTGTGCCTGTCACTACTGGTCTGTACTCCTTGATTGTCATTTTGTATTT
TGTAACAAGTAAAAATAAACTGTTATGAGTAGT

WO 2004/030615

PCT/US2003/028547

1039/6881

FIGURE 969

MNWHLPFLLLASVTLP SICS HFNPLSLEELGSNTGIQVFNQIVKSRPHDNIVISPHG IASVLGMLQLGADGR TKK
QLAMVMRYGVNGVGKILKKINKAIVSKKNKDIVTVANAVFVK NASEIEVPFVTRNKDVFQCEVRNVNFE DPASAC
DSINAWVKNETRDMIDNLLSPDLIDGVLTRLVLVNAVYFKGLWKS RFQPENTKKRTFVAADGKSYQVPM LAQLSV
FRCGSTSAPNDLWYNFIELPYHGESISMLIALPTESSTPLSAIIPHISTKTIDSWMSIMVPKR VQVILPKFTAVA
QTDLKEPLKVLGITDMFDSSKANFAKITRSENLVSHILQAKIEVSE DGTKASAATTAILIARS SPPWFIVDRP
FLFFIRHNPTGAVLFMGQINKP

WO 2004/030615

PCT/US2003/028547

1040/6881
FIGURE 970

ATGCGTGCTGAAAAGAGAAAAAGAATGCCCCAGAGGAGGTCAGCAGGCTTAAAAGTATTCTCAAAC TAGACGAT
GACGTTTTAATGAAAGATGTTCAAGAGATAGCAACTGTGGTGGTACCCAAACCCAAACATTGCCAAGAGAAAAATG
CAATGTGAGGTAAAAGATGAAAAAGATGACATGAAAAATGGAGACTGATATTAAGAGAAACAAAAAGACTCTTCTA
GACCAGCATGGACAGTACCCAATATGGATGAACCAAGGCCAAAGAAAAAGGCTAAAGGCCAAGCGAGAGAAAAAGA
AAGGAGAAAAACAAAGCAAAAGCAGTGAAGTGGCAAAAGGGTTTGGCCTGTAGTATTGTTTCCATAATAGTCCAT
TTCGCAGAAATAAGAAGGAGAATAAAACTTAGAGAAAAAGAGGAGGCCAAAGGGGGCAAGGTAGTGCTACTTGC
AGAAACCTGAAAAATATGTGTGACAAAGCCGCCATAATAAGTGCCAGCCGAGCTGCAGCAGCCCCTCTCAGGGGC
ACCGCAGCCTCCCCGGGCCCTACGGCCGCCGCCAGCAGGATGGCTGGAATGGCCTTAGTCATGAGGCTTTTAGA
ATTGTTTCAAGGCAGGATTATGCGTCAGAAGCAATCAATGGAGCAGCTGGTGGTGTATTGTTGGGTACTACCAAC
TCCTGTGTGGCAGTTATGGAAGGTAAACAAGCAAGGTGCTGGAGAATGCCGAAGGTGCCAGAACTACCCCTTCA
GTTGTGGCCTTTACAGCAGATGTACAGAAAGACATTAAAAATATTCCTTTAAAATTGTCTGTGCCTCCAATGGT
GATGCCTGGGTTGAGGCTCATGGGAACTGTATTCTCCAAGTCAGATCGGAGCATTGTGTGATGAAGATGAAA
GAGACTGCAGAAAATTACTTGGGGCACACAGCAAAAAATGCTGTGATCGCAGTCCCAGCTTATTTCAATGACTTG
CAGAGGCAGGCCACTAAAGATGCTGGCCAGATATCTGGACTGAATGTGCTTCGGGTGATTAATGAACCCACAGCT
GCTGCTCTTGCCATATGGTCTAGACAAATCAAAAGACAAAGTCATTGCTGTATATGATTTAGGTGGTGGAACCTTT
GATATTTCTATCCTGGAATTTAGAAAGGAGTATTCGAGGTGAAATCCACAAATGGGGACACTTTCTTAGGTGGG
GAAGACTTTGACCAGGCCTTGCTACAGCACATTGTGAAGGAGTTCAAGAGAGAGACGGGGGTGATTGACCAAA
GACAACGTGGCATTTCAGAGGGTGTGGGAAGCTGCTGAAAAGGCTAAATGTGAACCTCTCTCATCTGTGCAGACT
GACATCAATTTGCCCTATCTTACAATGGATTCTTCTGGACCCAAGCATTGGAATACAAAGTTGACCCATGCTCAA
TTTGAAGGGATTGTCACTGATCTAATCAGGAGGACTATCGCTCCATGCCAAAAAGCTATGCAAGATGCAGAAATC
AGCAAGAGTGATATAGGAGAAGTGATTCTTGTGGAGCCCCCAAGTAAAGCTGTCAATCCTGATGAGGCTGTGGCC
ATTGGAGCTGCCATTTCAGGGAGATGTGTTGGCCGGCGATGTCACAGATGTGCTGCTCCTTGATGTCAATCCCCTG
TCTCTGGGTATTGAAACTCTGCGAGGTGCTTTACCAAACCTTATTAATAGGAATACCACTATTCCAACCAAGAAG
AGCCAGGTATTCTCAACTGCTGCTGATGGGCAGACACAAGTGGAATTAAGTGTGTGAGGGTGAGAGAGAGATG
GCTGGAGACAACAACTCCTTGGACAGTTTACTTTGATTGGAATTCACCAGCCCCCTCGTGGAGTTCCTCAGATC
AAAGTTACATTTGACATTGATGCCAATGGGATCATAATGTTTCAGCTAAAGATAAAGGCACAGGACATGAGCAG
CAGATTGTAATCCAGTCTTCTGGTGGGTAAAGCAAAGATGATGTTGAAAATATGGTTAAAAATGCAGAGAAATAT
GCTAAGGAAGACCAGCGAAGGAAGGAATGA

WO 2004/030615

PCT/US2003/028547

1041/6881
FIGURE 971

CGGAGCTGTCCATCAGCACCAAAGGCCGCGGGCGGGCTCAGGGCATGGGGCCGCGGTTCTGGGGCGGGCCGAGCC
CCGGCTCCTGCGCCTTCCCCCTCCTCAGGCCAGCCGAGTTCCCGGACGCCGCGGGACTGGAGTGCCAGCCGGT
GTTGGACGTGGAGCGGCGCCGCCACCGCGCGACACCATTTCTCTCCGGCCAGCAGCCCCCTTCTCGCACGACG
GACTTTCCCTGGACCCAGTCAGTTGGAGCCTCTGGCGCCCCGCAACCCCGGCCCTCGGGCCTCTGCACAGCCT
CTTTACTCAGAAGCTCAGGTCGCCTCCAGCCCAGCACTATGCCGGGGACTGTGGCAACACTGCGGTTCCAGCTG
CTGCCCCCTGAGCCAGATGATGCCTTCTGGGGTGACCTTGTGAACAGCCCCCTGGAGCGCAGGTACCAGGCACTG
CCGGCCCTCGTCTGCATCATGTGCTGTTTGTGGAGTCGTCTACTGCTTCTTCGGTTACCGCTGCTTCAAGGCA
GTGCTCTTTCTACTGGGTTGCTGTTTGGCTCGGTGGTCATCTTCTCCTCTGCTACCGAGAGCGGGTGCTAGAG
ACACAGCTGAGTGCTGGGGCGAGCGCGGGCATCGCTCTGGGCATCGGGCTGCTCTGCGGGCTGGTGGCCATGCTA
GTGCGCAGCGTGGGCCTCTTCTGGTGGGGCTGCTGCTCGGCCTGCTGCTCGCAGCTGCTGCCCTGCTGGGCTCC
GCACCCTACTACCAGCCAGGCTCCGTGTGGGGTCCACTGGGGCTGTTGCTGGGGGGCGGCCTGCTCTGTGCCCTG
CTACTCTGCGCTGGCCCCGCCACTCACACCCTGGCCACCGCCGTGACTGGTGCTGCGCTGATCGCCACTGCC
GCTGACTACTTCGCCGAGCTGCTACTGCTGGGGCGCTACGTGGTGGAGCGACTCCGGGCTGCTCCTGTGCCCCA
CTCTGCTGGCGAAGCTGGGCCCTGCTGGCACTCTGGCCCCTGCTCAGCCTGATGGGCGTTCTGGTGCAGTGGAGG
GTGACAGCTGAGGGGGACTCCACACGGAAGTGGTCATCAGCCGGCAGCGCCGACGCGTGCAACTGATGCGGATT
CGGCAGCAGGAAGATCGCAAGGAGAAAAGGCGGAAAAGAGACCTCCTCGGGCTCCCCCTCAGAGGTCCCCGGGCT
CCTCCCAGGCCTGGGCCACCAGACCCTGCTTATCGGCGCAGGCCAGTGCCCATCAAACGCTTCAATGGAGACGTC
CTCTCCCCGAGCTATATCCAGAGCTTCCGAGACCGGCAGACCGGGAGCTCCCTGAGCTCCTTCATGGCCTCAGCC
ACAGATGCGGACTATGAGTATGGGTCCCGGGGACCTCTGACAGCCTGCTCAGGCCCCCAGTGCGGGTATAGCCA
TATCTGTCTGTCTAGACTCTGCAGTACCAGCTCTGCCAGCTCGAGGAGGCCTGCTAGGCTGCCACTCAGCCTCC
TGGCTTTGGCTGTCCCTCTCCCCAGCCTGGAGAGGGCTGGCCTGGTCACTAGAAGGGAGGATTGTCTCAGGCGAG
TCTTGGCCTGAGAGGAAAGCCCCCTCCCAAGCTCCCAAGAGGCTCCTGAGGAACTCGGGGTGTGAACCCCATGG
GGTGTGCTCAGGGTTGTGAGTGTGTTGCCCGTGTGTCTGTGTGTATGTGTGTGGGGGTGGGCAGGCTTGGAGGGG
ACGCTGGGACCCCTTGCCCTTAGATTTCTGACTGGTAGGGTTTCTCCAGGCTCAGCCCCACCTCTTCACTCCCTGCC
AAGGTCCCATGGGCCACCTCCTGCATGTCTCCGCGGAGGGGCTACCTTCCTTCCATCGCCCTGCCTCGCAGCCA
GACTCATCTAAGGGTTCTTGTCTTGTCTATGGGGCAAACGTAGCATCCCTCACCTGGTCCCTGGCCTCTGT
AAAGCCACCAGCCTGAGGGCAGTGGCAGGAGATGGGGGTGGGGGGTGTGCTGCTTGGGCTGGGTGGGAAGGGAG
TTGGGGAGGGGTTTAAATGCACGGTGCATGTCTGGTGTCTGTATGCCAACCTAGACACCTCATGCTTCTGTCTC
CCCCACCCCACTCTGTTTTACATCTTTTATAAATGTGCCAACTGTGTGGCCTCTGCCA

WO 2004/030615

PCT/US2003/028547

1042/6881
FIGURE 972

MPGTVATLRFQLLPPEPDDAFWGAPCEQPLERRYQALPALVCIMCCLFGVVYCFYGYRCFKAVLFLTGLLFGSVV
IFLLCYRERVLETQLSAGASAGIALGIGLLCGLVAMLVRSVGLFLVGLLLGLLLAAAALLGSAPYYQPGSVWGPL
GLLLGGGLLCALLTLRWRPPLTTLATAVTGAALIATAADYFAELLLLGRYVVERLRAAPVPPLCWRSWALLALWP
LLSLMGVLVQWRVTAEGDSHTEVVISRQRRRVQLMRIRQQEDRKEKRRKKRPFRAPLRGPRAPPRPGPPDPAYRR
RPVPIKRFNGDVLSPSYIQSFRDRQTGSSLSSFMASTADADYEYGSRGPLTACSGPPVRV

WO 2004/030615

PCT/US2003/028547

1043/6881
FIGURE 973

CGGAGCACATGCTGAGCGGAGCGGCTGGGGCTGCGCGGCGTGGCGGAGCAGCGCTCGCTCCCTCGCTCACTCGCT
CGCTCGCAGGGACACACGCAGGGGCTGACAGCTGTGCTGGTGCTGATAAGGGAAGCCACAAGGAGACGATCGAGG
AGAGAGACAAGCGGCAGCAGAGGCAGCAGCGGCAGAGGCAGCACCAGGGCTGCGGAGCTGCTGGGAGTGGGAGTG
ACTCCCCACCTCGGGCCCCCACCCTGTCCCTGTCTCTTCCCGCTTGCCCTGAGTTTAGAAGAGCAGCCGCTGC
CACCCTGCCACTCGGGAGGGCACCAGGGCTGCTGGCTAGGGAGGGACAGGGCAGGGAGGCTCTGGCCAGTCCCA
GCAGCCGGGGACAGATGCCGATCGAGATTGTGTGCAAAATCAAATTTGCTGAGGAGGATGCGAAACCCAAGGAGA
AGGAGGCAGGGGATGAGCAGAGCCTCCTCGGGGCTGTTGCCCTGGAGCAGCCCCCGAGACCTGGCCACCTTTG
CCAGCACCAGCACCCTGCATGGACTGGGCCGGGCTGTGGCCAGGCCCCACGGACTGCGCAGAACCTGTGGG
CACTGGCCCTACTCACCTCGCTGGCTGCCTTCTGTACCAGGCGGCTGGCTGGCCGGGGCTACCTGACCCGGC
CTCACCTGGTGGCAATGGACCCCGCTGCCCCAGCCCCAGTGGCGGGCTTCCCGGCTGTACCCCTCTGCAATATCA
ACCGCTTCCGGCATTCGGCACTCAGCGATGCCGACATCTTCCACCTGGCCAACTGACAGGGCTGCCCCCAAG
ACCGGGATGGGCACCGTGGCGCTGGCCTGCGCTACCCAGAGCCTGACATGGTAGACATCCTCAACCGCACTGGCC
ACCAGCTCGCCGACATGCTTAAGAGCTGCAACTTCAGTGGGCATCACTGTCCGCCAGCAACTTCTCTGTGGTCT
ATACTCGCTATGGGAAGTGTTACACCTTCAACGCGGACCCGCGGAGCTCGCTGCCAGCCGGGCAGGGGGCATGG
GCAGTGGCCTGGAGATCATGCTGGACATCCAGCAGGAGGAGTACCTGCCCATCTGGAGGGAGACAAATGAGACGT
CGTTTGAGGCAGGTATTCGGGTGCAGATCCACAGCCAGGAGGAGCCGCCCTACATCCACCAGCTGGGGTTCGGGG
TGTCCCCAGGCTTCCAGACCTTTGTGTCTGCCAGGAACAGCGGCTGACCTACCTGCCCCAGCCCTGGGGCAACT
GCCGCGCAGAGAGTGAGCTCAGGGAGCCTGAGCTTCAGGGCTACTCGGCCTACAGTGTGTCTGCCTGCCGGCTGC
GCTGTGAAAAGGAGGCCGTGCTTCAGCGCTGCCACTGCCGGATGGTGACATGCCAGGCAATGAGACCATCTGCC
CACCAATATCTACATCGAGTGTGCAGACCACACACTGGACTCCCTGGGTGGGGGCCCTGAGGGCCCGTGCTTCT
GCCCCACCCCTGCAACCTGACACGCTATGGGAAAGAGATCTCCATGGTCAGGATCCCCAACAGGGGCTCAGCCC
GGTACCTGGCGAGGAAGTACAACCGCAACGAGACCTACATACGGGAGAACTTCTTGGTCTTAGATGTCTTCTTG
AGGCCCTGACCTCTGAAGCCATGGAGCAGCGAGCAGCCTATGGCCTGTCAGCCCTGCTGGGAGACCTCGGGGGAC
AGATGGGCCTGTTTATTGGGGCCAGCATCCTCACGTTGCTGGAGATCCTCGACTACATCTATGAGGTGTCTTGGG
ATCGACTGAAGCGGTATGGAGGCGTCCCAAGACCCCTGCGGACCTCCACTGGGGGCATCTCCACTTTGGGGC
TTCAGGAGCTGAAGGAACAGAGTCCCTGCCCGAGCCTGGGCCGAGCGAGGGTGGGGGGGTGAGCAGTCTGCTCC
CCAATCACCACCACCCCAACGGTCCCCCAGGAGGTCTCTTTGAAGATTTTGCTTGCTAGGACGGTGCTGTGACTG
AAAGGACCCAGGAGTCTGGGACCCCTCCTGGGATCCCAGCACATTCTCCTGCTCCTGGGAGAGGCCTGGGGGGC
GTGCTCACTGGGAGGGCCAGGACTCAGTTCTGTCTCATCTCCCTGCCCTGATGTGAGCTGCTTTGCACAAA
GGTCTTCTTGTCCACACCCCTTATCCCAGGCTGGTGCCCCGGGAGGGCTGGAGACCAGGCCATGGGCCCTCAC
GGAGAGGAAGGAAGGAAGGAGAGGGAGGGGGAGGATAGAGCCCATCCCAGCCGGGGAGGGGAGCCCTCTGTAC
ATTTGTAAATATTTAGGGAAAGCCGGGTGGGGGGAGGGGATACAGATGTAGAAGGTGGGTAGGGCTACAGGGGTG
GGTGATTTAGGGACAGCCAGGGTCCCAGCCCCAATGTGAGCAGGATAGGGAGAGCCCCAGGACTCAGGAGTGCTG
GGCTGGTCTACTTCTTGGCCCTCTCCAGGCCAGCTCCCTCTTGGCAGGGGGAGAGGATGGCCAGCAGGCCCT
GGCCAGCTCCCAGTTCCCCCTGCACCAGCCCCACCCCTAGAGTCCCTTCTATAGGGAGGGGGCAGGAGACCTTC
CAGACTTCGGCTGAGCTTGGAGGGTGGGAAGGGAGCCTTCTCAGTCTCTCTCCCTCCAGTCTGATTTTATAAAG
TGCTGACGAG

WO 2004/030615

PCT/US2003/028547

1044/6881
FIGURE 974

MPLEIVCKIKFAEEDAKPKEKEAGDEQSLLGAVAPGAAPRDLATFASTSTLHGLGRACGPGPHGLRRTLWALALL
TSLAAFLYQAAGLARGYLTRPHLVAMDPAAPAPVAGFPAVTL CNINRFRHSALSDADIFHLANLTGLPPKDRDGH
RAAGLRYPEPDMVDILNRTGHQLADMLKSCNFSGHHC SASNFSVVYTRYGKCYTFNADPRSSLPSRAGGMGSGLE
IMLDIQQEEYLP IWRETNETSFEAGIRVQIHSQEEPPYIHQLGFGVSPGFQTFVSCQEQRLLTYLPQPWGNCRAES
ELREPELQGYSAYSVSACRLRCEKEAVLQRCHCRMVHMPGENETICPPNIYIECADHTLDSLGGGPEGFCFCPTPC
NLTRYGKEISMVRIPNRGSARYLARKYNRNETYIRENFLVLDVFFFEALTSEAMEQRAAYGLSALLGDLGGQMGLF
IGASILTLEILDYIYEVSWDRLKRVWRRPKTPLRTSTGGISTLGLQELKEQSPCPSLGRAEGGGVSSLLPNHHH
PHGPPGGLFEDFAC

WO 2004/030615

PCT/US2003/028547

1045/6881
FIGURE 975

CCTCGCCGCATCCACTCTCCGGCCGGCCGCTGCCCGCCGCTCCTCCGTGCGCCCGCCAGCCTCGCCCCGCGCCG
 TCACCATGAGCCAGGCCTACTCGTCCAGCCAGCGCGTGTCTCCTACCGCCGCACCTTCGGCGGGGCCCCGGGCT
 TCCCACTCGGCTCCCCGCTGAGTTGCCCCGTGTTCCCGCGGGCGGGTTTCGGCTCTAAGGGCTCCTCCAGCTCGG
 TGACGTCCCGCGTGTACCAGGTGTCGCGCACGTCCGGCGGGGCCGGGGGCTGGGGTTCGCTGCGGGCCAGCCGGC
 TGGGGACCAACCGCACGCCCTCCTCCTACGGCGCAGGCGAGCTGCTGGACTTCTCACTGGCCGACGCGGTGAACC
 AGGAGTTTCTGACCACGCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTCAATGACCGCTTCGCCAACTACATCG
 AGAAGGTGCGCTTCCTGGAGCAGCAGAACGCGGCGCTCGCCGCCGAAGTGAACCGGCTCAAGGGCCGCGAGCCGA
 CGCGAGTGGCCGAGCTCTACGAGGAGGAGCTGCGGGAGCTGCGGCGCCAGGTGGAGGTGCTCACTAACCAGCGCG
 CGCGCGTTCGACGTTCGAGCGCGACAACCTGCTCGACGACCTGCAGCGGCTCAAGGCCAAGCTGCAGGAGGAGATT
 AGTTGAAGGAAGAAGCAGAGAACAATTTGGCTGCCTTCCGAGCGGACGTGGATGCAGCTACTCTAGCTCGCATTG
 ACCTGGAGCGCAGAATTGAATCTCTCAACGAGGAGATCGCGTTCCTTAAGAAAGTGCATGAAGAGGAGATCCGTG
 AGTTGCAGGCTCAGCTTCAGGAACAGCAGGTCCAGGTGGAGATGGACATGTCTAAGCCAGACCTCACTGCCGCC
 TCAGGGACATCCGGGCTCAGTATGAGACCATCGCGGCTAAGAACAATTTCTGAAGCTGAGGAGTGGTACAAGTCGA
 AGGTGTCAGACCTGACCCAGGCAGCCAACAAGAACAACGACGCCCTGCGCCAGGCCAAGCAGGAGATGATGGAAT
 ACCGACACCAGATCCAGTCTACACCTGCGAGATTGACGCCCTGAAGGGCACTAACGATTCCCTGATGAGGCAGA
 TCGGGGAATTGGAGGACCGATTTGCCAGTGAGGCCAGTGGCTACCAGGACAACATTGCGCGCTGGAGGAGGAAA
 TCCGGCACCTCAAGGATGAGATGGCCCCGCATCTGCGCGAGTACCAGGACCTGCTCAACGTGAAGATGGCCCTGG
 ATGTGGAGATTGCCACCTACCGGAAGCTGCTGGAGGGAGAGGAGAGCCGATCAATCTCCCCATCCAGACCTACT
 CTGCCCTCAACTTCCGAGAAACCAGCCCTGAGCAAAGGGGTTCTGAGGTCCATACCAAGAAGACGGTGATGATCA
 AGACCATCGAGACACGGGATGGGGAGGTTCGTGAGTGAGGCCACACAGCAGCAGCATGAAGTGCTCTTAAAGACAGA
 GACCCTCTGCCACCAGAGACCGTCTCTACCCCTGTCTCACTGCTCCCTGAAGCCAGCCTTCTTCCATCCCAGGA
 CACCACACCCAGCCTCAGTCTCTCCCTTCACAGCCTCTGACCCCTCCTCACTGGCCATCCCTCGTGGTCCCCAACA
 GCGACATAGCCCATCCCTGCCTGGTTCACAGGGCATGCCCCGGCCACCTCTGCGGACCCAGCTGTGAGCCTTGGC
 TGTTGGCAGTGAGTGAGCCTGGCTCTTGTGCTGGATGGAGCCCAGGCGGGAGCGGTGGCCCTGTCCCTCCCACCT
 CTGTGACCTCAGGCACTAGCCTTTGGCTCTGGAGACAGCCCCAGAGCAGGGTGTGGGATACTGCAGGGCCAGGA
 CTGAGCCCCGACAGCCTCCCCAGCCCCCTAGCCCAGGAGAGAGAAAGCCAGGCAGGTAGCCAGGGGGACTAGCCCC
 TGTGGAGACTGGGGGGCTTGAAATTGTCCCCGTGGTCTCTTACTTTTCTTTCCCCAGCCCAGGGTGGACTTAGAA
 AGCAGGGGCTACAAGAGGGAATCCCCGAAGGTGCTGGAGGTGGGAGCAGGAGATTGAGAAGGAGAGAAAGTGGGT
 GAGATGCTGGAGAAGAGAGGAGAGAGAGAGGAGAGAGCGGTCTCAGGCTGGTGGGAGGGGCGCCACCTCCCC
 ACGCCCTCCCCTCCCCTGCTGTCAGGGGCTCTGGAGAGAAACAATAAAGAGATTACACACAAGCC

WO 2004/030615

PCT/US2003/028547

1046/6881
FIGURE 976

MSQAYSSSQRVSSYRRTFGGAPGFPLGSPVFPFRAGFGSKGSSSVTSRVYQVSRTSGGAGGLGSLRASRLG
TTRTPSSYGAGELLDFSLADAVNQEFLLTTRTNEKVELQELNDRFANYIEKVRFLQQNAALAAEVNRLKGREPTR
VAELYEEELRELRRQVEVLTNQRRARVDVERDNLLDDLQRLKAKLQEEIQLKEEAENNLAAFRADVDAATLARIDL
ERRIESLNEEIAFLKKVHEEEIRELQAQLQEQVQVEMDMSPDLTAALRDIRAQYETIAAKNISEAEWYKSKV
SDLTQAANKNNDALRQAKQEMMEYRHQIQSYTCEIDALKGTNDSLMRQMRELEDRFASEASGYQDNIAARLEEEIR
HLKDEMARHLREYQDLLNVKMALDVEIATYRKLEGEESRINLP IQTYSALNFRETSPEQRGSEVHTKKTVMIKT
IETRDGEVVSEATQQQHEVL

WO 2004/030615

PCT/US2003/028547

1047/6881
FIGURE 977

GCACGAGGGTGATGAAGGCCTACGAGTGCGGCGGGCCTGAAGGGGCACGCGGGGGACCTGCAAAGCTAGTGAGG
GGCGGGGCAGGCGGCGCGGTGGGGGCGGGCCGAGCCCGGAGGCCAGATGAGCGGACACAGCCCCACGCGGGGGC
CATGCAGGTGGCCATGAACGGTAAGGCCCGCAAAGAGGCGGTGCAGACTGCGGCTAAGGAACTCCTCAAGTTCGT
GAACCGGAGTCCCTCTCCTTTCCATGCTGTGGCTGAATGCCGCAACCGCCTTCTCCAGGCTGGCTTCAGTGAAC
CAAGGAGACTGAGAAATGGAATATTAAGCCCGAGAGCAAGTACTTCATGACCAGGAACTCCTCCACCATCATAGC
TTTTGCTGTAGGGGGCCAGTACGTTCTGGCAATGGCTTCAGCCTCATCGGGGGCCACACGGACAGCCCCTGCT
CCGGGTGAAACGTCGGTCTCGCCGAGCCAGGTGGGCTTCAGCAAGTCGGTGTGGAGACCTATGGTGGTGGGAT
CTGGAGCACCTGGTTTGACCGTGACCTGACTCTGGCTGGACGCGTCATTGTCAAGTGCCCTACCTCAGGTCGGCT
GGAGCAGCAGCTGGTGCACGTGGAGCGGCCATTCTTCGCATCCACACCTGGCCATCCATCTGCAGCGAAATAT
CAACGAGAACTTTGGGCCCAACACAGAGATGCATCTAGTCCCCATTCTTGCCACAGCCATCCAGGAGGAGCTGGA
GAAGGGGACTCCTGAGCCAGGGCCTCTCAATGCTGTGGATGAGCGGCACCATTCGGTCCTCATGTCCCTGCTCTG
TGCCCATCTGGGGCTGAGCCCCAAGGACATAGTGGAGATGGAGCTCTGCCTTGACAGACCCAGCCTGCGGTCTT
GGGTGGTGCCTATGATGAGTTCATCTTTGCTCCTCGGCTGGACAATCTGCACAGCTGCTTCTGTGCCCTGCAGGC
CTTGATAGATTCTGTGCAGGCCCTGGCTCCCTGGCCACAGAGCCTCACGTGCGCATGGTCACACTCTATGACAA
CGAAGAGGTGGGTCTGAGAGTGACAGGGAGCACAGTCACTGCTGACAGAGCTGGTGTGCGGCGGATCTCAGC
CTCGTGCCAGCACCCGACAGCCTTCGAGGAAGCCATACCCAAGTCCTTCATGATCAGCGCAGACATGGCCCATGC
TGTGCATCCCAACTACCTGGACAAGCATGAGGAGAACCACCGGCCTTTATTCCACAAGGGCCCCGTGATCAAGGT
GAACAGCAAGCAACGCTATGCTTCAAACGCGGTGTCAGAGGCCCTGATCCGAGAGGTGGCCAACAAAGTCAAGGT
CCCCCTGCAGGATCTCATGGTCCGGAATGACACCCCTGTGGAACCACCATTGACCTATCTTGGCTTCTCGGCT
GGGGCTGCGGGTGCTGGATTTAGGCAGCCCCCACTGGCCATGCACTCTATCCGGGAGATGGCCTGCACCACAGG
AGTCTCCAGACCCTCACCTCTTCAAGGGCTTCTTTGAGCTGTTCCCTTCTTAAGCCATAATCTCTTAGTGGA
TTGAGCCCTCTTGGAAGACTTCTCTGCCATCCCTTTGCACCTGAGAGGGGAAGTTCTCAGCTGAGCTGAAGCTG
GATTATTAAAGTGATTGTCACTCAGAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1048/6881
FIGURE 978

MQVAMNGKARKEAVQTAAKELLKFVNRSPSPFHAVAECRNRLQAGFSELKETEKWNIKPESKYFMTRNSSTIIA
FAVGGQYVPGNGFSLIGAHTDSPCLRVKRRSRRSQVGFQQVGVETYGGGIWSTWFDRLTLAGRVIVKCPTSGRL
EQQLVHVERPILRIPHLAIHLQRNINENFGPNTEMHLVPILATAIQEELEKGTPEPGPLNAVDERHHSVLMSSLLC
AHLGLSPKDIVEMELCLADTQPAVLGGAYDEFIFAPRLDNLHSCFCALQALIDSCAGPGSLATEPHVRMVTLYDN
EEVGSESAQGAQSLLTTELVLRRISASCQHPTAFEEAIPKSFMISADMAHAVHPNYLDKHEENHRPLFHKGPVIKV
NSKQRYASNAVSEALIREVANKVKVPLQDLMVRNDTPCGTTIGPILASRLGLRVLDLGSPLAMHSIREMACTTG
VLQTLTLFKGFFELFPLSHNLLVD

WO 2004/030615

PCT/US2003/028547

1049/6881
FIGURE 979

CTTTGCATTGTTTCCTCATCCGCCTCCTTGCTCGCCGCAGCCGCCTCCGCCGCGCGCCTCCTCCGCCGCCGCGGAC
TCCGGCAGCTTTATCGCCAGAGTCCCTGAACTCTCGCTTTCTTTTAAATCCCTGCATCGGATCACCGGCGTGCC
CCACCATGTCAGACGCAGCCGTAGACACCAGCTCCGAAATCACCACCAAGGACTTAAAGGAGAAGAAGGAAGTTG
TGGAAGAGGCAGAAAATGGAAGAGACGCCCCCTGCTAACGGGAATGCTAATGAGGAAAATGGGGAGCAGGAGGCTG
ACAATGAGGTAGACGAAGAAGAGGAAGAAGGTGGGGAGGAAGAGGAGGAGGAAGAAGAAGGTGATGGTGAGGAAG
AGGATGGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCAAGCGGGCAGCTGAAGATGATGAGGATGACGATG
TCGATACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAACTAAAAAAAAAAG
GCCGCCGTGACCTATTCACCTCCACTTCCCGTCTCAGAATCTAAACGTGGTCACCTTCGAGTAGAGAGGCCCGC
CCGCCCCACCGTGGGCAGTGCCACCCGCAGATGACACGCGCTCTCCACCACCCAACCCAAACCATGAGAATTTGCA
ACAGGGGAGGAAAAAAGAACCAAAACTTCCAAGGCCCTGCTTTTTTTCTTAAAAGTACTTTAAAAAGGAAATTTG
TTTGTATTTTTTATTTACATTTTATATTTTTGTACATATTGTTAGGGTCAGCCATTTTAAATGATCTCGGATGAC
CAAACCAGCCTTCGGAGCGTTCTCTGTCTACTTCTGACTTTACTTGTGGTGTGACCATGTTTCATTATAATCTCA
AAGGAGAAAAAAACCTTGTAaaaaaaAGCAAAATGACAACAGAAAAACAATCTTATTCCGAGCATTCCAGTAAC
TTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAG
GTTTCTTTTTTTTTCTTTTTTGTCTATGAAGTTGCTGTTTATTTTTTTTTGGCCTGTTTGATGTATGTGTGAAAC
AATGTTGTCCAACAATAAACAGG

WO 2004/030615

PCT/US2003/028547

1050/6881
FIGURE 980A

GCGGCAAGCCCCGCTCAGCCCCCTCTGGCAGGCTCCCGCCAGCGTCGCTGCGGCTCCGGCCCCGGGAGCGAGCGCC
CGGAGCTCGGAAAGATGCGGCGCCCCGCGCGGCCTGGGGGTCTCGGGGGATCCGGGGGTCTCCGGCTGCTCCTCT
GCCTCCTGCTGCTGAGCAGCCGCCCCGGGGGGCTGCAGCGCCGTTAGTGCCACGGCTGTCTATTTGACCGCAGGC
TCTGCTCTACCTGGAAGTCTGTATTTCAGGATGGCTTGTTTGGGCAGTGCCAGGTGGGAGTGGGGCAGGCCCGGC
CCCTTTTGCAAGTCACTCCCCAGTTCTCCAACGCTTACAAGGTGTGCTCCGACAACCTCATGTCCCAAGGATTGT
CCTGGCAGCATGACCTCACCCAGTATGTGATCTCTCAGGAGATGGAGCGCATCCCCAGGCTTCGCCCCCAGAGC
CCCGTCCAAGGGACAGGTCTGGCTTGGCACCCAAGAGACCTGGTCCTGCTGGAGAGCTGCTTTTACAGGACATCC
CCACTGGCTCCGCCCCCTGCTGCCCAGCATCGGCTTCCACAACCACCAAGTGGGCAAAGGTGGAGCTGGGGCCAGCT
CCTCTCTGTCCCCCTCTGCAGGCTGAGCTGCTCCCGCTCTCTTGGAGCACCTGCTGCTGCCCCACAGCCTCCCC
ACCCTTCACTGAGTTACGAACCTGCCTTGCTGCAGCCCTACCTGTTCCACCAGTTTGGCTCCCGTGATGGCTCCA
GGGTCTCAGAGGGCTCCCCAGGGATGGTCAGTGTGCGCCCCCTGCCCAAGGCTGAAGCCCCCTGCCCTCTTCAGCA
GAACTGCCTCCAAGGGCATATTTGGGGACCACCTGGCCACTCCTACGGGGACCTTCCAGGGCCTTACCTGCCC
AGCTTTTTCAAGACTCTGGGCTGCTCTATCTGCGCCAGGAGTTGCCAGCACCCAGCAGGGCCAGGGTGCCAAAGGC
TGCCAGAGCAAGGGAGCAGCAGCCGGGCAGAGGACTCCCCAGAGGGCTATGAGAAGGAAGGACTAGGGGATCGTG
GAGAGAAGCCTGCTTCCCCAGCTGTGCAGCCAGATGCGGCTCTGCAGAGGCTGGCCGCTGTGCTGGCGGGCTATG
GGGTAGAGCTGCGTCAGCTGACCCCTGAGCAGCTCTCCACACTCCTGACCCTGCTGCAGCTACTGCCCAAGGGTG
CAGGAAGAAATCCGGGAGGGGTGTAAATGTTGGAGCTGATATCAAGAAAACAATGGAGGGGCCGGTGGAGGGCA
GAGACACAGCAGAGCTTCCAGCCCGCACATCCCCATGCCTGGACACCCCACTGCCAGCCCTACCTCCAGTGAAG
TCCAGCAGGTGCCAAGCCCTGTCTCCTCTGAGCCTCCCAAAGCTGCCAGACCCCTGTGACACCTGTCTGTAG
AGAAGAAAAGCCCACTGGGCCAGAGCCAGCCACGGTGGCAGGACAGCCCTCAGCCCGCCAGCAGCAGAGGAAT
ATGGCTACATCGTCACTGATCAGAAGCCCCCTGAGCCTGGCTGCAGGAGTGAAGCTGCTGGAGATCCTGGCTGAGC
ATGTGCACATGTCTCAGGCAGCTTCATCAACATCAGTGTGGTGGGACCAGCCCTCACCTTCCGCATCCGGCACA
ATGAGCAGAACCTGTCTTTGGCTGATGTGACCCAACAAGCAGGGCTGGTGAAGTCTGAACTGGAAGCACAGACAG
GGCTCCAAATCTTGACAGACAGGAGTGGGACAGAGGGAGGAGGCAGCTGCAGTCTTCCCCAACTGCGCACAGCA
CCTCACCCATGCGCTCAGTGTGCTCACTCTGGTGGCCCTGGCAGGTGTGGCTGGGCTGCTGGTGGCTCTGGCTG
TGGCTCTGTGTGTGCGGCAGCATGCGCGGCAGCAAGACAAGGAGCGCCTGGCAGCCCTGGGGCCTGAGGGGGCCC
ATGGTGACACTACCTTTGAGTACCAGGACCTGTGCGGCCAGCACATGGCCACGAAGTCCTTGTCAACCGGGCAG
AGGGTCCACCGGAGCCTTACGGGTGAGCAGTGTGTCTCCAGTTACGCGACGCAGCCAGGCCAGCCCCAGCT
CCCACAGCAGCACCCCGTCTGGTGGGAGGAGCCGGCCCAAGCCAACATGGACATCTCCAGGGACACATGATTG
TGGCATACATGGAGGATCACCTGCGGAACCGGGACCGCCTTGCCAAGGAGTGGCAGGCCCTCTGTGCTTACCAAG
CAGAGCCAAACACCTGTGCCACCGCGCAGGGGGAGGGCAACATCAAAAAGAACCGGCATCCTGACTTCTTGCCT
ATGACCATGCCCCGATAAACTGAAGGTGGAGAGCAGCCCTTCTCGGAGCGATTACATCAACGCCAGCCCCATTA
TTGAGCATGACCCTCGGATGCCAGCCTACATAGCCACGCAGGGCCCCGTGTCCCATACCATCGCAGACTTCTGGC
AGATGGTGTGGGAGAGCGGCTGCACCGTCATCGTCATGCTGACCCCGCTGGTGGAGGATGGTGTCAAGCAGTGTG
ACCGCTACTGGCCAGATGAGGGTGCCTCCCTCTACCAGTATATGAGGTGAACCTGGTGTGCGAGCACATCTGGT
GCGAGGACTTTCTGGTGGGAGCTTCTACCTGAAGAAGCTGCAGACCCAGGAGACGCGCACGCTCACGCAGTTCC
ACTTCTCAGCTGGCCGGCAGAGGGCACACCGGCCCTCCACGCGGCCCTGCTGGACTTCCGAGGAAGGTGAACA
AGTGCTACCGGGGCGCTCCTGCCCATCATCGTGACTGCAGTGTATGGTGGGGGAGGACCGGCACCTACATCC
TCATCGACATGGTCTGAACCGCATGGCAAAGGAGTGAAGGAGATTGACATCGCTGCCACCTGGAGCATGTCC
GTGACCAGCGGCTGGCCTTGTCCGCTCTAAGGACCAGTTTGAATTTGCCCTGACAGCCGTGGCGGAGGAAGTGA
ATGCCATCCTCAAGGCCCTGCCCCAGTGAGACCTGGGGGCCCTTGGCGGGCAGCCAGCCTCTGTCCCTCTTTG
CCTGTGTGAGCATCTCTGTGTACCCACTCCTCACTGCCCCACCAGCCACCTTGGGCATGCTCAGCCCTTCCTA
GAAGAGTCAGGAAGGGAAAGCCAGAAGGGGCACGCTGCCAGCCTCGCATGCCAGAGCCTGGGGCATCCAGAG
CCCAGGGCATCCCATGGGGGTGCTGCAGCCAGGAGGAGAGGAAGGACATGGGTAGCAATTCTACCCAGAGCCTT
CTCCTGCCTACATTCCCTGGCCTGGCTCTCCTGTAGCTCTCCTGGGGTTCTGGGAGTTCCCTGAACATCTGTGTG
TGTCCCCCTATGCTCCAGTATGGAAGAATGGGGTGGAGGGTGGCCACACCCGGCTCCCCCTGCTTCTCAGCCCCG
GGCCTGCCTCTGACTCACACTTGGGCGCTCTGCCCTCCCTGGCCTCACGCCCAGCCTCCTCCACCACCCCTCCCA
CCATGCGCTGCTCAACCTCTCTCCTTCTGGCGCAAGAGAACATTTCTAGAAAAAACTACTTTTGTACCAGTGTGA

WO 2004/030615

PCT/US2003/028547

1051/6881
FIGURE 980B

ATAAAGTTAGTGTGTTGTCTGTGCAGCTGCAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1052/6881
FIGURE 981

MRRPRRP GGLGGSGGLRLLLLCLLLLLSSRPGGCSAVSAHGCLFDRRLCSHLEVCIQDGLFGQCQVGVGQARPLLQV
TSPVLQRLQGVLRQLMSQGLSWHDDLTQYVISQEMERIPRLRPPEPRPRDRSGLAPKRPGPAGELLLQDIPTGSA
PAAQHRLPQPPVVGKGGAGASSLSPLQAELLPLLEHLLLPQPPHPSLSYEPALLQPYLFHQFGSRDGSRVSEG
SPGMVSVGPLPKAEAPALFSRTASKGIFGDHPGHSYGDLPGPSAQLFQDSGLLYLAQELPAPSRARVPRLPEQG
SSSRAEDSPEGYEKEGLGDRGEKPASPAVQPDAAALQRLAAVLAGYGVELRQLTPEQLSTLLTLLQLLPKGAGRNP
GGVVNVGADIKKTMEGPVEGRDTAELPARTSPMPGHFTASPTSSEVQQVPSPVSSPEPPKAARPPVTPVLEKKSP
LGQSQPTVAGQPSARPAEEYGYIVTDQKPLSLAAGVKLLEILAETHVMSSGSFINISVVGPAITFRIRHNEQNL
SLADVTQQAGLVKSELEAQTGLQILQTGVGQREEAAVLPQTAHSTSPMRSVLLTLVALAGVAGLLVALAVALCV
RQHARQQDKERLAALGPEGAGDITTFEYQDLCRQHMAKSLFNRAEGPPEPSRVSSVSSQFSDAAQASPSHSST
PSWCEEPAQANMDISTGHMILAYMEDHLNRNDRDLAKEWQALCAYQAEPNTCATAQGEKNIKNRHPDFLPYDHAR
IKLKVESSPSRSDYINASPIIEHDPMPAYIATQGPLSHTIADFWQMVWESGCTVIVMLTPLVEDGVKQCDRYWP
DEGASLYHVYEVNLVSEHIWCEDFLVRSFYLNKVNQTQETRTLTFHFLSWPAEGTPASTRPLLDFFRRKVNKCYRG
RSCPIIVHCSDGAGRTGTIYLIDMVLNRMAGVKEIDIAATLEHVRDQRPGLVRSKDQFEFALTAVAEVNAILK
ALPQ

WO 2004/030615

PCT/US2003/028547

1053/6881
FIGURE 982

AGTTCTCACTGAGACCTGTCACCCCGACTCAACGTGAGACGCACCGCCCGGACTCACCATGCGTGAATGCATCTC
AGTCCACGTGGGGCAGGCAGGTGTCCAGATGGGCAATGCCTGCTGGGAGCTCTATTGCTTGGAACATGGGATTCA
GCCTGATGGGCAGATGCCCAGTGACAAGACCAATTGGTGGAGGGGACGACTCCTTCACCACCTTCTTCTGTGAAAC
TGGTGCTGGAAAACACGTACCCCGGGCAGTTTTTGTGGATCTGGAGCCTACGGTCATTGATGAGATCCGAAATGG
CCCATACCGACAGCTCTTCCACCCAGAGCAGCTCATCACTGGGAAAAGAGGATGCTGCCAACAACTATGCCCGTGG
TCACTATACCATTGGCAAGGAGATCATTGACCCAGTGCTGGATCGGATCCGCAAGCTGTCTGACCAGTGCACAGG
ACTTCAGGGCTTCCTGGTGTTCACAGCTTTGGTGGGGGCACTGGCTCTGGCTTCACCTCACTCCTGATGGAGCG
GCTCTCTGTTGACTATGGCAAGAAATCCAAGCTGGAATTCTCCATCTACCCAGCCCCCAGGTGTCTACAGCCGT
GGTCGAGCCCTACAACCTCTATCCTGACCACCCACACCACCTGGAGCACTCAGACTGTGCCTTCATGGTGGACAA
CGAAGCAATCTATGACATCTGCCGCCGCAACCTAGACATCGAGCGCCCAACCTACACCAACCTCAATCGCCTCAT
TAGCCAAATTGTCTCCTCCATCACAGCTTCTCTGCGCTTTGACGGGGCCCTCAATGTGGACCTGACAGAGTTCCA
GACCAACCTGGTGGCCTACCCTCGCATCCACTTCCCCCTGGCCACCTATGCACCAGTCATCTCTGCAGAAAAGGC
ATACCACGAGCAGCTGTCCGTGGCAGAGATACCAATGCCTGCTTTGAGCCTGCCAACCAGATGGTAAAGTGTGA
TCCCCGGCACGGCAAGTACATGGCCTGCTGCCTGCTGTACCGTGGAGATGTGGTGCCCAAGGATGTCAACGCTGC
CATTGCCGCCATCAAGACCAAGCGCAGCATTTCAGTTTGTGGACTGGTGCCCCACAGGCTTCAAGGTGGTATCAA
CTACCAGCCTCCCCTGTGGTGCCTGGGGGTGACCTGGCCAAGGTGCAGCGTGCCGTGTGCATGCTGAGCAACAC
GACCGCCATCGCCGAGGCCTGGGCCCCGCTGGACCACAAGTTCGACCTGATGTATGCCAAGAGGGCGTTTGTGCA
CTGGTATGTGGGTGAGGGCATGGAGGAGGGTGAGTTCTCCGAGGCCCGTGAGGATATGGCTGCCCTGGAGAAGGA
TTATGAGGAGGTGGGCATCGACTCCTATGAGGACGAGGATGAGGGAGAAGAATAAAGCAGCTGCCTGGAGCCTAT
TCACTATGTTTATTGCAAAATCCTTTGAAATAAACAGTTTCCTTGACGGTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1054/6881
FIGURE 983

MRECISVHVGQAGVQMGNACWELYCLEHGIQPDGQMP SDKTIGGGDDSF TTTFFCETGAGKHVPRAVFVDLEPTVI
DEIRNGPYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDPVLDRIKRLSDQCTGLQGFLVFHSFGGGTGSGFT
SLLMERLSVDYGKKSLEFSIYPAPQVSTAVVEPYN SILTHTTLEHSDCAFMDNEAIYDICRRNLDIERPTYT
NLNRLISQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAATAAIKTKRSIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGIDSYEDEDEGEE

WO 2004/030615

PCT/US2003/028547

1055/6881
FIGURE 984

GGGCCTGCAGTTGGCAGGAGGGTCCCCGGGCCAGAGCCAGCGGGCCGTGCTGAGACGGCGTACGTGCCCTGCGT
GAGTGCGTGGCGGCGGCGCGTGCCTAGGGGAGTGGGCGGTGAGGCCTGGTCCACGTGCGTCCCTTCCCGGGACC
CCCGCAGCTTGGCGCCCAGCGGCTACGTGAGCCAAGGCACCCGGATGTCCGCGCCCCCTCTCCGAGTGACCAGTCC
CGGCCTCCGGTCCCGCAGTGCCCGCAGCCTCGGCCGGCGTCCACGCATTGCCATGGTGAAGTGTGGGCAACTACTG
CGAGGCCGAAGGGCCCGTGGGTCCGGCTGGATGCAGGATGGCCTGAGTCCCTGCTTCTTCTTACGCTCGTGCC
CTCGACGCGGATGGCTCTGGGGACTCTGGCCTTGGTGCTGGCTCTTCCCTGCAGACGCCGGGAGCGGCCCGTGG
TGCTGATTGCTGTCTTGGGGGGCGGCCCTCGCATCTCTCCCTACGTGCTGCAGCTGCTTCTGGCCACACTTCA
GGCGGCGCTGCCCCCTGGCCGGCCTGGCTGGCCGGGTGGGCACTGCCCGGGGGCCCCACTGCCAAGCTATCTACT
TCTGGCCTCCGTGCTGGAGAGTCTGGCCGGCGCCTGTGGCCTGTGGCTGCTTGTCTGAGCGGAGCCAGGCACG
GCAGCGTCTGGCAATGGGCATCTGGATCAAGTTCAGGCACAGCCCTGGTCTCCTGCTCCTCTGGACTGTGGCGTT
TGCAGCTGAGAACTTGGCCCTGGTGTCTTGGAAACAGCCACAGTGGTGGTGGCAAGGGCAGACTTGGGCCAGCA
GGTTCAGTTTAGCCTGTGGGTGCTGCGGTATGTGGTCTCTGGAGGGCTGTTGTCTGGGTCTCTGGGCCCTGG
ACTTCGTCCCGAGTCTATACATTGCAGGTTTCAAGAGGACCAAGATGTGGAAGGAGCCAGGTTCCGTCAGC
AGCCCAACAGTCTACCTGGCGAGATTTTGGCAGGAAGCTCCGCCCTCTGAGTGGCTACCTGTGGCCTCGAGGGAG
TCCAGCTCTGCAGCTGGTGGTGTCTATCTGCCGGGGCTCATGGGTTTGGAAACGGGCACTCAATGTGTGGTGCC
TATATTCTATAGGAACATTGTGAAGTGTGCTGAGTGAAGGCACCTTGGAACTCTCTGGCCTGGACTGTTACAG
TTACGTCTTCTCAAGTTTCTCCAGGGGGTGGCACTGGCAGTACAGGCTTCGTGAGCAACCTGCGCACCTTCTT
GTGGATCCGGGTGCAGCAGTTCACGTCTCGCGGGTGGAGCTGCTCATCTTCTCCACCTGCACGAGCTCTCACT
GCGCTGGCACCTGGGGCGCCGCACAGGGGAGGTGCTGCGGATCGCGGATCGGGGCACATCCAGTGTACAGGGCT
GCTCAGCTACCTGGTGTTCATGTATCCCCACGCTGGCCGACATCATATTGGCATCATCTACTTCAGCATGTT
CTTCAACGCCTGGTTTGGCCTCATTGTGTCTCTGTGATGAGTCTTTACCTACCCCTGACCATTGTGGTCACTGA
GTGGAGAACCAAGTTTTCGTGCTGCTATGAACACACAGGAGAACGCTACCCGGGCACGAGCAGTGGACTCTCTGCT
AAACTTCGAGACGGTGAAGTATTACAACGCCGAGAGTTACGAAGTGAACGCTATCGAGAGGCCATCATCAAATA
TCAGGGTTTGGAGTGAAGTTCGAGCGCTTCACTGGTTTTACTAAATCAGACCCAGAACCTGGTGATTGGGCTCGG
GCTCCTCGCCGGCTCCCTGCTTTGCGCATACTTTGTCACTGAGCAGAAGCTACAGGTGGGGACTATGTGCTCTT
TGGCACCTACATTATCCAGCTGTACATGCCCTCAATTGGTTTGGCACCTACTACAGGATGATCCAGACCACTT
CATTGACATGGAGAACATGTTTGACTTGCTGAAAGAGGAGACAGAAGTGAAGGACCTTCTGGAGCAGGGCCCT
TCGCTTTTCAAGGGCCGTATTGAGTTTGAAGACGTGCACTTACAGCTATGCCGATGGGCGGGAGACTCTGCAGGA
CGTGTCTTTCACTGTGATGCCTGGACAGACACTTGGCCTGGTGGGCCCCTCTGGGGCAGGGAAGAGCACAAATTT
GCGCCTGCTGTTTTCGCTTCTACGACATCAGCTCTGGCTGCATCCGAATAGATGGGCAGGACATTTACAGGTGAC
CCAGGCCTCTCTCCGGTCTCACATTGGAGTTGTGCCCCAAGACACTGTCTCTTTAATGACACCATCGCCGACAA
TATCCGTTACGGCCGTGTACAGCTGGGAATGATGAGGTGGAGGCTGCTGCTCAGGCTGCAGGCATCCATGATGC
CATTATGGCTTTCCCTGAAGGGTACAGGACACAGGTGGGCGAGCGGGGACTGAAGCTGAGCGGCGGGGAGAAGCA
GCGCGTCGCCATTGCCCGCACCATCCTCAAGGCTCCGGGCATCATTCTGCTGGATGAGGCAACGTACGCGCTGGA
TACATCTAATGAGAGGGCCATCCAGGCTTCTCTGGCCAAAGTCTGTGCCAACCGCACCACTCGTAGTGGCACA
CAGGCTCTCAACTGTGGTCAATGCTGACCAGATCTCGTCATCAAGGATGGCTGCATCGTGGAGAGGGGACGACA
CGAGGCTCTGTTGTCCCGAGGTGGGTGTATGCTGACATGTGGCAGCTGCAGCAGGGACAGGAAGAAACCTCTGA
AGACACTAAGCCTCAGACCATGGAACGGTGACAAAAGTTTGGCCACTTCCCTCTCAAAGACTAACCAGAAAGGA
ATAAGATGTGCTCTCTTTCCCTGGCTTATTTTCATCCTGGTCTTGGGGTATGGTGCTAGCTATGGTAAGGGAAAGG
GACCTTTCCGAAAACATCTTTTGGGGAAATAAAAAATGTGGACTGTG

WO 2004/030615

PCT/US2003/028547

1056/6881
FIGURE 985

GTGCACTTCAGCTATGCCGATGGGTGAGGCCTTCCTTTTGCTTCCTTTGCTTTTCCGTTTCATTTGCACACTGCCT
TCCTGCTTCTCAGTGCTCTGAATCCCTGCTTTTGGAAGAGCCTGGGCAGGGGAGGGGCAGGGCCTACTAGCAG
CTCTGGTGATGGAAGGTGCCTGCTGAGCAACCCACCTTTTCCTTGACAGGCGGGAGACTCTGCAGGACGTGTCTTT
CACTGTGATGCCTGGACAGACACTTGCCTGGTGAGAGGAGACCCAGCCACTTGGCCCAGATGCCTCAAGCTTCC
CTCATTCACTGCCCATGGTAGCTTGTGACCCAGGCTGTGGAGTCAGAGAGCCCAGTCACGATAGGCAACCGGATT
GAATGGTGCAGCCTCCATGGACACTGGTGACCTCTTGGAGAGGGAACCTCAAAAGCCAGTGGGCCTCGGCCGGCT
GCGGTGGCACATGCCTGTAATCCCAGCACTTTGGGAGGCTTAGGTGGCCAGATCACCTAAGGTGGGCCCATCTGG
GGCAGGGAAGAGCACAATTTTGCCTGCTGTTTCGCTTCTACGACATCAGCTCTGGCTGCATCCGAATAGATGG
G

WO 2004/030615

PCT/US2003/028547

1057/6881
FIGURE 986

GCTGCCCCGGTATCCCCGTGTGGGGCAGGAAGTGGGCTTCCAGATTCCCAGTATCCCCGGTAGGGTCTGCTTCTG
 CTCGCTCGGGAAGGGCGGTGGCCGTCCCATTACTCAACCAACCCTCAACGCACTGGTCCTCCCAGTTCCCTCCCC
 TCAGTGGGTAAACAAACACACACCAGCGCTTGACTCGACAGACTCGAAAACAACATCTACTCAGAAAAGTTGTTT
 CTTTCCTATCTCCTTAAACTTTCCCACTTCCACATATCGGAGCTTCTTCCCACCTCGGCCTACTCAAGCATGAGA
 TCGGAGGCGGGAGGGCGGCGACTGGCGGCGCGATGGACCTGACCGGGCTCCTGCTGGACGAAGAAGGCACCTTCT
 CCGTCGCCGGCTTCCAGGACTTCACGTTCTTCCCAGGACACCAGAAGCTGAGTGCCCGGATCCGAAGGAGGCTCT
 ACTATGGCTGGGACTGGGAAGCCGACTGTAGCCTGGAGGAGCTCTCCAGCCCGGTGGCAGACATTGCTGTGCAAC
 TGCTCCAGAAGGCAGCCCCAGCCCTATTGCGCGACTCCAGAAGAAATATGTAGCTCATGTGTCCCGGGAGGCAT
 GCATCTCCCCATGTGCTATGATGCTGGCTCTGGTGTACATTGAACGGCTCCGGCACCGAAACCCAGACTACTTGC
 AGCATGTGTCACTCTGACTTGTTCCTGATCTCCATGATGGTGGCCAGTAAGTACCTCTATGATGAAGGGGAGG
 AGGAGGAGGTCTTCAACGACGAATGGGGAGCTGCTGGGGGTGTGGCCGTGCCCACTCTCAATGCCTTGGAGAGGG
 GCTTCCTGAGTGCCATGGATTGGCATCTCTACACTGACCCCTCGGGAGATCTTTGAGGTGCTGAGCTGGTTGGAGA
 GCTGTGTGGCTGAGCAGCAGGGACGGTGGCGAGGCTGGTACACCTACACAGACCTGTGTGTGCTGCTGGAGCAGC
 CGACCTGGCAGTTGGCCCTGGGCTCCCTCTGCCAGCGGCTGGTAAAGCTGTCTTGCCTGTTAGCTGTGGCATATG
 TGAGCAGTGTGGCCCTGGCTGTGGCATCGGTGGCCGTAATACATCAGTCTTTGGGGCTGTCTGTCATCCCTACAC
 CTGGGCGCGCTGACCTTGGACTGACCTCCCGTTGCCTCCTGGAGCCCTGCATACCTTCTGTGCCACAATGCCTGC
 CGTCTCTCGCTAATGTCTCCAGCTGCCTGGAAGGCAGCATGGGGCTGCGGTCACTCTGGGGCAGTCTTCTGGCCT
 CACTGACTCCTCCACCATTGCCTCCCCCAGACCCCCCTGCCCCCTCCCCTCTTCTTTCATAACTGCCACCTTTGCC
 AGAAGCTCCAGAGAGACTCCCCAACCTGCCATGCCTGCCTCCACCCCAACCGTACAGTCCCCACTGCGCTGTCCA
 GCCCCCTGGTACCATACTATGGCCTGGCTCCCCCTGGCCTTGGAGCCCGGTGCTCCTTTCACTTCTCAGCCTC
 AGCAATGTTCCCTTTTCACTGTATGGAGCTGGCTCGCCTCAAGTCTTTTCGTTTTCCAGGCTAGGTAGGGCTGT
 GAGGAATGCATTAAAGAGGGTTTGGGAGTTTCTGAGAACCTGGAGGAGCAAAGCTTGATTGAGATCCTGTCTGCCT
 CGCTGGGTCTTGGCAGGTCCCCCTGTCTCCTGGGTGGGAGCTTATGGGGTGGTGGGGCAGAAGGACTGAAGGTA
 ATTCACTCCTAGATCGCAGTGGCTGGCTGCTTGGCCAGGACAGTGATGCCGCCAGGGAGAGCTTCCGCTTGGTGA
 CCAGGGACATGTCCCAGATGGACATAGAAGCCCCCTCTCTGCCTCCCTGGGATTTTTTAGACTTTTACTTTTGATT
 TCCCTAGGATGGAAGAGTATAGGTGGGAGATAAGGGAAGTGGGGTGAGAGGAGAAAGGAAATGTTGGCATGGGCC
 TGTGTGATGTCCCTGAGGCAGAAGAGC

WO 2004/030615

PCT/US2003/028547

1058/6881
FIGURE 987

MDLTGLLLDEEGTFSLAGFQDFTFLPGHQKLSARIRRRRLYYGWDWEADCSLEELSSPVADI AVELLQKAAPSPIR
RLQKKYVAHVSREACISPCAMMLALVYIERLRHRNP DY LQHVSSDLFLISMMVASKYLYDEGEEEEVFNDEWGA
AGGVAVPTLNALERGFLSAMDWHLYTDPREIFEVL SWLESCVAEQGRWRGWYTYTDLCV LLEQPTWQLALGSLC
QRLVKLSCLLAVAYVSSVALAVASVAVIHQSLGLSC IPTPGPPDLGLTSRCLLEPCIPSPQCLPSLANVSSCLE
GSMGLRSLWGSLLASLT P P P L P P P D P P A P P T L L H N C H L C Q K L Q R D S P T C H A C L H P N R T V P T A L S S P W Y H T Y G L A P
PWPWSPVLLSLPQPQQCSLFSVMELARLKS F V F P G

WO 2004/030615

PCT/US2003/028547

1059/6881
FIGURE 988

GAAGATATGCGGCGTCTGCGTCTGCAGCTGCAGGGGAGGAGGACTGGGTCTTCCCTCTGAAGTTGAAGTATTG
GAGTCCATCTATCTAGATGAACTACAGGTGATTAAAGGAAATGGCAGAACTTCACCATGGGAGATCTACATCACT
TTGCATCCTGCCACTGCAGAGGACCAGGATTCACAGTATGTCTGCTTCACTCTGGTGCTTCAGGTCCCAGCAGAG
TATCCCCATGAGGTGCCACAGATCTCTATCCGAAATCCCCGAGGACTTTCAGATGAACAGATCCACACGATCTTA
CAGGTGCTGGGCCACGTGGCCAAGGCTGGGCTGGGCACTGCCATGCTGTATGAACTCATTGAGAAAGGGAAGGAA
ATTCTCACAGATAACAACATCCCTCATGGCCAGTGTGTCTATCTGCCTCTATGGTTTCCAGGAGAAGGAGGCCCTT
ACCAAAACACCCTGTTACCACTACTTCCACTGCCACTGCCTTGCTCGGTACATCCAGCACATGGAGCAAGAGCTG
AAGGCACAAGGACAGGAGCAGGAACAGGAACGGCAGCATGCTACAACCAACAGAAGGCAGTCGGTGTGCAGTGT
CCAGTGTGCAGAGAGCCCCCTCGTGTATGATCTTGCCTCACTGAAAGCAGCCCCCTGAACCCCAACAGCCCATGGAG
CTGTACCAGCCCAGTGCAGAGAGCTTGCGCCAGCAAGAAGAACGCAAGCGGCTCTACCAGAGGCAGCAGGAGCGG
GGGGGAATCATTGACCTTGAGGCTGAGCGAAACCGATACTTCATCAGCCTTCAGCAGCCTCCTGCCCTGCGGAA
CCTGAGTCAGCTGTAGATGTCTCCAAGGATCCCAACCCAGCACCCTTGAGCAGAGAACTATCCACCTCACCA
GCCGTCCAATCCACTTTGCCACCTCCTCTGCCTGTGGCGACCCAGCACATATGTGAGAAGATTCCAGGGACCAGG
TCAAATCAGCAAAGGTTGGGCGAAACCCAGAAAGCTATGCTAGATCCCCCAAGCCCAGTCGAGGTCCCTGGCGA
CAGCCCGAACGGAGGCACCCAAAGGGAGGGGAGTGCCACGCCCCCTAAAGGTACCCGTGACACCCAGGAACCTGCCA
CCTCCTGAGGGGCCCCCTCAAGGAGCCCATGGACCTAAAGCCAGAACCCCATAGCCAAGGAGTTGAAGGTCCTCCA
CAAGAGAAGGGGCTGGCAGCTGGCAGGGGCCCCCACCCTCGCAGGACTCGGGACTGTGTTTCGCTGGGAGCGCTCT
AAAGGCCGGACACCCGGTTCTTCTACCTCGCCTGCCTCGGGGCCAGTAGCATACCGGCCTGGTACTCGGAGGG
AGTCCCTGGGCCTGGAATCTAAGGATGGTTCTTAGCAGGACTTGGTGGGGGAACAGGGAATTGGGGATGGGAGG
GAGGCAATAAAGATATTTGGCCTTC

WO 2004/030615

PCT/US2003/028547

1060/6881
FIGURE 989

MAASASAAAGEEDWVLPSEVEVLESIYLDELQVIKNGRTSPWEIYITLHPATAEDQDSQYVCFTLVLPVPAEYP
HEVPQISIRNPRGLSDEQIHTILQVLGHVAKAGLTAMLYELIEKGKEILTDNNIPHGQCVICLYGFQEKEAFTK
TPCYHYFHCHCLARYIQHMEQELKAQGQEQEQERQHATTQKAVGVQCPVCREPLVYDLASLKAAPQPMPMELY
QPSAESLRQQEERKRLYQRQQERGGIIDLEAERNRYFISLQPPAPAEPESAVDVSKGSQPPSTLAAELSTSPAV
QSTLPPPLPVATQHICEKIPGTRSNQORLGETQKAMLDPKPSRGPWRQPERRHPPKGGECHAPKGTRDTQELPPP
EGPLKEFMDLKPEPHSQGVEGPPQEKGPSWQGPPPRRTRDCVRWERSKGRTPGSSYPRLPRGQ

WO 2004/030615

PCT/US2003/028547

1061/6881
FIGURE 990

GGCACGAGGGCCAGCTGCTGTAGAAAGAGGGGAGGAAACAAGCCAGTGCAAGGGGAGCAAAAGAGAAAAGGAGCCA
GGCTGGGCTTCCTGATCCCACAGCATCGCAGAGCTCGGGAGGCACAGCTCACAGACACAGGAAACACAGGACTGC
TATTCTGCTCTCCTGCCCCAGGTGATCTGGTGCCAGCTGGTGGAACAGTGGGTGATGGCGTCCCTGCTGCAAGAC
CAGCTGACCACTGATCAGGACTTGCTGCTGATGTCAGGAAGGCATGCCGATGCGCAAGGTGAGGTCCAAAAGCTGG
AAGAAGCTAAGATACTTCAGACTTCAGAATGACGGCATGACAGTCTGGCATGCACGGCAGGCCAGGGGCAGTGCC
AAGCCAGCTTCTCAATCTCTGATGTGGAGACAATACGTAATGGCCATGATTCCGAGTTGCTGCGTAGCCTGGCA
GAGGAGCTCCCCCTGGAGCAGGGCTTACCATTGTCTTCCATGGCCGCCGCTCCAACCTGGACCTGATGGCCAAC
AGTGTGAGGAGGGCCAGATATGGATGCGAGGGCTCCAGCTGTTGGTGGATCTTGTCACCAGCATGGACCATCAG
GAGCGCTGGACCAATGGCTGAGCGATTGGTTTTCAACGTGGAGACAAAATCAGGATGGTAAGATGAGTTTCCAA
GAAGTTCAGCGTTATTGACCTAATGAATGTGGAAATGGACCAAGAATATGCCTTCAGTCTTTTTTCAGGCAGCA
GACACGTCCCAGTCTGGAACCCCTGGAAGGAGAAGAATTCGTACAGTTCTATAAGGCATTGACTAAACGTGCTGAG
GTGCAGGAAGTGTGAAAGTTTTTCAGCTGATGGGCAGAAGCTGACTCTGCTGGAATTTTTGGATTTCTCCAA
GAGGAGCAGAAGGAGAGAGACTGCACCTCTGAGCTTGCTCTGGAACCTCATTGACCGCTATGAACCTTCAGACAGT
GGCAAAGTGCAGCATGTGCTGAGTATGGATGGCTTCCTCAGCTACCTCTGCTCTAAGGATGGAGACATCTTCAAC
CCAGCCTGCCTCCCCATCTATCAGGATATGACTCAACCCCTGAACCACTACTTCATCTGCTCTTCTCATAACACC
TACCTAGTGGGGGACCAGCTTTGCGGCCAGAGCAGCGTCGAGGGATATATACGGGCCCTGAAGCGGGGTGCCGC
TGCGTGGAGGTGGATGTATGGGATGGACCTAGCGGGGAACCTGTGCTTTACCACGGACACACCCCTGACCTCCCGC
ATCCTGTTCAAAGATGTCGTGGCCACAGTAGCACAGTATGCCTTCAGACATCAGACTACCCAGTCATCTTGTC
CTGGAGACCCACTGCAGCTGGGAGCAGCAGACCATGGCCCGTCATCTGACTGAGATCCTGGGGGAGCAGCTG
CTGAGCACCACTTGATGGGGTGTGCCCCACTCAGCTGCCCTCGCTGAGGAGCTTCGGAGGAAGATCCTGGTG
AAGGGGAAGAGTTAACACTTGAGGAAGACCTGGAATATGAGGAAGAGGAAGCAGAACCTGAGTTGGAAGAGTCA
GAATTGGCGCTGGAGTCCCAGTTTGAGACTGAGCCTGAGCCCCAGGAGCAGAACCTTCAGAATAAGGACAAAAAG
AAGAAATCCAAGCCCATCTTGTGTCCAGCCCTCTCTTCCCTGGTTATCTACTTGAAGTCTGTCTCATTCCGCAGC
TTCACACATTCAAAGGAGCACTACCACTTCTACGAGATATCATCTTCTCTGAAACCAAGGCCAAGCGCCTCATC
AAGGAGGCTGGCAATGAGTTTGTGTCAGACAATACTTGGCAGTTAAGCCGTGTGTATCCCAGCGGCCTGAGGACA
GACTCTTCCAAGTACAACCCCCAGGAAGTCTGGAATGCAGGCTGCCAGATGGTGGCCATGAATATGCAGACTGCA
GGGCTTGAAATGGACATCTGTGATGGGCATTTCCGCCAGAATGGCGGCTGTGGCTATGTGCTGAAGCCAGACTTC
CTGCGTGATATCCAGAGTTCTTTCCACCCTGAGAAGCCCATCAGCCCTTTCAAAGCCCAGACTCTCTTAATCCAG
GTGATCAGCGGTGAGCAACTCCCCAAGTGGACAAGACCAAGAGGGGTCCATTGTGGATCCACTGGTGAAAGTG
CAGATCTTTGGCGTTTCGTCTAGACACAGCACGGCAGGAGACCAACTATGTGGAGAACAATGGTTTTAATCCATAC
TGGGGGCAGACACTATGTTTCCGGGTGCTGGTGCCCTGAACCTTGCCATGCTGCGTTTTGTGGTAATGGATTATGAC
TGGAAATCCCGAAATGACTTTATTGGTCAGTACACCCTGTCCTTGACCTGCATGCAACAAGGTTACCGCCACATT
CACCTGCTGTCCAAAGATGGCATCAGCCTCCGCCAGCTTCCATCTTTGTGTATATCTGCATCCAGGAAGGCCTG
GAGGGGGATGAGTCTTGAGGTGGGCATTTACGGGAAGGGTTGGTATGCTGGCTTTAGACGGGGAGAAACATCTG
GAAGGATGCTCGAGAGAAACAAATGGAGGTGGTGAAATCAAGCTTTGGATTGTGCATTCTAGGCACAAAATTAC
CTCATTCTTCTAACAAGCAATCTGGGACCTGATTTTCCACCTTTTTCTCTTTTCTTCCCTTCTTTGTTTTCA
TAAGCCTTTGGTATCTTTCTGCCCCTTTTCTTTGTGTACTCTATACCTGGAGTTCCCTTCTTCTCTTGCTGTAG
GCTCAATCCCATACCGACATCTACAACCTAATCTTTCCATCAACTCTGTGTGAAGGCAGGTTGCAACTAGAAATT
CAGAGGGGCTTGGAATAGAGAAACCTAAAGAAGCATCATCCCTCCATCCCCAAGCTTCTCAAAGCCCCAAGCCA
AGGGAAGGATAAATCAAGGCTCAAGGCTTCCCCAGCAAAGATTAGGGAAAGAGACTTGACCCCAGGACTGTACTA
CGACTCTTAAGAGAACACTGCACAGCACTCAAAGTCCCCACTGGACTGCTTCTCCTTAGCCCCACTGGTATAA
ATACATCTCTCTCCAATTTGGCAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1062/6881
FIGURE 991

MASLLQDQLTTDQDLLLLMQEGMPMRKVRSKSWKKLRYFRLQNDGMTVWHARQARGSAKPSFSISDVETIRNGHDS
ELLRSIAEELPLEQGFTIVFHGRRSNLDLMANSVEEAQIWMRGLQLLDLVTSMQHQLDQWLSDFQRGDKNQ
DGKMSFQEVQRLHLMLNVEMDQEYAFSLFQAADTSQSGTLEGEFVQFYKALTKRAEVQELFESFSADGQKLTLL
EFLDFLQEEQKERDCTSELALELIDRYEPSDSGKLRHVLSMDGFLSYLCSKDGDIFNPACLPYQDMTQPLNHVF
ICSSHNTYLVGDQLCGQSSVEGYIRALKRGCRCVEVDVWDGPGSEPVVYHGHTLTSRILFKDVVATVAQYAFQTS
DYPVILSLETHCSWEQQQTMARHLTEILGEQLLSTTLDGVLPTQLPSPEELRRKILVKGKKLTLEEDLEYEEEEA
EPELEESLALLESQFETEPEPQEONLQNKDKKKKSKPILCPALSSLVYLYKSVSFRSFTHSKEHYHFEISSFSE
TKAKRLIKEAGNEFVQHNTWQLSRVYPSGLRTDSSNYPQELWNAGCQMAMNMQTAGLEMDICDGHFRQNGGCG
YVLKPDFLRDIQSSFHPEKPI SPFKAQTLLIQVISGQQLPKVDKTKEGSIVDPLVKVQIFGVRLDTARQETNYVE
NNGFNPHYWGQTLCFRVLVPELAMLRFVVMYDVKSRNDFIGQYTLPWTCMQQGYRHHLLSKDGISLRPASIFVY
ICIQEGLEGDES

WO 2004/030615

PCT/US2003/028547

1063/6881
FIGURE 992

TTCTCCCCCAGGCTCACTCACCATGACCAAGCTGAGCGCCCAAGTCAAAGGCTCTCTCAACATCACCACCCCGGG
GCTGCAGATATGGAGGATCGAGGCCATGCAGATGGTGCCTGTTCTTCCAGCACCTTTGGAAGCTTCTTCGATGG
TGA CTGCTACATCATCTCTGGCTATCCACAAGACAGCCAGCAGCCTGTCTATGACATCCACTACTGGATTGGCCA
GGACTCATCCCTGGATGAGCAGGGGGCAGCTGCCATCTACACCACACAGATGGATGACTTCTGAAGGGCCGGGC
TGTGCAGCACCCGCGAGGTCCAGGGCAACGAGAGCGAGGCCTTCCGAGGCTACTTCAAGCAAGGCCTTGTGATCCG
GAAAGGGGGCGTGGCTTCTGGCATGAAGCACGTGGAGACCAACTCCTATGACGTCCAGAGGCTGCTGCATGTCAA
GGGCAAGAGGAACGTGGTAGCTGGAGAGGTAGAGATGTCTTGGAAAGAGTTTCAACCGAGGGGATGTTTTCTCTCT
GGACCTTGGGAAGCTTATCATCCAGTGGAAATGGACCGGAAAGCACCCGTATGGAGAGACTCAGGGGCATGACTCT
GGCCAAGGAGATCCGAGACCAGGAGCGGGGAGGGCGCACCTATGTAGGCGTGGTGGACGGAGAGAAATGAATTGGC
ATCCCCGAAGCTGATGGAGGTGATGAACCACGTGCTGGGCAAGCGCAGGGAGCTGAAGGCGGCCGTGCCCGACAC
GGTGGTGGAGCCGGCACTCAAGGCTGCACTCAAAGTGTACCATGTGTCTGACTCCGAGGGGAATCTGGTGGTGAG
GGAAGTCGCCACACGGCCACTGACACAGGACCTGCTCAGTCACGAGGACTGTTACATCTGGACCAGGGGGGCCT
GAAGATCTACGTGTGGAAAGGGAAAGAAAGCCAATGAGCAGGAGAAGAAGGGAGCCATGAGCCATGCGCTGAACCT
CATCAAAGCCAAGCAGTACCCACCAAGCACACAGGTGGAGGTGCAGAATGATGGGGCTGAGTCGGCCGCTCTTTCA
GCAGCTCTTCCAGAAGTGGACAGCGTCCAACCGGACCTCAGGCCTAGGCAAAACCCACACTGTGGGCTCCGTGGC
CAAAGTGGAAACAGGTGAAGTTCGATGCCACATCCATGCATGTCAAGCCTCAGGTGGCTGCCCAGCAGAAGATGGT
AGATGATGGGAGTGGGGAAGTGCAGGTGTGGCGCATTGAGAACCTAGAGCTGGTACCTGTGGATTCCAAGTGGCT
AGGCCACTTCTATGGGGGCGACTGCTACCTGCTGCTCTACACCTACCTCATCGGCGAGAAGCAGCATTACCTGCT
CTACGTTTGGCAGGGCAGCCAGGCCAGCCAAGATGAAATTACAGCATCAGCTTATCAAGCCGTATCTTGGACCA
GAAGTACAATGGTGAACCAGTCCAGATCCGGGTCCCAATGGGCAAGGAGCCACCTCATCTTATGTCCATCTTCAA
GGGACGCATGGTGGTCTACAGGGAGGCACCTCCCGAACTAACAACCTTGGAGACCGGGCCCTCCACACGGCTGTT
CCAGGTCCAGGGAACTGGCGCCAACAACCAAGGCCTTTGAGGTCCAGCGCGGGCCAATTTCTCAATTCCAA
TGATGTCTTTGTCTCAAGACCCAGTCTTGCTGCTATCTATGGTGTGGGAAGGGTTGTAGCGGGGACGAGCGGGA
GATGGCCAAGATGGTTGCTGACACCATCTCCCGGACGGAGAAGCAAGTGGTGGTGGGAAGGGCAGGAGCCAGCCAA
CTTCTGGATGGCCCTGGGTGGGAAGGCCCCCTATGCCAACCAAGAGACTACAGGAAGAAAACCTGGTCATCAC
CCCCGGCTCTTTGAGTGTTCACAAGACTGGGCGCTTCTTGGCCACAGAGATCCCTGACTTCAATCAGGATGA
CTTGAAGAGGATGATGTGTTCTACTAGATGTCTGGGACCAGGTCTTCTTCTGGATTGGGAAACATGCCAACGA
GGAGGAGAAGAAGGCCGAGCAACCACTGCACAGGAATACCTCAAGACCCATCCAGCGGGCGTGACCCTGAGAC
CCCCATCATTGTGGTGAAGCAGGGACACGAGCCCCCACCCTTACAGGCTGGTTCTTGGCTTGGGATCCCTTCAA
GTGGAGTAACACCAAATCCTATGAGGACCTGAAGCGGAGCTTGGCAACTCTAGGGACTGGAGCCAGATCACTGC
TGAGGTCAACAAGCCCCAAAGTGGACGTGTTCAATGCTAACAGCAACCTCAGTTCTGGGCCTCTGCCATCTTCCC
CCTGGAGCAGCTAGTGAACAAGCCTGTAGAGGAGCTCCCCGAGGGTGTGGACCCAGCAGGAAGGAGGAACACCT
GTCCATTGAAGATTTCACTCAGGCCTTTGGGATGACTCCAGCTGCCTTCTCTGCTCTGCCTCGATGGAAGCAACA
AAACCTCAAGAAAGAAAAAGGACTATTTTGAAGAAGTAGCTGTGGTTGTAAAGCAGTACCCTACCCTGATTGTA
GGGTCTCATTTTCTCACCAGATATTAGTCTACACCAATTGAAGTGAAATTTTGCAGATGTGCCTATGAGCACAAA
CTTCTGTGGCAATGCCAGTTTGTTTAATAATGTACCTATTCTTCAGAAAGATGATACCCC

WO 2004/030615

PCT/US2003/028547

1064/6881
FIGURE 993

TGCTCCCTTTTCTGTCTCTGTCCATGCTGCCATGTTTCTCTGCTGCCAAATTGGGCCCCTTGGCCCCTTCCGGT
TCTGCTTCCTGGGGGCAGGGTTCCCTGCCCTTGGACCCCCAGTCTGGGAACGGTGGACATCAAGTGCCTTGCATAGA
GCCCCCTCTTCCCCGCCAGCTTTCCCAGGGGCACAGCTCTAGGCTGGGAGGGGAGAACCAGCCCCTCCCCCTGC
CCCACCTCCTCTCCCCAGGGTCTAACGGTTAAGGGGACCCACATACCAGTGCCAAGGGGGATGTCAAGTGGTGAT
GTCGTTGTGCTCCCCTCCCCCAGAGCGGGTGGGCGGGGGGTGAATATGGTTGGCCTGCATCAGGTGGCCTTCCCA
TTTAAGTGCCTTCTCTGTGACTGAGAGCCCTAGTGTGATGAGAACTAAAGAGAAAGCCAGACCCCT

WO 2004/030615

PCT/US2003/028547

1065/6881
FIGURE 994

ATGGACTCTGGGAGGCGTTTGGGCCCAGAGAAGTGGATCCGCCGCTTGCGCCGCATGGAGTCCGAATCGGAAAGC
GGGGCTGCTGCTGACACCCCCCTGAGACCTAAGCTTCCATGGTGATGAAGAGATTATCGAGGTGGTAGAA
CTTGATCCCCGGTCCGCCGGACCCAGATGACCTGGCCCAGGAGATGGAAGATGTGGACTTTGAGGAAGAAGAGGAG
GAAGAGGGCAACGAAGAGGGCTGGGTTCTAGAACCCCAGGAAGGGGTGGTCGGCAGCATGGAGGGCCCCGACGAT
AGCGAGGTACCTTTGCATTGCACTCAGCATCTGTGTTTTGTGTGAGCCTGGACCCCAAGACCAATACCTTGGCA
GTGACCGGGGGTGAAGATGACAAAGCCTTCGTATGGCGGCTCAGCGATGGGGAGCTGCTCTTTGAGTGTGCAGGC
CATAAAGACTCTGTGACTTGTGCTGGTTTTAGCCATGACTCCACTCTAGTGGCCACAGGGGACATGAGTGGCCTC
TTGAAAGTGTGGCAGGTGGACACTAAGGAGGAGGTCTGGTCTTTGAAGCGGGAGACCTGGAGTGGATGGAGTGG
CATCTCGGGCACCTGTCTCTGTTGGCGGGCACAGCTGACGGCAACACCTGGATGTGGAAAGTCCCGAATGGTGAC
TGCAAGACCTTCCAGGGTCCCAACTGCCAGCCACCTGTGGCCGAGTCTCCCTGATGGGAAGAGAGCTGTGGTA
GGCTATGAAGATGGGACCATCAGGATTTGGGACCTGAAGCAGGGAAGCCCTATCCATGTACTGAAAGGGACTGAG
GGTCACCAGGGCCCCACTCACCTGTGTTGCTGCCAACCAGGATGGCAGCTTGATCCTAACTGGCTCTGTGGACTGC
CAGGCCAAGCTGGTCAGTGCCACCACCGGCAAGGTGGTGGGTGTTTTTAGACCTGAGACTGTGGCCTCCCAGCCC
AGCCTGGGAGAAGGGGAGGAGAGTGAAGTCCAACCTCGGTGGAGTCTTGGGCTTCTGCAGTGTGATGCCCCTGGCA
GCTGTTGGCTACCTGGATGGGACCTTGGCCATCTATGACCTGGCTACGCAGACTCTTAGGCATCAGTGTGAGCAC
CAGTCGGGCATCGTGAGCTGCTGTGGGAGGCAGGCACTGCCGTGGTATATACCTGCAGCCTGGATGGCATCGTG
CGCCTCTGGGACGCCCCGACCGGCCGCTGCTTACTGACTACCGGGGCCACACGGCTGAGATCCTGGACTTTGCC
CTCAGCAAAGATGCCTCCCTGGTGGTGACCACGTCAGGAGACCACAAAGCGAAAGTATTTTGTGTCCAAAGGCCT
GACCGTT**TA**ATGGCTGCAGCCCCCTGCCTGTGTGTCTGGTGTGAGGGGACGAAGGGACCCCTGCCCTGTCTGCCA
GCAGAGGCAGTAGGGCACAGAGGGAAGAGGAGGTGGGGCCCTGGATGACTTCCAGCCTCTTCAACTGACTTGC
TCCCTCTCCTTTTCTTCTTTAGAGACCCAGCCAGGGCCCTCCCACCCTTGCCCAGACCTGGTGGGCCCTTC
AGAGGGAGGGGTGGACCTGTTTCTCTTTCACTTTCAATTTGCTGGTGTGAGCCATGGGGTGTGATTTGTATGTGG
GGAGTAGGTGTTTGAGGTTCCCGTTCTTTCCCTTCCCAAGTCTCTGGGGGTGGAAGGAGGAAGAGATACTAGTT
AAAGATTTTAAAAATGTAAATAAAATATACTTCCCAG

WO 2004/030615

PCT/US2003/028547

1066/6881
FIGURE 995

MDSGRRLGPEKWIRRLRMESESESGAAADTPPLETLSFHGDEEIIIEVVELDPGPPDPDDLAQEMEDVDFEEEE
EEGNEEGWVLEPQEGVVGSMEGPDDSEVTFALHSASVFCVSLDPKTNLAVTGGEDDKAFVWRLSDGELLFECAG
HKDSVTCAGFSHDSTLVATGDMGGLLKVWQVDTKEEVWSFEAGDLEWMEWHPRAPVLLAGTADGNTWMWKVPNGD
CKTFQGPNCPCATCGRVLPDGKRAVVGIEDGTIRIWDLKQGSPIHVLKGTEGHQGPLTCVAANQDGSILITGSVDC
QAKLVSATTGKVVGVRFPETVASQPSLGEGESESNVESLGFCVMPPLAAVGYLDGTLAIYDLATQTLRHQCQH
QSGIVQLLWEAGTAVVYTCSLDGIVRLWDARTGRLLTDYRGHTAEILDFALSKDASLVVTTSGDHKAKVFCVQRP
DR

WO 2004/030615

PCT/US2003/028547

1067/6881
FIGURE 996

GGCACGAGCTCTCCCTCCGTCCTTGCTCCCTTACCCACCCTCACCGGCCCTTGTTTCTCCTTCCCCTGGGGGCA
GCCGCCGCCATGATCCTGCTGGAGGTGAACAACCGCATCATCGAGGAGACGCTCGCGCTCAAGTTCGAGAACGCG
GCCGCCGGAACAAACCGGAAGCAGTAGAAGTAACATTTGCAGATTTTCGATGGGGTCCTCTATCATATTTCAAAT
CCTAATGGAGACAAAACAAAAGTGATGGTCAGTATTTCTTTGAAATTCTACAAGGAAC TTCAGGCACATGGTGCT
GATGAGTTATTAAAGAGGGTGACGGGAGTTTCTTGGTAAATCCAGAATCAGGATACAATGTCTCTTTGCTATAT
GACCTTGAAAATCTTCCGGCATCCAAGGATTCCATTGTGCATCAAGCTGGCATGTTGAAGCGAAATTGTTTTGCC
TCTGTCTTTGAAAATACTTCCAATTCCAAGAAGAGGGCAAGGAAGGAGAGAACAGGGCAGTTATCCATTATAGG
GATGATGAGACCATGTATGTTGAGTCTAAAAAGGACAGAGTCACAGTAGTCTTCAGCACAGTGTTTAAGGATGAC
GACGATGTGGTCATTGGAAAGGTGTTTCATGCAGGAGTTCAAAGAAGGACGCAGAGCCAGCCACACAGCCCCACAG
GTCCTCTTTAGCCACAGGGAACCTCCTCTGGAGCTGAAAGACACAGACGCCGCTGTGGGTGACAACATTGGCTAC
ATTACCTTTGTGCTGTTCCCTCGTCACACCAATGCCAGTGCTCGAGACAACACCATCAACCTGATCCACACGTTT
CGGGACTACCTGCACTACCACATCAAGTGCTCTAAGGCCTATATTACACACGTATGCGGGCGAAAACGCTCTGAC
TTCCTCAAGGTGCTGAACCGCGCACGCCAGATGCCGAGAAAAAGAAATGAAAACAATCACGGGGAGACGTTT
TCATCCCGCTTAATCTTGGGAATAAGAGGAGGAAGCGGCTGGCAACTGAAGGCTGGAACACTTGCTACTGGATAAT
CGTAGCTTTTAATGTTGCGCTCTTCAGGTTCTTAAGGATTCTCCGTTTTGGTTCCATTTTGTACACGTTTGGA
AAATAATCTGCAGAAACGAGCTGTGCTTGCAAAGACTTCATAGTTCCCAAGAATTAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1068/6881
FIGURE 997

MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTKVMVSI SLKFYKELQAHGADEL
LKRVGSGFLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKRNCFASVFEKYFQFQEEGKEGENRAVIHYRDDE
TMYVESKKDRVTTVVFSTVFKDDDDVVIGKVFMQEFKEGRRASHTAPQVLF SHREPPLELKDTDAAVGDNIGYITF
VLFPRHTNASARDNTINLIHTFRDYLHYHIKCSKAYIHTRMRAKTSDFLKVLNRARPD AEKKEMKTIITGKTFSSR

WO 2004/030615

PCT/US2003/028547

1069/6881
FIGURE 998

GCGGCGGCGAGAGGATGAACAACAAGTTGACGCTTTGAAAGATGATGACAGTGGGGACCATGATCAGAATGAAG
AAAACAGCACACAGAAAGATGGTGAGAAGGAAAAACGGAACGAGACAAGAATCAGAGCAGTAGCAAGAGAAAGG
CTGTTGTCCCTGGACCGGCAGAGCATCCCCTGCAGTACAACCTACACTTTTTGGTACTCCAGGAGAACCCCCGGCC
GTCCCACGAGCTCACAGAGCTATGAACAGAATATCAAACAGATTGGCACCTTGCCTCTGTGGAGCAGTTCTGGA
GGTTTTATAGCCACATGGTACGTCCTGGGGACCTGACAGGCCACAGTGACTTCCATCTCTTCAAAGAAGGAATTA
AACCCATGTGGGAGGATGATGCAAATAAAAATGGTGGCAAGTGGATTATTCGGCTGCGGAAGGGCTTGGCCTCCC
GTTGCTGGGAGAATCTCATTTTTGGCCATGCTGGGGGAACAGTTCATGGTTGGGGAGGAGATCTGTGGGGCTGTGG
TGTCTGTCCGCTTTCAGGAAGACATTATTTCAATATGGAATAAGACTGCCAGTGACCAAGCAACCACAGCCCGAA
TCCGGGACACACTTCGGCGAGTGCTTAACCTACCTCCCAACACCATTATGGAATACAAAACCTCACACCGACAGCA
TCAAATGCCAGGCAGGCTGGGCCCCCAAAGGCTCCTTTTTCAAACCTCTGGAAGCCGCGGTTGAATGTGCCAT
GACCCCTCTCCCTCTCTGGATGGCACCATCATTGAAGCTGGCGTCATCGGAGTCTGTTGTTCTGTTGGCGTGCTAC
CTGGAAGATCCTTCTGTGGTGGACAAGAGGAATTGGAAGAGCATTATGTTTTAAGAACAGGCTGACACGCAGC
AGCTACAACAACAGCTGAGATCACTTAATAAATGGTGCTAAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1070/6881
FIGURE 999

MNNKFDALKDDDSGDHDQNEENSTQKDGEKEKTERDKNQSSSKRKAVVPGPAEHPLQYNYTFWYSRRTPGRPTSS
QSYEQNIKQIGTFASVEQFWRFYSHMVRPGDLTGHSDFHLFKEGIKPMWEDDANKNGGKWIIRLRKGLASRCWEN
LILAMLGEQFMVGEEICGAVSVRFQEDIISIWNKTASDQATTARIRDTLRRVLNLPNTIMEYKTHTDTSIKMPG
RLGPQRLLFQNLWKPRLNVP

WO 2004/030615

PCT/US2003/028547

1071/6881
FIGURE 1000

GGCACGAGGAGAGCCTCGAGCCTGCGAGGAGCGCGCCGCCAGCTCCCTGCGTCCCGTCCCGCGTCCCCGCG
TTCCCGCGTCTGCGATCCGCGGCC**ATG**GCCAGTGAGGAGCTGGCGTGCAAGCTGGAGCGCCGGCTGCGGCGCGA
GGAGGCCGAGGAGAGTGGCCCCAGCTGGCTCCCCTCGGCGCCCCAGCCCCGGAGCCCAAGCCCCGAGCCCCGAGCC
TCCCGCCCGTGCGCCACGGCCAGCGCCGACGCGGAGCTGAGCGCCAGCTGAGCCGGCGGGCTGGACATCAACGA
GGGCGCTGCGCGGCCCGGCGCTGCAGGGTCTTCAACCCCTACACGGAGTTCCCGGAGTTCCAGCCGCCGCCTCAT
CAAGGACCTGGAGAGCATGTTCAAAGTGTATGACGCTGGGCGGGATGGCTTCATCGACCTGATGGAGCTGAAGCT
GATGATGGAGAAGCTGGGGGCCCCCAGACCCACCTGGGCCTGAAGAGCATGATCAAGGAGGTGGATGAGGACTT
CGATGGCAAGCTCAGCTTCCGGGAGTTCTGCTCATTTTTCCACAAGGCCGCGGCAGGGGAGCTGCAGGAGGACAG
TGGGCTGATGGCGCTGGCAAAGCTTTCTGAGATCGATGTGGCCCTGGAGGGTGTCAAAGGTGCCAAGAACTTCTT
TGAAGCCAAGGTCCAAGCCTTGTATCGGCCAGTAAGTTTGAAGCAGAGTTGAAAGCTGAGCAAGATGAGCGGAA
GCGGGAGGAGGAGGAGAGGCGGCTCCGCCAGGCAGCCTTCCAGAACTCAAGGCCAACTTCAATACAT**TAGT**CCTG
CTGACCTTGCCCTCTGCCACAGCTGTGCTCACAGATGCCCCGAGAAGAGATGACTAGGCATCTTCATCACTGC
TGTCGGTCCCCCTCCCTGAGCCAGCATCTCCATCCACCACCCCGTGCCAGCTCCCGTGCCAGCCTTCATTCTCTCC
AGTGTTCAAGCCCCCTCCAGGAGGGTCTGGGGTGGGCCAGATGCCTGCCCCACCTCTGTCTCTCTGCTCTCTCT
CTGCCCTTCTTATAGCCAGAACTTGTATCTTCTCAGCAACCTTCACTTTGTCTTGTCCCTTTACCATTCCCCAT
CAAAGAGTAGTCTGCTATATCAATTTGTGTAGATATGTCTGTCTTTTTGGGTCTCAGAGAAAATGCCCATTTTC
TCGGAGAATTCTCTGCACTCCTCTCTGCTTCACTTCAACTTCCCTGTTCTCATCTTTGGTAGGATTCTGCCAGT
TGCTTTTGCATCTTCTGTTCTCTGGGTAATGGTGGGTCTTAATGGAGGCTGGGTGGACCACTGCCCGTCCACTCTT
CAACAGGAGGAACAGCATGCCACCACAGTAACACACATTAGAGAAAGGACAGAGGTCTGCTCCTTCTGCCACCT
TTCTCCTGGCCCCCTTAGCATTCCCCCAGTCCCTCCCTCTTACCTTGCTCCGTCTATGTCTTCCAGCTCAGCCT
TTTCCCCACTCTTAAATACTGTACTACTTCACTGTAAGAACGAAAGAATAGTTAGGATACCAATGAGTAAAAGG
TTCTGTCTCACTCTGACTCTGTGCAAATTGTATTACAGTAGACCGCTGACGTTCCAAGTGACAGATCCAGGGCC
TTTCAAACATCCCCAAAGTCATGGCCATACTACCATTAGCCAGTTTCTAACATCTGTTTCAGGGTATCCAGCTG
TAGATGTTCTTATCCCCATACTTGTGAGTTATTGGGGTTGCTCACAAATACTAGGGGTTTTTGTGTATTTTAA
ACAAATATATCCTAATGTCATATTTATTCTCTTTTGTAACTGCTGTCTTTACAATAAAGAAATCATCTGCCTTTC
TAAAAAAAAAAAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1072/6881
FIGURE 1001

MASEELACKLERRLRREEAEESGPQLAPLGAPAPEPKPEPEPPARAPTASADAELSAQLSRRLDINEGAARPRRC
RVFNPYTEFFPEFSRRLIKDLESMFKLYDAGRDFIDLMELKLMMEKLGAPQTHLGLKSMIKEVDEDFDGKLSFRE
FLLIFHKAAAGELQEDSGLMALAKLSEIDVALEGVKGAKNFFEAKVQALSSASKFEAELKAEQDERKREEEERRL
RQAAFQKLFNFNT

WO 2004/030615

PCT/US2003/028547

1073/6881
FIGURE 1002

ATGGTCCCCCTGCTGGAACCATGGCAACATCACCCGCTCCAAGGCGGAGGAGCTGCTTTCCAGGACAGGCAAGGAC
GGGAGCTTCCTCGTGCGTGCCAGCGAGTCCATCTCCCGGGCATAACGCGCTCTGCGTGCTGTATCGGAATTGCGTT
TACACTTACAGAATTCTGCCCCAATGAAGATGATAAATTCAGTGTTCAGAAATCTGAACCTGACTTCAGCCGATAC
TGGCAGAGAAAGGGTGTAACGATGAGGAAGGAAGTGCACGCGCAGGATGCAGTAGTAGACAGGGAGCTGGACTC
AAGGTGTGGGGAGACCACAGGCAAGTCCCTGGAGGCAAAAATCCTCCAGAAGTTGTCAAGAGGGAGAGCGTGGTG
AGCAGAACGCCCCCTCAGGAAGACAGCTTATGAGGATGGAAGGAATTGCTTCGAGGAGCGATGTGATTTGA

WO 2004/030615

PCT/US2003/028547

1074/6881
FIGURE 1003

MVPCWNHGNI TRSKAEELLSRTGKDG SFLVRASESISRAYALCVLYRNCVYTYRILPNEDDKFTVQKSEPDFSRY
WQRKGVNDEEGSARAGCSSRQGAGLKVWGDHRQVPGGKNPPEVVKRESVVSRTPLRKTAYEDGRNCFEERCD

WO 2004/030615

PCT/US2003/028547

1075/6881
FIGURE 1004

CTTCGGGTGTACGTGCTCCGGGATCTTCAGCACCCGCGGCCCATCGCCGTCGCTTGGCTTCTTCTGGACTCAT
CTGCGCCACTTGTCCGCTTCACACTCCGCCGCCATCATGTTGAAGCTCGCGAAGGCAGGTAAAAATCAAGGTGAC
CCCAAGAAAATGGCTCCTCCTCAAAGGAGGTAGAAGAAGATAGTGAAGATGAGGAAATGTCAGAAGATGAAGAA
GATGATAGCAGTGGAGAAGAGGTCGTACCTCAGAAGAAAGGCAAGAAGGCTGCTGCAACCTCAGCAAAGAAG
GTGGTCGTTTTCCCAACAAAAAAGGTTGCAGTTGCCACACCAGCCAAGAAGCAGCTGTCACTCCAGGCAAAAAG
GCAGCAGCAACACCTGCCAAGAAGACAGTTACACCAGCCAAGCAGTTACCACACCTGGCAAGAAGGGAGCCACA
CCAGGCAAAGCATTGGTAGCAACTCCTGGTAAGAAGGGTGCTGCCATCCAGCCAAGGGGGCAAAGAATGGCAAG
AATGCCAAGAAGGAAGACAGTGATGAAGAGGAGGATGATGACAGTGAGGAGGATGAGGAGGATGACGAGGACGAG
GATGAGGATGAAGATGAAATTGAACCAGCAGCGATGAAAGCAGCAGCTGCTGCCCTGCCTCAGAGGATGAGGAC
GATGAGGATGACGAAGATGATGAGGATGACGATGACGATGAGGAAGATGACTCTGAAGAAGAAGCTATGGAGACT
ACACCAGCCAAGGAAAGAAAGCTGCAAAAGTTGTTCTGTGAAAGCCAAGAACGTGGCTGAGGATGAAGATGAA
GAAGAGGATGATGAGGACGAGGATGACGACGACGACGAAGATGATGAAGATGATGATGATGAAGATGATGAGGAG
GAGGAAGAAGAGGAGGAGGAAGAGCCTGTCAAAGAAGCACCTGGAAAACGAAAGAAGGAAATGGCCAAACAGAAA
GCAGTCTCTGAAGCCAAGAAACAGAAAGTGGAAAGGCACAGAACCGACTACGGCTTTCAATCTCTTTGTTGGAAC
CTAACTTTAACAATCTGCTCCTGAATTAATAAAGTGGTATCAGCGATGTTTTTGGCTAAAAATGATCTTGCTGTT
GTGGATGTCAGAAATGGTATGACTAGGAAATTTGGTTATGTGGATTTTGAATCTGCTGAAGACCTGGAGAAAGCG
TTGGAACCTCACTGGTTTGAAAGTCTTTGGCAATGAAATTAAGTAGAGAAACAAAAGGAAAAGACAGTAAGAAA
GAGCGAGATGCGAGAACACTTTTGGCTAAAAATCTCCCTTACAAAGTCACTCAGGATGAATTGAAAGAAGTGTTT
GAAGATGCTGCGGAGATCAGATTAGTCAGCAAGGATGGGAAAAGTAAAGGGATTGCTTATATTGAATTTAAGACA
GAAGCTGATGCAGAGAAAACCTTTGAAGAAAAGCAGGGAAACAGAGATCGATGGGCGATCTATTTCCCTGTACTAT
ACTGGAGAGAAAGGTCAAAATCAAGACTATAGAGGTGAAAAGAATAGCACTTGGAGTGGTGAATCAAAAACCTCTG
GTTTTAAGCAACCTCTCCTACAGTGCAACAGAAGAAACTCTTCAGGAAGTATTTGAGAAAGCAACTTTTATCAAA
GTACCCCAAGAACCAAAATGGCAAAATCTAAAGGGTATGCATTTATAGAGTTTGCTTCATTGCAAGACGCTAAAGAA
GCTTTAAATTCCTGTAATAAAAGGGAAATTTAGGGGCAGAGCAATCAGGCTGGAGTTGCAAGGACCCAGGGGATCA
CCTAATGCCAGAAGCCAGCCATCCAAAACCTCTGTTTGTCAAAGGCCTGTCTGAGGATACCACTGAAGAGACATTA
AAGGAGTCATTTGACGGCTCCGTTCCGGGCAAGGATAGTTACTGACCGGGAAACTGGGTCTCCAAAGGGTTTGGT
TTGTAGACTTCAACAGTGAGGAGGATGCCAAAGCTGCCAAGGAGGCCATGGAAGACGGTGAAATTGATGGAAT
AAAGTTACCTTGGACTGGGCCAAACCTAAGGGTGAAGGTGGCTTCGGGGTTCGTGGTGGAGGCAGAGGCGGCTTT
GGAGGACGAGGTGGTGGTAGAGGAGGCCGAGGAGGATTTGGTGGCAGAGGCCGGGGAGGCTTTGGAGGGCGAGGA
GGCTTCCGAGGAGGCAGAGGAGGAGGAGGTGACCACAAGCCACAAGGAAAGAAGACGAAGTTTGAATAGCTTCTG
TCCCTCTGCTTTCCCTTTTCCATTTGAAAGAAAGGACTCTGGGGTTTTTACTGTTACCTGATCAATGACAGAGCC
TTCTGAGGACATTCCAAGACAGTATACAGTCCTGTGCTCCTTGGAATCCGCTCTAGTTAACATTTCAAGGGCA
ATACCGTGTTGGTTTTGACTGGATATTCATATAAACTTTTTAAAGAGTTGAGTGATAGAGCTAACCCCTTATCTGT
AAGTTTTGAATTTATATTGTTTCATCCCATGTACAAAACCATTTTTCTCTAC

WO 2004/030615

PCT/US2003/028547

1076/6881
FIGURE 1005

MVKLAKAGKNQGDPKKMAFPPEVEEDSEDEEMSEDEEDDSSGEEVVIPQKKGKKAAATS AKKVVSPTKKVAVA
TPAKKAAVTPGKKAAATPAKKTVPKAVTTPGKKGATPGKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEED
DDSEDEDEDEDEDEDEDEIEPAAMKAAAAAPASEDEDEDEDEDEDEDDDEEDDSEEEAMETTPAKGKKA
PVKAKNVAEDEDEDEDEDEDEDDDDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE
TEPTTAFNLFVGNLNFNKSAPELKTGISDVFAKNDLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLK
IKLEKPKGKDSKKERDARTLLAKNLPYKVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADA
GTEIDGRSISLYYTGEKGQNQDYRGKNSTWSGESKTLVLSNLSYSATEETLQEVFEKATFIKVPQ
AFIEFASFEDAALNSCNKREIEGRAIRLELQGPRGSPNARSQPSKTLFVKGLSEDTEETLKE
VTDRETGSSKGFVDFNSEEDAKAAKEAMEDGEIDGNKVTLDWAKPKGEGGFGGRGGRGGF
FGGRGRGGFGGRGGRGGFRGGRGGGGDHKPQGKKTKE

WO 2004/030615

PCT/US2003/028547

1077/6881
FIGURE 1006

TGAACTGAGCGGCCCCCTGAGCTGACAGATACACTGCGCAGCTGGAACGGCGAGCGAGCCGACGGGCGAGTGAGGG
GCGCAGCCATGATCACCTCGGCCGCTGGAATTATTTCTCTTCTGGATGAAGATGAACCACAGCTTAAGGAATTTG
CACTACACAAATTGAATGCAGTTGTTAATGACTTCTGGGCAGAAATTTCCGAGTCCGTAGACAAAATAGAGGTTT
TATACGAAGATGAAGGTTTCCGGAGTCGGCAGTTTGCAGCCTTAGTGGCATCTAAAGTATTTTATCACCTGGGGG
CTTTTGAGGAGTCTCTGAATTATGCTCTTGGAGCAGGGGACCTCTTCAATGTCAATGATAACTCTGAATATGTGG
AACTATTATAGCAAAATGCATTGATCACTACACCAACAATGTGTGGAAAAATGCAGATTTGCCTGAAGGAGAAA
AAAAACCAATTGACCAGAGATTGGAAGGCATCGTAAATAAAATGTTCCAGCGATGTCTAGATGATCACAAGTATA
AACAGGCTATTGGCATTGCTCTGGAGACACGAAGACTGGACGCTTTTGAAGAGACCATACTGGAGTGAATGATG
TCCAGGAATGTTAGCTTATAGCCTTAAGCTCTGCATGTCTTTAATGCAGAATAAACAGTTTCGGAATAAAGTAC
TAAGAGTTCTAGTTAAAAATCTACATGAACCTGGAGAAACCTGATTTCAATCAATGTTTGTGTCAGTGCTTAATTTTCT
TAGATGATCCTCAGGCTGTGAGTGATATCTTAGAGAACTGGTAAAGGAAGACAACCTCCTGATGGCATATCAGA
TTTGTTTTGATTTGTATGAAAGTGCTAGCCAGCAGTTTTTGTCACTGTAAATCCAGAATCTTCGAAGTGTGGCA
CCCCATTGCTTCTGTGCCTGGATCCACTAATACGGGTACTGTTCCGGGATCAGAGAAAGACAGTGACTCGATGG
AAACAGAAGAAAAGACAAGCAGTGCAATTTGTAGGAAAGACACCAGAAGCCAGTCCAGAGCCTAAGGACCAGACTT
TGAAAATGATTAAAAATTTAAGTGGTGAAATGGCTATTGAGTTACATCTGCAGTTCTTAATACGAAACAATAATA
CAGACCTCATGATTCTAAAAAACACAAAGGATGCAGTACGGAATTTCTGTATGTCATACTGCAACCGTTATAGCAA
ACTCTTTTATGCACTGTGGGACAACCAGTGACCAAGTTTCTTAGAGATAATTTGGAATGGTTAGCCAGAGCCACTA
ACTGGGCAAAATTTACTGCTACAGCCAGTTTGGGTGTAATTCATAAGGGTCATGAAAAGAAGCATTACAGTTAA
TGGCAACATACCTTCCCAAGGATACTTCTCCAGGATCAGCCTATCAGGAAGGTGGAGGTCTCTATGCACTAGGTC
TTATTTCATGCCAATCATGGTGGTGATATAATTGACTATCTGCTTAATCAGCTTAAGAAGCCAGCAATGATATCG
TTAGACACGGTGGCAGTCTGGGCCTTGGTTTGGCAGCCATGGGAACGTCACGTCAAGATGTTTATGATTTGCTAA
AAACAAACCTTTATCAGGATGATGCAGTAACAGGGGAAGCAGCTGGCCTGGCCCTAGGTTTGGTTATGTTGGGCT
CTAAAAATGCTCAGGCTATTGAGGACATGGTTGGTTATGCACAAGAACTCAACATGAGAAGATTCTCGGTGGTC
TTGCACTTGGCATAGCTTTAGTAATGTATGGGAGGATGGAAGAGGCTGATGCTCTCATTGAATCTCTCTGTCGTG
ACAAGGACCCAATTCTTCGAAGGTCTGGAATGTATACTGTAGCCATGGCTTATTGTGGCTCTGGTAACAACAAG
CAATTCGACGCCTGCTACATGTTGCTGTAAGTGATGTTAATGATGATGTCAGGAGGGCAGCAGTAGAATCACTTG
GGTTCATTCTATTTCAGAACCCCTGAACAGTGCCCAAGTGTGCTCTTTGTTGTGTCAGAGAGTTACAACCCCTCATG
TGCGCTACGGAGCTGCAATGGCCTTGGGGATATGCTGTGCTGGTACAGGAACAAGGAAGCCATTAATTTGCTAG
AACCAATGACAAACGACCCCGTGAACCTACGTGAGGCAAGGGGCACTCATAGCTTCAGCTCTCATCATGATCCAGC
AGACTGAAATCACTTGTCCAAAGGTGAATCAGTTCAGACAGCTGTATTCCAAAGTCATCAATGATAAGCATGATG
ATGTCATGGCCAAGTTTGGCGCTATTCTGGCCCAGGGCATACTGGATGCAGGTGGTCATAATGTCACAATCTCCT
TGCAGTCCAGGACTGGGCATACTCATATGCCTTCTGTGGTTGGCGTCTTGTATTTACCCAGTTTTGGTTCTGGT
TTCTCTTTTACACTTCTGTCTATTGGCTTATACCCCTACCTGTGTCTATTGGCCTTAACAAGGACTTAAAGATGC
CGAAAGTTTCAGTATAAATCGAACTGTAAACCATCCACATTTGCATATCCTGCCCTCTGGAAGTACCAAAAGAAA
AAGAAAAGGAAAAGGTTTCTACTGCTGTATTATCTATAACTGCCAAGGCTAAAAAGAAGGAAAAAGAAAAGGAAA
AAAAGGAGGAGGAGAAAAATGGAAGTGGATGAGGCAGAGAAAAAGGAGGAAAAAGAGAAGAAAAAGAACCTGAGC
CAAACCTCCAGTTATTGGATAAACCAGCCCGAGTTATGCCTGCCAGCTTAAGGTCCTAACCATGCCGGAGACCT
GTAGATACCAAGCCTTTCAAACCACTCTCTATTGGAGGCATCATCATTCTGAAGGATACCAGTGAAGACATTGAGG
AGCTGGTGGAAACCTGTGGCAGCACATGGCCCAAAATCGAGGAGGAGGAACAAGAGCCAGAACCCCAAGAACCAT
TTGAGTATATTGATGATTAAAGGGCCAGAGGATCTCACTTGCTTATCTGAAGAAGATTGTCCAGGCTCATATTGGG
AATGCTTATGAGGAAATTCATGCCGAGACCTGCTATTCAATGCATGTATCGTTGCCTCTGCACTGACCTGAAGAA
CCCTGCTCCAAGTCTTTGGTTGAAGAGAAGATATATGACTGTTGAGTGTGCTCTTTCACAGAACTTGGTTTTCA
AATAAATATAAGATCTCCAGATGGACAAG

WO 2004/030615

PCT/US2003/028547

1078/6881
FIGURE 1007

CTGCAAGCCGCCGGAGCCGGGCAACCAGTGGGAAGGAGCCTGGGAGAGGCCAGGCCTCCCCGGACTGCTAGCCTGC
TTTTCTGGGGTCCCTGGAGCCGGAGGAAGAACCAGGATGTTGCTGCCTGCAGAAGCTCAGCTCAGGAAGACTTC
CAGGAACCTGAGGAGGAGCTGCCACTAACAGCCATATTTCCCAATGGAGACTGTGATGACCTTGGGAAGGGGTCA
AAAGCCTGTGATGGAGTCGTACACACTCCTGCTGAGCCCACCGGAGACTCAAGATGAAGGCTGGACCCTTGCCT
GTCCCTGGCTCTAACCTACAGACTGGGGCCTGGCTCCGTCTTACTGGCCCCAGGTCTCCATGGAGACTGCAGAA
ACCCCCGCTGCTGGAGGCCTGCCACACTCACAGTTACCAGCTAGACAGTGGGGCTTACTAAGACAAGCAGGACC
TAAACAGTGTCTCCCTGGGAACCTACTCCCCACCCAGCATTTCCTAAGTCTGATCACAGGGAGGTTATTTTGT
CTCTCTGTCTCGGTTTCTCTGAGCCACTGAGACAGATGGCTGTCCGCTTTGAGGCTCTGCAGAGCTGTGGCACC
CATGGTGTGTCTGCAGTGTCTGAGGCATGCATGGGCACCCATCGTTGAGAGTGCAGCTGGGAAGAACTCTGAA
CCAGAAGTCATCAGAGCTGAGGCATGGCCTTGAACATGTCACTCAGTCTCTGGGGCTTCTGTTTCACAAATGCAT
GAGGGGGCCACCAGCCAGTGGCTTTAAACCAGGGGCAGGTTGTCCCTCCAGGCAGCATTGGAAATGTGTGTGTG
TTGAGGGGGTCACAGTGAAGTGTGGGGGCACCCCTGGCATCTAGTGGGCATCCCACAATGTGCAGAACAGTCTCTG
ACAGCAAAGAATTGGTCCATTCAATGCCAATTGTAGTACCTTTGAGACATTCTGGCTGAGCCATGCCCTTCTCCC
TGTCAGAGTCCCCAGAGCAGAGAGGGTTCAGGCTTCCCTGGACCTTGGCTCCCAGAGCAAGCCAAAATAAAGACT
ACACTGTTGCCTTGGGGGCTTGTCTGGGCCAGGGCCAAGACGGTCTGCGTGCTGCAGGGCCAGGACAGAAATAGCC
ACACATGCCGGTGAGAACAAAGAGCCTCTTTCTTTCTCATGTTGACATCGACTTTCTGTGCCAAGTCCCTTTGGGT
ATAAGGATGCTAGGGAATTCCTATAGGCACCAAACAGAAGGAAAGCTAGGGGCTTGGACTACTGGGTATAGGACT
TGCTCTAGCTCTCAGGTCTTAGCCCAAGCTCAATGCAAACACAGCCCCCTCCGGGCTCTCTGTTTCTGTGAGGTTT
TGGAATCCCTTCTCTGTGTCCGTGAGTCTGACAGAATCGATGATGTTCCCTTAGAGCTGGGAAATCCATGTGTT
TATTCACGGAGGGAATCACCATTACCTCCCTTGTCTTCTTTGCCTGCCTTGGAGAAATCCAGAGTCTTCGGAAT
GGCAAAGGCAGCTCCTGGATTTCCCTGGAGGGGAGGCACTAGCTGAGGGAAGTAGCTCCCTTCATTTCATGATGCA
CAGTTTACGCAGCAGACACAACTGCGCCTACTATTTGCTCGGTGCCCTGCAAGGTGCTGCCTAACTTTGATTT
GTTATTTTCAGCTCTCTCCAGGATAGTGCCAAATGGTGCAATGGGAACCTGTTTGTCTGGGGGGCTCTAGATCAC
TGGCTCCAGAACTCCCGCTGCCAGGGTAGCCCCCTACCCCCAGCCCCCTGCTCCTGGACAGCAGTGGGTCTCACC
TTTAGCCTCTGCCCCAGTTCTGGTCTGACCCAACAGAGGGGCTCTATGATATTAAGAAGGGGCCCTTCTGCTC
TGTGCTCAACCTATTCTCCATAATAGGGAGTCTAATCCTATTCCCTCCCTGCTGATGAGGATGGTGTGAGGAT
GAGGAGGACGGCATCTCATTGGGGGCTTTTGGCAGTGGGCCTCATTTTAATCCTGCAGGGCTGCCTGCCAGTGG
ATCTATCCAGCTGCTTCTTGTAGCCAAGAATGAGTTCAATGAATTGTGATTCACTGATTTTATTGATTTTGT
TAAACAGGGAGACTGGTATTTTGAAGCTGCTATCATTTTCTATTCTTTATTAATTTCTTTGTAATCATCTTA
TTAAAGTTTTCTTATTTAGTGGG

WO 2004/030615

PCT/US2003/028547

1079/6881
FIGURE 1008

METVMILEGGQKPFVMESYTLTLLSPPETQDEGWTALSLALTYRLGPGSVLLAPRSPWRLQKPPPAGGLPHSQLPA
RQWGLLRQAGPKTVSPLGTYSPPSIC

WO 2004/030615

PCT/US2003/028547

1080/6881
FIGURE 1009

GGGACGCGAGCGGGATCCAACTTCCGGTGCCTGCAGAGCTCGGAGCGGGCGGAGGCAGAGACCGAGGCTGCACCG
GCAGAGGCTGCGGGGCGGACGCGCGGGCCGGCGCAGCCATGGTGAAGATTAGCTTCCAGCCC GCCGTGGCTGGCA
TCAAGGGCGACAAGGCTGACAAGGCGTCGGCGTCGGCCCCTCGCGCCGGCCTCGGCCACCGAGATCCTGCTGACGC
CGGCTAGGGAGGAGCAGCCCCACACATCGATCCAAGAGGGGGGGCTCAGTGGGCGGCGTGTGCTACCTGTTCGA
TGGGCATGGTTCGTGCTGCTCATGGGCTCGTGTTCGCTCTGTCTACATCTACAGATACTTCTTCTTGCAGCAGC
TGGCCCGAGATAACTTCTTCCGCTGTGGTGTGCTGTATGAGGACTCCCTGTCTCCAGGTCCGGACTCAGATGG
AGCTGGAAGAGGATGTGAAAATCTACCTCGACGAGAACTACGAGCGCATCAACGTGCCTGTGCCCCAGTTTGGCG
GCGGTGACCCTGCAGACATCATCCATGACTTCCAGCGGGGTCTGACTGCGTACCATGATATCTCCCTGGACAAGT
GCTATGTCATCGAACTCAACACCACCATTGTGCTGCCCCCTCGCAACTTCTGGGAGCTCCTCATGAACGTGAAGA
GGGGGACCTACCTGCCGCGAGACGTACATCATCCAGGAGGAGATGGTGGTCACGGAGCATGTGAGTGACAAGGAGG
CCCTGGGGTCTTTCATCTACCACCTGTGCAACGGGAAAGACACCTACCGGCTCCGGCGCCGGGCAACGCGGAGGC
GGATCAACAAGCGTGGGGCCAAGAACTGCAATGCCATCCGCCACTTCGAGAACACCTTCGTGGTGGAGACGCTCA
TCTGCGGGGTGGTGTGAGGCCCCCTCTCCCCAGAACCCCCCTGCCGTGTTCCTCTTTCTTCTTCCGGCTGCTCT
CTGGCCCTCCTCCTTCCCCCTGCTTAGCTTGTACTTTGGACGCGTTTCTATAGAGGTGACATGTCTCTCCATTCC
TCTCCAACCCCTGCCACCTCCCTGTACCAGAGCTGTGATCTCTCGGTGGGGGGGCCATCTCTGCTGACCTGGGTG
TGGCGGAGGGAGAGGCGATGCTGCAAAGTGTTCCTGTGTCCCACTGTCTTGAAGCTGGGCCTGCCAAAGCCTGG
GCCACAGCTGCACCGGCAGCCCAAGGGGAAGGACCGGTTGGGGGAGCCGGGCATGTGAGGCCCTGGGCAAGGGG
ATGGGGCTGTGGGGGCGGGGCGGCATGGGCTTCAGAAGTATCTGCACAATTAGAAAAGTCTCAGAAGCTTTTTC
TTGGAGGGTACACTTTCTTCACTGTCCCTATTCTTAGACCTGGGGCTTGAGCTGAGGATGGGACGATGTGCCAG
GGAGGGACCCACCAGAGCACAAGAGAAGGTGGCTACCTGGGGGTGTCCAGGGACTCTGTGAGTGCCTTCAGCCC
ACCAGCAGGAGCTTGAGTTTGGGGAGTGGGGATGAGTCCGTCAAGCACAACCTGTTCTGTGAGTGGAAACCAAGA
AGCAAGGAGCTAGGACCCCCAGTCTGCCCCCAGGAGCACAAGCAGGGTCCCCTCAGTCAAGGCAGTGGGATGG
GCGGCTGAGGAACGGGGCAGGCAAGGTCACTGCTCAGTCACGTCCACGGGGACGAGCCGTGGGTTCTGCTGAGT
AGGTGGAGCTCATTGCTTTCTCCAAGCTTGGAAGTGTTCGAAAGATAACACAGAGGGAAAGGGAGAGCCACCTG
GTACTTGTCCACCCTGCCTCCTCTGTTCTGAAATTCCATCCCCCTCAGCTTAGGGGAATGCACCTTTTCCCTTT
CCTTCTCACTTTTGCATGTTTTTACTGATCATTGATATGCTAACCGTTCTCAGCCCTGAGCCTTGGAGAGGAGG
GCTGTAACGCCTTCAGTCAGTCTCTGGGGATGAAACTCTTAAATGCTTTGTATATTTCTCAATTAGATCTCTTT
TCAGAAGTGTCTATAGAACAATAAAAATCTTTTACTTCTG

WO 2004/030615

PCT/US2003/028547

1081/6881
FIGURE 1010

MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGGSVGGVCYLSMGMVVLLMGLVFA
SVYIYRYFFLAQLARDNFFRCGVLYEDSLSSQVRTQMELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQR
GLTAYHDISLDKCYVIELNTTIVLPPRNFWELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGK
DTYRLRRRATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

WO 2004/030615

PCT/US2003/028547

1082/6881
FIGURE 1011

GATCACCACCATCGAGGCAGTGAAGTGCAAGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGC
TGAGCACCTCCAGCGAGAAGTTGAGGGAGAAAGGCAGGCCCGGGAAGAGAGGTATGAAGGTTGTTGAAAATCGGG
CCTTAAAAGATGAAGAAAAGATGGAACTCCAGGAAATCTAACTCCAAGAAGCTAAGCACATTGCAGAAGAGGCAG
ATAGGAAGTATGAAGAGGTGGCTCATAAGTTGGTGATCATTGAAGGAGACTTGGAAGGCACGGAGGAACGAGCTG
AGCTGGGAGAGTCCCGTTGCCAAGAGATGGATGAGCAGATTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTG
CTGCTGAAGAAATGTACTCTCAAAAAGAAGACAAATATGAGGAAGAGATCAAGATTCTTACTGATAAACTCAAGG
AGGCAGAGACCAGTGCTGAGTTTGCTGAGAGATCGGTAGCCAAGCTGGAAAAGACAATTGATGACTTGGAAGATA
AACTGAAACGCACCAAAGAGGAGCACCTCTGTACACAAAGGATGCTGGACCAGACTCTGATTGACCTGAATGAGA
TGTAGAACGCCCCAGTCCCACCCTGCTGCTGCTCCTCCCTCTTCTCAGAGAATCCAGCTGGGCTAGAGGCTGAGC
ACCTTTGGAAACAACATTTAAGGGAATGTGAGCACAATGCATAATGTCTTTAAAAGCATGTTGTGATG

WO 2004/030615

PCT/US2003/028547

1083/6881
FIGURE 1012

GTTTTGCCTGCTAGCATCTCCCTGTAACCTCTCCCAATCTTGAGGAGTGATCCCTGTCCAGCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGGATCTTCACCATGACAAGAGCCATGGAAGAGGCTCTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCCTCCTAGACAACCTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACCTGTCTCTTCTGGTGACATTGTTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTTACAGAAGCTTCAAACGTGTTGGTGCTTCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCAC
CACAACCCCTCAACCAAGCTGTTCAACCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCTGTCTGCCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCTCAAGAGATGC
CCCCTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAGAAAAGATGTATCTGGTCAACTCCAAAAGGAGAC
ATAAGAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCCCTCAAAAGAAAGATGACTCAACTTGTAACCTCCACGGTAGAGACAAGGGCCCCAAAAGGCGAGAAGTGAAT
GTGCCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGACGCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACCTCAGAGGTGATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCCGAAAGTCCAGATCGAAAGAAAAGAAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTACCGAAGAGGAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAATGAAACACGGATCCTCAGTGAAGTGCATTTCGGAATG
AGGATGGAACCTTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAAGAAGTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGCGGAAAAACTCGGATGAATGCGAGGTGTGCTGTC
AAGGGGGACAACCTTCTGTGCTGCGGTACTTGTCCACGAGTCTTCCATGAGGACTGTACATCCCCCTGTGGAAG
CCAAGAGGATGTGTGGAGTTGCACCTTCTGCAGGATGAAGAGGTCTTCAGGAAGCCAACAGTGCCATCATGTAT
CTAAGACCCTGGAGAGGCAGATGCAGCCTCAGGACCAGCTGATTGAGATTACGGTGAGCCCTTTCAGGAAGCAA
TGTGGTTGGACCTGGTTAAGGAAAGGCTGATTACGGAATGTACACGGTGGCATGGTTTGTGCGAGACATGCGCC
TGATGTTTCGCAACCATAAAACATTTTACAAGGCTTCTGACTTTGGCCAGGTAGGACTTGACTTAGAGGCAGAAT
TTGAAAAAGATCTCAAAGACGTGCTCGGTTTTTCATGAAGCCAATGACGGCGGTTTCTGGACTCTTCTTGAACCT
GTTCTGTAAAGACTGAAGCATCCCCACCTCAGGATTCAGCTGATGGGACCCTGGCTGGACTGTTGATTGCCAGT
GAGTCTGGGATGTAATTGGCTGCCCTCAGGACCCAAACCCAGACACTTCATAGGATTATCACACCCTCCATCTTT
ATTCTTTCTTTTACCTTTAAAAGTCTATATCTA

WO 2004/030615

PCT/US2003/028547

1084/6881
FIGURE 1013

MFTMTRAMEEALFQHFHMQKLGIAIAIHKPFPFFEGLLDNSIIITKRMYESLEACRNLI PVSRVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMP SLLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSSTPSDKKGKKRRCI WSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLVVDKVTQRKDDSTWNSEVMRVQKARTKARKSRSEKKKEKD ICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKMKHGSSVKIRNEDGTWLT PNEFEVEGKGRNAKNWKRNI RCEGMTL
GELLKRKNSDECEVCCQGGQLCCGTCPRVFHEDCHIPPVEAKRMLWSCTFCRMKRSSGSQQCHHVSKTLERQMQ
PQDQLIRDYGEPPQEAMWLDLVKERLITEMYTVAWFVRDMRLMFRNHKTFYKASDFGQVGLDLEAEFEKDLKDVL
GFHEANDGGFWTLP

WO 2004/030615

PCT/US2003/028547

1085/6881
FIGURE 1014

GTTTTGCCTGCTAGCATCTCCCTGTAACCTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCTGGAAAGGGG
CAGGAACGACAACTCAAAGTCCAGGATGTTTACCATGACAAGAGCCATGGAAGAGGCTCTTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACCTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACCTGTCTCTTCTGGTGACATTGTTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTACAGAAGCTTCAAACGTGTTGGTGCTTCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCAC
CACAACCCCCCTCAACCAAGCTGTTACCCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCTGTCTGCTCTCCCTGCACTACCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCCTCAAGAGATGC
CCCCTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAAGAAAGATGTATCTGGTCAACTCCAAAAAGGAGAC
ATAAGAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCTCAAAAGAAAGATGACTCAACTTGTAACCTCCACGGTAGAGACAAGGGCCCCAAAAGGCGAGAAGTGAAT
GTGCCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAAGTCAGAGGTTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCCGAAAGTCCAGATCGAAAGAAAAAGAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTCACCGAAGAGGAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAATGAAACACGGATCCTCAGTGAAGTGCATTTCGGAATG
AGGATGGAAGTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAAGAACTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGAGTGGACTTTTGCTCTGTCCTCCAAGAATAAATC
TCAAGAGAGAGTTAAATAGCAAGTGAATTTCTACTACCCCTCTCAGTCACCATGTTGCAGACTTTCCCTGTCTGGA
GGCTCACCTTAGAGCTTCTGAGTTTCCAAGCTCTGAGTCACCTCCACATTTGGGCATGGCATCTTCAAAACAATT
AATTTGCATAGTTAATTTGGGATGGGGAAGCAAATGACTCTAAAAATAAAAAATTAAATGAAAAAGCTCAAAAAAAA
AAAAAAAAAAAA

WO 2004/030615

PCT/US2003/028547

1086/6881
FIGURE 1015

MFTMTRAMEEALFQHFMHQKLGIAIAIHKPFPFFEGLLDNSIIITKRMYESLEACRNLIIPVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQPPSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVAS
DNLIPIQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRKCIWSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLVVDKVTQRKDDSTWNSEVMRVQKARTKARKSRSEKKKKEKDICSSEKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKMKKHGSSVKCIRNEDGTWLTNFEFEVEGKGRNAKNWKNIRCEGRTL
GELLKSGLLLCPPRINLKRELNSK

WO 2004/030615

PCT/US2003/028547

1087/6881
FIGURE 1016

GTTTTGCCTGCTAGCATCTCCCTGTAACCTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGGATGTTTACCATGACAAGAGCCATGGAAGAGGCTCTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACCTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTTCTACCCAACTGGAGAGGACTTTTAACCTGTCTCTTCTGGTGACATTGTTTCAAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTACAGAAGCTTCAAACGTGTTGGTGCTTCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCAC
CACAACCCCTCAACCAAGCTGTTACCCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCTGTCTGCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCTCAAGAGTGC
CCCCTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAGAAAAGATGTATCTGGTCAACTCCAAAAGGGAGAC
ATAAGAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCTCAAAAGAAAGATGACTCAACTTGTAACCTCCACGGTAGAGACAAGGGCCCCAAAAGGCGAGAAGTGAAT
GTGCCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACCTCAGAGGTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCCGAAAGTCCAGATCGAAAGAAAAGAAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTCACCGAAGAGGAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTCAAGCGAAAGGGATTTTATATAAGAAGAAAATGAAACACGGATCCTCAGTGAAGTGCATTTCGGAATG
AGGAIGGAACTTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAAGAAGTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGCGGAAAAACTCGGATGAATGCGAGGTGTGCTGTC
AAGGGGGACAACCTCTCTGCTGCGGTACTTGTCCACGAGTCTTCCATGAGGACTGTACATCCCCCTGTGGAAG
CCAAGAGGATGCTGTGGAGTTGCACCTTCTGCAGGATGAAGAGGTCTTCAGGAAGCCAACAGTGCCATCATGTAT
CTAAGACCCTGGAGAGGCAGATGCAGCCTCAGGACCAGCTGAAATGTGAGTTCTCTCTCTTGAAGGCCTACTGTC
ATCCACAAAGCTCCTTTTTTACGGGCATCCCATTTAATATTCGAGATTACGGTGAGCCCTTTAGGAAGCAATGT
GGTTGGACCTGGTTAAGGAAAGGCTGATTACGGAAATGTACACGGTGGCATGGTTTGTGCGAGACATGCGCCTGA
TGTTTCGCAACCATAAAACATTTTACAAGGCTTCTGACTTTGGCCAGGTAGGACTTGACTTAGAGGCAGAATTTG
AAAAAGATCTCAAAGACGTGCTCGGTTTTTCATGAAGCCAATGACGGCGGTTTCTGGACTCTTCTCTGACCCCTGTT
CTGTAAAGACTGAAGCATCCCCACCTCAGGATTCAGCTGATGGGACCCTGGCTTGGACTGTTGATTGCCAGTGAG
TCTGGGATGTAATTGGCTGCCCTCAGGACCCAAACCCAGACACTTCATAGGATTATCACACCCTCCATCTTTATT
CTTTCTTTTTACCTTTAAAAGTCTATATCTA

WO 2004/030615

PCT/US2003/028547

1088/6881
FIGURE 1017

MFTMTRAMEEALFQHFMHQKLGIAIAIHKPFPFFEGLLDNSIIITKRMYESLEACRNLI PVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMP SLLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSSTPSDKKGKKRRCI WSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLVVDKVTQRKDDSTWNSEVMRVQKARTKARKSRSEKKEKKEKD ICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKMKHGSSVKIRNEDGTWLT PNEFEVEGKGRNAKNWKRNI RCEGMTL
GELLKRKNSDECEVCCQGGQLCCGTCPRVFHEDCHIPPVEAKRMLWSCTFCRMKRSSGSQQCHHVSKTLERQMQ
PQDQLKCEFLLLKAYCHPQSSFFTGIPFNIRDYGEFFQEAMWLDLVKERLITEMYTVAWFVRDMRLMFRNHKTFY
KASDFGQVGLDLEAEFEKDLKDV LGFHEANDGGFWTL P

WO 2004/030615

PCT/US2003/028547

1089/6881
FIGURE 1018

ATGCTGGGTACGCTGCGGCCATGGAGGGCGAGGACGTGGAAGACGACCAGCTGCTGCAGAAGCTCAGGGCCAGT
CGCCGCCGCTTCCAGAGGCGCATGCAGCGGCTGATAGAGAAGTACAACCAGCCCTTCGAGGACACCCCGGTGGTG
CAAATGGCCACGCTGACCTACGAGACGCCACAGGGATTGAGAATTTGGGGTGAAGACTAATAAAGGAAAGAAAC
AAAGGAGAGATCCAGGACTCCTCCATGAAGCCCGCGGACAGGACAGATGGCTCCGTGCAAGCTGCAGCCTGGGGT
CCTGAGCTTCCCTCGACCCGCACAGTCCTGGGAGCCGATTCAAAAAGCGGTGAGGTGATGCCACGTCAGACCAG
GAAGAGTCAGTTGCTTGGGCCCTTAGCACCTGCAGTGCCTCAAAGCCCTTTGAAAAATGAATTAAGAAGGAAATAC
TTGACCCAAGTGGATATACTGCTACAAGGTGCAGAGTATTTTGAAGTGTGCAGGTAAACAGAGCTGGAAGGGATGTA
CGTGTGACTCCGCTGCCTTCACTGGCCTCACCTGCCGTGCCTGCCCCGGATACTGCAGTCGTATCTCCGGAAAG
AGTCCTGGTGACCCAGCGAAACCAGCTTCATCTCCAGAGAATGGGATCCTTTGCATCCTTCCACAGACATG
GCCTTAGTACCTAGAAATGACAGCCTCTCCCTACAAGAGACCAGTAGCAGCAGCTTCTTAAGCAGCCAGCCCTTT
GAAGATGATGACATTTGCAATGTGACCATCAGTGACCTGTACGCAGGGATGCTGCACTCCATGAGCCGGCTGTTG
AGCACAAAGCCATCAAGCATCATCTCCACCAAAACGTTTCATCATGCAAAACTGGAAGTGCAGGAGGACACAGA
TATAAGAGCAGGATGAACAAAACATATTGCAAAGGAGCCAGACGTTCTCAGAGGAGCTCCAAGGAGAACCTTCATA
CCCTGCTCTGAGCCTGTGAAAGGGACAGGGGCATTAAGAGATTGCAAGAACGTATTAGATGTTTTCTTGCCGTAAG
ACAGGTTTAAAATTGGAAAAAGCTTTTCTTGAAGTCAACAGACCCCAATCCATAAGTTAGATCCAAGTTGGAAG
GAGCGCAAAGTGACACCCTCGAAGTATTCTTCCCTGATTTACTTCGACTCCAGTGCAACATATAATCTTGATGAG
GAAATAGATTTAGGACATTAAATGGTTAATTTCTCTGTAAGAAATAGTTTCCAGACCAACAATACGACAGGGC
CATGGAGAGAACCCTCAGAGGGAGATTGAAATCCGATTGATCAGCTTCATCGGGAATATTGCCTGAGTCCCAGG
AACCAGCCTCGCCGGATGTGCCCTCCCGGACTCCTGGGCCATGAACATGTACAGAGGGGGTCTGCGAGTCTGGT
GGCCTTCAGGGCTTAGAAACCCGAGGCTGAGTTTACCTTCCAGCAAAGCAAAGCAAAGGTTTAAAGTGAGGCT
TTTGAAAACCTAGGCAAAGATCTCTGGAAGCAGGTAGGTGCCCTGCCAAGAGCGATTTCATCTTCATCACTTCCA
AAGACCAACCCACACACAGCGCAACTCGCCCGCAGCAGACATCTGACCTTCACGTTTCAGGGAAATAGTTCTGGA
ATATTTAGAAAGTCAGTGTCAACCAGCAAACCTCTTTCAGTCCCAGATAAAGAAGTGCCAGGCCACGGAAGGAAT
CGTTACGATGAAATTAAGAAGAATTTGACAAGCTTCATCAAAAGTATTGCCTCAAATCTCTGGGCAGATGACA
GTGCCCTTTATGTATTGGAGTGTCTACAGATAAAGCAAGTATGGAAGTTCGATATCAAACAGAAGGCTTCTTAGGA
AAATTAATCCAGACCCTCACTTCCAGGGTTTCCAGAAGTTGCCATCATCACCCCTGGGGTGCAGAAAAAGTCTA
CTGGGCTCAACTGCAATTGAGGCTCCTTCATCTACATGTGTGCTCGTGCCATCACGAGGGATGGCACGAGGGAC
CATCAGTTCCCTGCAAAAAGACCCAGGCTATCAGAACCCAGGGCTCCGGACGCCAGGGCAATTCCTGGGTGCC
TCAGATGGGGTGGACAACACCGTCAGACCGGGAGACCAGGGCAGCTCTTCACAGCCCAACTCAGAAGAGAGAGGA
GAGAACACGTCTTACAGGATGGAAGAGAAAAGTGATTTTCATGCTAGAAAAATTGGAAACTAAAAGTGTGTAGCTA
GGTTATTTCCGAGTGTTATTTATCTTCCACTTGCTCTCTGTTTGTATTTTGTGTTTGTGTTTGTGTTTGTGAGAC
TGTGAGGACTTGGTTGACTTCTCTGCCCTTAAAGTAAATATTAGTGAAATTGGTTCCATCAGAGATAACCTCGAG
TTCTTGGTGTAGAAATTATGTGAATAAAGTTGCTCAATTAGAAAAA

WO 2004/030615

PCT/US2003/028547

1090/6881
FIGURE 1019

MLHMSRLLSTKPSSIIISTKTFIMQNWNCRRRHRYKSRMNKTYCKGARRSQRSSKENFIPCSEPVKGTGALRDCK
NVLDVSCRKTGLKLEKAFLEVNRPQIHKLDPSWKERKVTPSKYSSLIYFDSSATYNLDEENRFRTLKWLI SPVKI
VSRPTIRQGHGENRQREIEIRFDQLHREYCLSPRNQPRRMCLPDSWAMNMYRGGPASPGGLOGLETRRLSLPSSK
AKAKSLSEAFENLGKRSLEAGRCLPKSDSSSSLPKTNPTH SATRPQQTSDLHVQGNSSGIFRKSVSPSKTLSVPD
KEVPGHGRNRYDEIKEEFDKLHQKYCLKSPGQMTVPLCIGVSTDKASMEVRYQTEGFLGKLNPDPHFQGFQKLPS
SPLGCRKSLLGSTAIEAPSSTCVARAITRDGTRDHQFPAKRPRLSEPQGSGRQGNLGLASDGV DNTVRPGDQGSS
SQPNSEERGENTS YRMEEKSDFMLEKLETKSV

WO 2004/030615

PCT/US2003/028547

1091/6881
FIGURE 1020

AAGACCGTCCCGGATGGCCTCGGGGACTGCCAGTGTGTGGAGGTGAGCTCCGGGATTGCCGGCATTCCCGCTTCT
GCTGGTTGCTTCATGCTGCAGGCTGCGGCCGTGAGCCCTCGCTCGCATTGGTGGCGCTGAGGTGCCGGGGCAGCA
AGTGACATGTCGTCGGGCCTCCGCGCCGCTGACTTCCCCCGCTGGAAGCGCCACATCTCGGAGCAACTGAGGCGC
CGGGACCGGCTGCAGAGACAGGCGTTTCGAGGAGATCATCTGCAGTATAACAAATTGCTGGAAAAGTCAGATCTT
CATTAGTGTGGCCAGAACTACAGGCTGAAAAGCATGACGTACCAAACAGGCACGAGATAAGTCCCGGACAT
GATGGCACATGGAATGACAATCAGCTACAAGAAATGGCCCAACTGAGGATTAAGCACCAAGAGGAAGTACTGAA
TTACACAAGAAACGTGGGGAGTTAGCTCAACTGGTGATTGACCTGAATAACCAAATGCAGCGGAAGGACAGGGAG
ATGCAGAAAGAGCTTGCAGAAGCAGCAAAGGAACCTCTACCAGTCGAACAGGATGATGACATTGAGGTCTTGTG
GATGAAACTTCTGATCACACAGAAGAGACCTCTCCTGTGCGAGCCATCAGCAGAGCAGCCACTAAGCGACTCTCG
CAGCCTGCTGGAGGCCTTCTGGATTCTGTCTACTAATATCTTTGGGAGACGCTCTGTCTCTTCCCTTCCAGTCCCC
CAGGACAATGTGGATACTCATCCTGGTTCTGGTAAAGAAGTGAGGGTACCAGCTACTGCCTTGTGTGTCTTCGAT
GCACATGATGGGGAAGTCAACGCTGTGCAGTTCAGTCCAGGTTCCCGGTTACTGGCCACTGGAGGCATGGACCGC
AGGGTTAAGCTTTGGGAAGTATTTGGAGAAAAATGTGAGTTCAAGGGTTCCCTATCTGGCAGTAATGCAGGAATT
ACAAGCATTGAATTTGATAGTGCTGGATCTTACCTCTTAGCAGCTTCAAATGATTTTGCAAGCCGAATCTGGACT
GTGGATGATTATCGATTACGGGTAAAGACCCAGTTAAGAAAGTTAGTGCAATCTCCAACTTCATGTGGTGTATC
AAGGCACAACTGGCAGGTGCTTAATTAGGGGACTTTGTTTTCCAAAAATCATGCTTGATTACCCCTGCCCTTC
CTTCTCCTTGGGGAAATCTGTGTTTCCACTTTATACTCTTTGTCCAAACTCAGTTTCAAATATTTGCATG
GGACCTCACATTTGCATGAAAACCTTGAATACTCTTCATAAGGACTAAATACTTTGGTAGATAGCAATTTTGG
CTTAATGGCACAGAACTTAGCAACAGCATGTGAATTGTGATTCTGTGGGCTCTAAAACCTAATTACCTAAAGTG
GGATATAGAAGTACAAATGGATGTATCATAGGGATAAGACAATTCTGAAACAAAACTCCAAGCTGAGAAAGAGG
GGACAGGTGTCAGAGCAGGGAGAAATGATTGGATGTTGAGGAAAGCTGCATTTGAACCAAACCTTGCCAAGAATT
CTCTTGGCATCTGACAGAGAGACCAAACTTGGTTGTATCATTTTTGATTGGGGCAGGGGCGGAGGSCGAAGCA
TGTAACCTAATTTGCAGACATTTTTTTTCCCATAAGCCTGAAGGAATCATCACATAAGCTTATTAAATACAAGC
TATTGAAAGATATAATGGAGGATGAATTTGGCATTAGTAGGCATTTTACT

WO 2004/030615

PCT/US2003/028547

1092/6881
FIGURE 1021

MSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIILQYNKLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDG
TWNDNQLQEMAQLRIKHQEELTELHKKRGELAQLVIDLNNQMQRKDREMOKELAEAAKEPLPVEQDDDI EVIVDE
TSDHTEETSPVRAISRATKRLSQPAGGLLDSVTNIFGRRSVSSFPVPQDNVDTHPGSGKEVRVPATALCVFDAH
DGEVNAVQFSPGSRLLATGGMDRRVKLWEVFGEKCEFKGSLSGSNAGITSIEFDSAGSYLLAASNDFASRIWTV
DYRLRV RPS

WO 2004/030615

PCT/US2003/028547

1093/6881
FIGURE 1022A

AAGAGAGAAGGCTTCTGCCAGCTCCTGCAGCAGATGAAGAACAAGCACTCAGAGCAGCCGAGCCCGACATGATC
ACCATCTTCATCGGCACCTGGAACATGGGTAACGCCCCCTCCCAAGAAGATCACGTCTGGTTTCTCTCCAAG
GGGCAGGGAAAGACGCGGGACGACTCTGCGGACTACATCCCCATGACATTTACGTGATCGGCACCCAAGAGGAC
CCCCTGAGTGAGAAGGAGTGGCTGGAGATCCTCAAACACTCCCCTGCAAGAAATCACCAGTGTGACTTTTAAACA
GTCGCCATCCACACGCTCTGGAACATCCGCATCGTGGTGCTGGCCAAGCCTGAGCAGGAGAACC GGATCAGCCAC
ATCTGTACTGACAACGTGAAGACAGGCATTGCAAACACACTGGGGAAACAAGGGAGCCGTGGGGGTGTCGTTCATG
TTCAATGGAACCTCCTTAGGGTTTCGTCAACAGCCACTTGACTTCAGGAAGTGAAGAAGAACTCAGGCGAAACCAA
AACTATATGAACATTCTCCGGTTCTGGCCCTGGGCGACAAGAAGCTGAGTCCCTTAACATCACTCACC GCTTC
ACGCACCTCTTCTGGTTTGGGGATCTTAACCTACCGTGTGGATCTGCCTACCTGGGAGGCAGAAACCATCATCCAG
AAAATCAAGCAGCAGCAGTACGCAGACCTCCTGTCCACGACCAGCTGCTCACAGAGAGGGAGGCAGAAAGGTC
TTCCTACACTTCGAGGAGGAAGAAATCAGTTTTGCCCAACCTACCGTTTTGAGAGACTGACTCGGGACAAATAC
GCCTACACCAAGCAGAAAGCGACAGGGATGAAGTACAACCTTGCCCTTCTGGTGTGACCGAGTCTCTGGAAGTCT
TATCCCCTGGTGCACGTGGTGTGTGAGTCTTATGGCAGTACCAGCGACATCATGACGAGTGACCACAGCCCTGTC
TTTGCCACATTTGAGGCAGGAGTCACTTCCCAGTTTGTCTCCAAGAAGCTCCCGGGACTGTTGACAGCCCAAGGA
CAGATTGAGTTTTCTCAGGTGCTATGCCACATTGAAGACCAAGTCCCAGACCAAATTTACCTGGAGTTCCACTCG
AGCTGCTTGGAGAGTTTTGTCAAGAGTCAGGAAGGAGAAAATGAAGAAGGAAGTGAGGGGGAGCTGGTGGTGAAG
TTTGGTGAGACTCTTCCAAAGCTGAAGCCCATTATCTCTGACCCTGAGTACCTGCTAGACCAGCAGACATCCTCATC
AGCATCAAGTCTCTGACAGCGACGAATCCTATGGCGAGGGCTGCATTGCCCTTCGGTTAGAGGCCACAGAAACG
CAGCTGCCCATCTACACGCCTCTCACCACCATGGGGAGTTGACAGGGCACTTCCAGGGGGAGATCAAGCTGCAG
ACCTCTCAGGGCAAGACGAGGGGAGAAGCTCTATGACTTTGTGAAGACGGAGCGTGATGAATCCAGTGGGCCAAAG
ACCCTGAAGAGCCTCACCAGCCACGACCCCATGAAGCAGTGGGAAGTCACTAGCAGGGCCCCCTCCGTGCAGTGGC
TCCAGCATCACTGAAATCATCAACCCCAACTACATGGGAGTGGGGCCCTTTGGGCCACCAATGCCCTGCACGTG
AAGCAGACCTTGTCCCCTGACCAGCAGCCACAGCCTGGAGCTACGACCAGCCGCCCAAGGACTCCCCGCTGGGG
CCCTGCAGGGGAGAAAGTCTCCGACACCTCCCGGCCAGCCGCCATATACCCAAGAAGTTTTTACCCTCAACA
GCAAACCGGGGTCTCCCTCCCAGGACACAGGAGTCAAGGCCAGTGACCTGGGGAAGAACGCAGGGGACACGCTG
CCTCAGGAGGACCTGCCGTGACGAAGCCCCGAGATGTTTGAGAACCCCCCTGTATGGGTCCCTGAGTTCTTCCCT
AAGCCTGCTCCCAGGAAGGACAGGAATCCCCAAAATGCCGCGGAAGGAACCCCGCCCTGCCCGGAACCCGGC
ATCTTGTGCGCCAGCATCGTGCTACCAAAGCCCAGGAGGCTGATCGCGGCGAGGGGCCGGGCAAGCAGGTGCCC
GCGCCCCGGCTGCGCTCCTTCAGTGCTCATCCTCTGCCGAGGGCAGGGCGGCCGGCGGGGACAAGAGCCAAGGG
AAGCCCAAGACCCCGGTGAGCTCCAGGCCCGGGTGCCGGCCAAGAGGCCCATCAAGCCTTCCAGATCGGAAATC
AACCAGACAGCCCCGCCACCCGACGCCGCGGCCGCGCTGCCAGTCAAGAGCCCGGGCGGTGCTGCACCTCCAG
CACTCCAAGGGCCGCGACTACCGCGACAACACCGAGCTCCCGCATCACGGCAAGCACCGGCCGGAGGAGGGGCCA
CCAGGGCCTCTAGGCAGGACTGCCATGCAGTGAAGCCCTCAGTGAGCTGCCACTGAGTCGGGAGCCAGAGGAAC
GGCGTGAAGCCACTGGACCTCTCCCGGGACCTCCTGCTGGCTCCTCTGCCAGCTTCTATGCAAGGCTTTGT
GTTTTCAGGAAGGGCCTAGCTTCTGTGTGGCCACAGAGTTCACTGCCTGTGAGACTTAGCACCAAGTGCTGAG
GCTGGAAGAAAAACGCACACCAGACGGGCAACAAACAGTCTGGGTCCCAGCTCGCTCTTGGTACTTGGGACCCC
AGTGCCTCGTTGAGGGCGCCATTCTGAAGAAAGGAAGTGCAGCGCCGATTTGAGGGTGGAGATATAGATAATAAT
AATATTAATAATAATAATGGCCACATGGATCGAACACTCATGATGTGCAAGTGCTGTGCTAAGTGCTTTACGAA
CATTCGTATATCAGGATGACCTCGAGAGCTGAGGCTCTAGCCACCTAAAACCACGTGCCCAAACCCACAGTTT
AAAACGGTGTGTGTTCCGAGGGGTGAAAGCATTAAAGAAGCCCAGTGCCCTCCTGGAGTGAGACAAGGGCTCGGCC
TTAAGGAGCTGAAGAGTCTGGGTAGCTTGTGTAGGGTACAAGAAGCCTGTTCTGTCCAGCTTCAGTGACACAAGC
TGCTTTAGCTAAAGTCCGCGGGTTCCGGCATGGCTAGGCTGAGAGCAGGGATCTACCTGGCTTCTCAGTTCTTT
GGTTGGAAGGAGCAGGAAATCAGCTCCTATTCTCCAGTGGAGAGATCTGGCCTCAGCTTGGGCTAGAGATGCCAA
GGCCTGTGCCAGGTTCCCTGTGCCCTCCTCGAGGTGGGCAGCCATCACCAGCCACAGTTAAGCCAAGCCCCCAA
CATGTATTCCATCGTGCTGGTAGAAGAGTCTTTGCTGTTGCTCCCGAAAGCCGTGCTCTCCAGCCTGGCTGCCAG
GGAGGGTGGGCTCTTGGTTCCAGGCTCTTGAAATAGTGCAGCCTTTTCTTCTATCTCTGTGGCTTTTCAAGCTCT
GCTTCTTGGTTATTAGGAGAATAGATGGGTGATGTCTTCTTATGTTGCTTTTTCAACATAGCAGAATTAATG
TAGGGAGCTAAATCCAGTGGTGTGTGTAATGCAGAAGGAATGCACCCACATTCCCATGATGGAAGTCTGCGT

WO 2004/030615

PCT/US2003/028547

1094/6881
FIGURE 1022B

AACCAATAAATTGTGCCTTTCTCACTCA

WO 2004/030615

PCT/US2003/028547

1095/6881
FIGURE 1023

MKNKHSEQPEPDMITIFIGTWNMGNA PPPKKITSWFLSKGQGKTRDDSADYIPHDIYVIGTQEDPLSEKEWLEIL
KHS LQEITSVTFKTVAIHTLWNIRIVVLAKPEHENRISHICTDNVKTGIANTLGNGAVGV SFMFNGTSLGFVNS
HLTSGSEKKLRRNQNYMNLRF LALGDKKLS PFNITHR FTHLFWFGDLN YRVLDLPTWEAETIIQKIKQQQYADLL
SHDQLLTERREQKVFLHFEEEEITFAPTYR FERLTRDKYAYTKQKATGMKYNLPSWCDRVLWKSYP LVHVVCQSY
GSTSDIMTSDHSPVFATFEAGVTSQFVSKNGPGTVDSQGQIEFLRCYATLKT KSQTKFYLEFHSSCLESFVKSQE
GENEEGSEGELVVKFGETLPKLPKPIISDPEYLLDQHILISIKSSDSDES YGEGCIALRLEATETQLPIYTPLTHH
GELTGHFQGEIKLQTSQGKTREKLYDFVKTERDESSGPKTLKSLTSHDPMKQWEVTSRAPPCSGSSITEIINPNY
MGVGPFPGPPMPLHVKQTLSPDQQPTAWSYDQPPKDSPLGPCRGESPPTPPGQPPISP KKF LPSTANRGLPPRTQE
SRPSDLGKNAGDTLPQEDLPLTKPEMFENPLYGSLSSF PKPAPRKDQESPKMPRKEPPPCPEPGILSPSIVLTKA
QEADRGE GPGKQVPAPRLRSFTCSSAEGRAAGGDKSQGKPKTPVSSQAPVPAKRPIKPSRSEINQQTPPTPTPR
PPLPVKSPAVLHLQHSGRDYRDNTELP HHGKHRPEEGPPGPLGRTAMQ

WO 2004/030615

PCT/US2003/028547

1096/6881
FIGURE 1024

CGAGCGGACTCGACTCGGCACCGCTGTGCACCATGCGCCGGGCCCTGTGCCGCTCCCGCGGCGCGGCCTCTGGC
TGCTCCTGGCCCATCACCTCTTCATGACCACTGCCTGCCAGGAGGCTAACTACGGTGCCCTCCTCCGGGAGCTCT
GCCTCACCCAGTTCCAGGTAGACATGGAGGCCGTCGGGGAGACGCTGTGGTGTGACTGGGGCAGGACCATCAGGA
GCTACAGGGAGCTGGCCGACTGCACCTGGCACATGGCGGAGAAGCTGGGCTGCTTCTGGCCCAATGCAGAGGTGG
ACAGGTTCTTCCTGGCAGTGCATGGCCGCTACTTCAGGAGCTGCCCCATCTCAGGCAGGGCCGTGCGGGACCCGC
CCGGCAGCATCCTCTACCCCTTCATCGTGGTCCCCATCACGGTGACCCTGCTGGTGACGGCACTGGTGGTCTGGC
AGAGCAAGCGCACTGAGGGCATTGTGTAGCGGGGCCAGGCTGCCCCGCGGGTGACCCAGGCTGCAGGGTGAGG
CCAGGCAGGCCTGGGTAGGGGCAGCTTCTGGAGCCTTGGGACAGAGCAGGCCCACAATGCCCCCTTCTTCCAGC
CAAGAAGAGCTCACAGGAGTCCAGAGTAGCCGAGGCTCTGGTATTAACTGGAAGCCCCCTGGCTGGAGGCCAC
CGCCACCCTAGGAAGGGGGCAGGGACGTGACCTTGACTTACCTCTGGAAGGGTCCCAGCCTAGACTGCTTACCC
CATAGCCACATTTGTGGATGAGTGGTTTGTGATTAAAAGGGATGTTCTTG

WO 2004/030615

PCT/US2003/028547

1097/6881
FIGURE 1025

MARALCRLPRRGLWLLLAHHLFMTTACQEANYGALLRELCLTQFQVDMEAVGETLWCDWGRTIRSYRELADCTWH
MAEKLGCFWPNAEVDREFFLAVHGRYFRSCPISGRAVRDPPGSILYPFIVVPITVILLVTALVVWQSKRTEGIV

WO 2004/030615

PCT/US2003/028547

1098/6881
FIGURE 1026A

GGCACGAGGCCGCTCCCCGGCGGGCTGGCTCCTGGCCCCGGAAGCGCGAGCGTTCACTTAGCGGCGAGTGGCTCC
GTCTCCGCGGACAGAGCGCGCGCCCCCTGGCCCCGCGCGAGGGGCTCCCCGGCGGGTCCCCGAGCATTTCCCG
CCGGGTGGAGCGGGCCGAGCCCGGCAGGATGACACAGCCCCGCGGCCGCTCAAAGCCGGGAGATCGACTGTTTGGAG
CCCGGAAGCGCAGAAGCTGGCGGAAGCCCGGCTCGCTGCAAAACGGGCGGCCCGCGCGGAGGCTCGCGAGATCCG
CATGAAGGAGCTGGAGCGGCAGCAGAAGGAGGAAGACAGTGAGCGCTACTCTCGTAGATCCAGAAGAAACACATC
GGCTTCTGATGAAGACGAGCGCATGTCAGTGGGTAGTCTGTGAAGCCTGAGGGTAGAAGAGAGACCAGAAAAAGA
TTTTACTGAGAAGGGTCTCGTAACATGCCGGGCTGTCTGCAGCCACGCTGGCCTCTCTGGGTGGGACTTCCTC
TCGGAGAGGCAGCGGAGACACCTCCTTCTCCATCGACACCGAGGCATCCATCAGGGAAATCAAGGACTCTCTAGC
AGAAGTTGAAGAGAAATATAAGAAGGCTATGGTTTCCAATGCTCAGCTAGACAATGAAAAGACAACTTCATGTA
CCAGTTGATACCCTAAAAGATATGTTGCTGGAGCTTGAAGAACAGCTGGCTGAATCTAGGCGGCAGTACGAAGA
GAAAAACAAAGAATTTGAAAGGGAAAAACACGCCACAGTATACTGCAATTTTCAGTTTGCTGAAGTCAAGGAGGC
CCTGAAGCAAAGAGAGGAAATGCTCGAGAAACATGGAATAATCCTAAATTCAGAAATAGCTACCAATGGAGAGAC
TTCCGACACCTCAATAATGTTGGATACCAAGGTCTACCAAGATGACAAAAGAAGAGTTAAATGCCCTCAAGTC
TACAGGGGATGGGACCTAGGAAGAGCCAGTGAAGTGGAGGTGAAAAATGAAATCGTGGCGAATGTGGGGAAAAG
AGAAATCTTGACAATACTGAGAAAGAACAACACAGAGGACACAGTGAAGGACTGTGTGGACATAGAGGTATT
CCCTGCTGGTGAGAATACCGAGGACCAGAAATCCTCTGAAGACACTGCCCCATTCTAGGAACCTTAGCAGGTGC
TACCTATGAAGAACAGGTTCAAAGCCAAATTCCTTGAGAGCAGTTCTCTCCCTGAAAACACAGTACAGGTTGAGTC
AAATGAGGTCATGGGTGCACCAGATGACAGGACCAGAACTCCCCTTGAGCCATCCAATGTTGGAGTGACTTAGA
TGTTGGGAACCCACACAGAGAATGTGGGAGAGGCAGCAGTGAAGTGAAGAGCAGGCAGGCACAGTGGCCTC
GTGTCCCTTTAGGGCATAGTGATGACACAGTTTATCATGATGACAAATGTATGGTAGAGGTCCCCAAGAGTTAGA
GACAAGCACAGGGCATAGTTTATAGAGAAAGAAATCACCAACCAGGAAGCAGCTGAGCCCAAGGAGGTTCCAGCGCA
CAGTACAGAAAGTAGGTAGGGATCACAACGAAGAAGAGGGTGAAGAAACAGGATTAAGGGACGAGAAACCAATCAA
GACAGAAGTTTCTGGTTCTCCAGCAGGAACTGAGGGCAACTGTGAGGAAGCGACAGGTCCAAGTACAGTAGACAC
TCAAAATGAACCTTAGATATGAAAGAGCCCGATGAAGAAAAGAGTGACCAACAGGGAGAGGCATTGGACTCATC
GCAGAAGAAGACAAAGAAACAAGAAAAAGAAAAACAAGAAGAAAAATCCCCAGTACCCGTAGAAACCTTAAAGA
TGTTAAAAAAGAGTTAACGTATCAGAACACAGATTTAAGTGAATTAAGGAAGAAGAGCAGGTAAAGTCTACTGA
CAGAAAGTCAGCAGTGAAGCCCCAAACGAGGTGACTGAAAATCCAAACAGAAAATTGCAGCAGAAAGCAGTGA
AAATGTTGATTGTCCGGAGAATCCTAAATTAAGTTGGATGGAAAACCTTGACCAAGAAGGTGATGATGTACAAAC
AGCAGCTGAGGAGGTACTAGCTGATGGAGACACATTAGATTTTGAGGATGACACCGTTCAATCATCAGGCCCCGAG
GGCTGGTGGTGAAGAATTAGATGAAGGTGTTGCAAAAGATAATGCTAAAATAGATGGTGGCACTCAAAGCAGTCC
TGCAGAACCAAAGAGCGAAGACGCAGATCGCTGCACCTGCCCGAACATGAAAGTCCCTCACAGGACATTAGTGA
TGCCTGTGAAGCAGAAAGTACAGAGAGGTGTGAGATGTCAGAACATCCAAGTCAGACCGTCAGGAAAGCTTTAGA
CAGCAATAGCCTAGAGAACGATGACTTGTCCGCACCAGGAAGAGAGCCAGGGCACTTCAATCCAGAAAGCAGAGA
AGATACCAGAGGAGGGAATGAGAAGGGCAAAAGCAAAGAAGACTGTACCATGTCTTAAGCTGAGGCAGGCGGCAG
GCGCGGTGCACAGGAAGTCTCAGTGTGAAGGGTCTTTTCTCTCCACTGCCAATGTAAGTAGAATGTTCTAAAT
CATAGAGAGGCACTGTATGACAATTACCAGGTGCTCTACTGCTTTAAGTTATAGACTGTTACTTGTAGATTTCCA
TGTAATCATTGAGGTTATCACCCAGATTAGAAAGACATATTTGTTATCAGTGTACGTTCTAATTGAGAGCATTCC
AGTAGTATCAACAATAATGTCTACTGTTTATAGTCCACTTAATAAAAAATAGAGGCATTACTATTTGCCCTTAGG
CTGATAGGAATGTGGGTTTTCTTGACCAAAATATATCAGCATCTAATTGAAATGACCAATAGCATTCCTTAGACTT
CTGTATTATGAATATAATTGATATTTAAATTAATGTCTTGTTCACATATGTGTACTTTTATATTTTAAAA
TGATACATTATAACCTGTATGGTATTTTATTTAAAGGAGATAAACAGCCAAATAGCAAATAGGTCAGTGAATGATA
AGATTTGCACCTTAGAACAAATAATCATTTTAAAGGATAACAAGTAAATGTCTGAAAGCATGAGGGGCTTTATTTGC
CTTTACCTCATATGAGTCTTTGATCTTGAACCGATACTTTTGGATCTCATTGTTGATATACCTGAATTTACTTTG
TAAGAGATTTTAACTTCACTTCTATGCTGATGATGATCAAATTCATTTTATAGAAAGATTTAAAGTTTTTTCTG
GAAGTGATATATGTCAAATTACATTTCTACTGCAGTATTTGAGCAGGGACAGTCATTTTAAATGTTTTTGGC
CGGGCGTGGTGGCTCATGCCTGTAATCTCAGTACATTGGGAGGCCAAGGCAGGTGGATCACCTGAGGTCAAGAGT
TCGAGGCCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTGGCCGGGCGTGATGGTG
GGCGCCTGTAATCCCAGCCACTCCAGAGGCTGAGGCAGGAGAATCGCTTGAACCTGCGAGGCAGAGATTGCAGTG

WO 2004/030615

PCT/US2003/028547

1099/6881

FIGURE 1026B

AGCCAAGATCAAGCCATTGTACTCCAGCCTGGACAACAAGAGCGAAACTCTGTCTA

WO 2004/030615

PCT/US2003/028547

1100/6881
FIGURE 1027

MTSPAAAQSREIDCLSPFAQKLAEARLAAKRAARAEAREIRMKELERQQKEEDSERYSRRSRNTSASDEDERMS
VGSRGSLRVEERPEKDFTEKGSRNMPGLSAATLASLGGTSSRRGSGDTSFSIDTEASIREIKDSLAEVEEKYKKA
MVSNAQLDNEKTNFMVQVDTLKDMLLELEEQLAESRRQYEEKNKEFEREKHAHSILQFQFAEVKEALKQREEMLE
KHGIILNSEIATNGETSDTLNNGVYQGPTKMTKEELNALKSTGDGTLGRASEVEVKNEIVANVGKREILHNTEKE
QHTEDTVKDCVDIEVFPAGENTEDQKSSSED TAPFLGTLGATYEEQVQSQILESSSLPENTVQVESNEVMGAPDD
RTRTPLEPSNCWSDLDGGNHTENVGEAAVTQVEEQAGTVASCPLGHSDDTVYHDDKCMVEVPQELETSTGHSLEK
EFTNQEAAPKEVPAHSTEVGRDHNEEEGEETGLRDEKPIKTEVPGSPAGTEGNCQEATGPSTVDTQNEPLDMKE
PDEEKSDQQGEALDSSQKTKNKKKKNNKKKSPVPVETLKDVKKELTYQNTDLSEIKEEEQVKSTDRKSAVEAQN
EVTENPKQKIAAESSENVDCPENPKIKLDGKLDQEGDDVQTAAEEVLADGDTLDFEDDTVQSSGPRAGGEELDEG
VAKDNAKIDGATQSSPAEPKSEDADRCTLPEHESPSQDISDACEAESTERCESHPSTVRKALDSNSLENDL
SAPGREPGHFNPESTRGNEKGKSKEDCTMS

WO 2004/030615

PCT/US2003/028547

1101/6881
FIGURE 1028A

CAGTTTGGAGCTCAGTCTTCCACCAAAGGCCGTTTCTCTGGGCTCCAGCCTCCTGCAAGGACTGCAAGAG
TTTTCTCCGCAGCTCTGAGTCTCCACTTTTTTGGTGGAGAAAGGCTGCAAAAAGAAAAGAGACGCAGTGAGTG
GGAAAAGTATGCATCCTATTCAAACCTAATTGAATCGAGGAGCCCAGGGACACACGCCTTCAGGTTTGCTCAGGG
GTTTATATTGGTGCTTAGACAAATTCAAATGAGGAAACATCGGCACCTTGCCCTTAGTGGCCGCTCTTTGCTC
TTTCTCTCAGGCTTTCTTACAACCTCATGCCCAGCAGCAGCAAGCAGATGTCAAAAATGGTGCGGCTGCTGATATA
ATATTTCTAGTGGATTCTCTTGGACCATTGGAGAGGAACATTTCCAACCTTGTTTCGAGAGTTTCTATATGATGTT
GTAAAATCCTTAGCTGTGGGAGAAAATGATTTCCATTTTGCTCTGGTCCAGTTCAACGGAAACCCACATACCGAG
TTCCTGTTAAATACGTATCGTACTAAACAAGAAGTCCTTTCTCATATTTCCAACATGTCTTATATTGGGGGAACC
AATCAGACTGGAAAAGGATTAGAATACATAATGCAAAGCCACCTCACCAAGGCTGCTGGAAGCCGGGCCGGTGAC
GGAGTCCCTCAGGTTATCGTAGTGTTAACTGATGGACACTCGAAGGATGGCCTTGCTCTGCCCTCAGCGGAACTT
AAGTCTGCTGATGTTAACGTGTTTGCAATTGGAGTTGAGGATGCAGATGAAGGAGCGTTAAAAGAAATAGCAAGT
GAACCGCTCAATATGCATATGTTCAACCTAGAGAATTTTACCTCACTTCATGACATAGTAGGAACTTAGTGTC
TGTGTGCATTATCCGTGAGTCCAGAAAGGGCTGGGGACACGGAAACCTTAAAGACATCAAGCACAAGACTCT
GCTGACATTATTTTCTTATTGATGGATCAAACAACACCGGAAGTGTCAATTTGCGAGTCATTCTCGACTTCCTT
GTAAATCTCCTTGAGAACTCCCAATTGGAACCTCAGCAGATCCGAGTGGGGTGGTCCAGTTTAGCGATGAGCCC
AGAACCATGTTCTCCTTGGACACCTACTCCACCAAGGCCAGGTTCTGGGTGCAGTGAAGCCCTCGGGTTTGCT
GGTGGGGAGTTGGCCAATATCGGCCTCGCCCTTGATTTCTGGTGGAGAACCCTTACCCGGGCAGGGGCGAGC
CGCGTGGAGGAAGGGGTTCGCCAGGTGCTGGTCTCATAAAGTGCCGGGCTTCTAGTGACGAGATTCTCGTACGGG
GTGGTAGCACTGAAGCAGGCTAGCGTGTTCTCATTCGGCCTTGAGGCCAGGCCGCTCCAGGGCAGAGCTTCAG
CACATAGCTACCGATGACAACCTTGGTGTTTACTGTCCCGAATTCCGTAGCTTTGGGGACCTCCAGGAGAAATTA
CTGCCGTACATTGTTGGCGTGGCCCAAAGGCACATTGTCTTGAAACCGCCAACCAATTGTACACAAGTCATTGAA
GTCAACAAGAGAGACATAGTCTTCTGGTGGATGGCTCATCTGCAGTGGGACTGGCCAACCTTCAATGCCATCCGA
GACTTCATTGCTAAAGTCATCCAGAGGCTGGAATCGGACAGGATCTTATCCAGGTGGCAGTGGCCCAGTATGCA
GACACTGTGAGGCCTGAATTTTATTCAATACCCATCCAACAAAAGGGAAGTCATAACCGCTGTGCGGAAAATG
AAGCCCTTGACGGCTCGGCCCTGTACAGGGCTCTGCTCTAGACTTTGTTTCGTAACAACCTATTACAGAGTTCA
GCCGGCTACCGGGCTGCCGAGGGGATTCTAAGCTTTTGGTGTGATCACAGGTGGTAAGTCCCTAGATGAAATC
AGCCAGCCTGCCAGGAGCTGAAGAGAAGCAGCATATGGCCTTTGCCATTGGGAACAAGGGTGCCGATCAGGCT
GAGCTGGAAGAGATCGCTTTCGACTCCTCCTTGGTGTTCATCCAGCTGAGTTCCGAGCCGCCCATTTGCAAGGC
ATGCTGCCTGGCTTGCTGGCACCTCTCAGGACCTCTCTGGAACCCCTGAAGTTCACTCAAACAAAAGGGATATC
ATCTTTCTTTGGATGGATCAGCCAACGTTGGAAAAACCAATTTCCCTTATGTGCGGACTTTGTAATGAACCTA
GTTAACAGCCTTGATATTGGAATGACAATATTCTGTGTTGGTTTAGTGCAATTTAGTGACACTCTGTAAACGGAG
TTCTCTTTAAACACATACCAAGCAAGTCAGATATCCTTGGTCATCTGAGGCAGCTGCAGCTCCAGGGAGGTTCG
GGCCTGAACACAGGCTCAGCCCTAAGCTATGTCTATGCCAACCACTTCACGGAAGCTGGCGGCAGCAGGATCCGT
GAACACGTGCCGCAGCTCCTGCTTCTGCTCACAGCTGGGCAGTCTGAGGACTCCTATTTGCAAGCTGCCAACGCC
TTGACACGCGCGGCATCCTGACTTTTTTGTGTGGGAGCTAGCCAGGCGAATAAGGCAGAGCTTGAGCAGATTGCT
TTTAACCCAAGCCTGGTGATCTCATGGATGATTTTCACTCCTGCCAGCTTTGCCTCAGCAGCTGATTCAGCCC
CTAACCACATATGTTAGTGAGGTGTGGAGGAAGTACCCTCGCTCAGCCAGAGAGCAAGCGAGACATTCTGTTC
CTCTTTGACGGCTCAGCCAATCTTGTGGGCCAGTTCCCTGTTGTCCGTGACTTTCTCTACAAGATTATCGATGAG
CTCAATGTGAAGCCAGAGGGGACCCGAATTGCGGTGGCTCAGTACAGCGATGATGTCAAGGTGGAGTCCCGTTTT
GATGAGCACCAGAGTAAGCCTGAGATCCTGAATCTTGTGAAGAGAATGAAGATCAAGACGGGCAAAGCCCTCAAC
CTGGGCTACGCGCTGGACTATGCACAGAGGTACATTTTGTGAAGTCTGCTGGCAGCCGGATCAGAGGTGGAGTG
CTTCAGTTTCTGGTGCTGCTGGTTCGAGGAAGGTATCTGACCGTGTGGATGGGCCAGCAAGTAACCTGAAGCAG
AGTGGGGTTGTGCTTTTCTCTTCCAAGCCAAGAACGCAGACCTGCTGAGTTAGAGCAGATCGTGCTGTCTCCA
GCGTTTATCCTGGCTGCAGAGTCGCTTCCAAGATTGGAGATCTTCATCCACAGATAGTGAATCTCTTAAATCA
GTGCACAACGGAGCACCAGCACCAGTTTCAAGGTGAAAAGGACGTGGTGTCTGCTTGTGCTGCTGAGGGCGTC
AGGAGCGGTTTCCCTCTGTTGAAAGAGTTTGTCCAGAGAGTGGTGGAAAGCCTGGATGTGGGCCAGGACCGGGTC
CGCGTGGCCGTGGTGCAGTACAGCGACCGGACAGGCCGAGTTCTACCTGAATTCATACATGAACAAGCAGGAC
GTCGTCAACGCTGTCCGCCAGCTGACCCTGCTGGGAGGGCCGACCCCCAACACCGGGGCCGCCCTGGAGTTTGTC

WO 2004/030615

PCT/US2003/028547

1102/6881
FIGURE 1028B

CTGAGGAACATCCTGGTCAGCTCTGCGGGAAGCAGGATAACAGAAGGTGTGCCCCAGCTGCTGATCGTCCTCACG
GCCGACAGGTCTGGGGATGATGTGCGGAACCCCTCCGTGGTCGTGAAGAGGGGTGGGGCTGTGCCCATTTGGCATT
GGCATCGGGAACGCTGACATCACAGAGATGCAGACCATCTCCTTCATCCCGACTTTGCCGTGGCCATTCCCACC
TTTCGCCAGCTGGGGACCGTCCAACAGGTCATCTCTGAGAGGGTGACCCAGCTCACC CGCAGGAGCTGAGCAGG
CTGCAGCCGGTGTTCAGCCTCTACCGAGCCAGGTGTTGGTGGCAAGAGGGACGTGGTCTTTCTCATCGATGGG
TCCCAAAGTGCCGGGCTGAGTTCCAGTACGTTTCGCACCCTCATAGAGAGGCTGGTTGACTACCTGGACGTGGGC
TTTGACACCACCCGGGTGGCTGTCATCCAGTTTCAGCGATGACCCCAAGGTGGAGTTCCTGCTGAACGCCCATTC
AGCAAGGATGAAGTGCAGAACGCGGTGCAGCGGTGAGGCCCAAGGGAGGGCGGCAGATCAACGTGGGCAATGCC
CTGGAGTACGTGTCCAGGAACATCTTCAAGAGGCCCTGGGGAGCCGATTGAAGAGGGCGTCCCGCAGTTCTCTG
GTCTCATCTCGTCTGGAAAGTCTGACGATGAGGTGGACGACCCGGCGGTGGAGCTCAAGCAGTTTGGCGTGGCC
CCTTTTCAGATCGCCAGGAACGCAGACCAGGAGGAGCTGGTGAAGATCTCGCTGAGCCCCGAATATGTGTTCTCG
GTGAGCACCTTCCGGGAGCTGCCCAGCCTGGAGCAGAACTGCTGACGCCCATCACGACCCTGACCTCAGAGCAG
ATCCAGAAGCTCTTAGCCAGCACTCGCTATCCACCTCCAGCAGTTGAGAGTGATGCTGCAGACATCGTCTTTCTG
ATCGACAGCTCTGAGGGAGTTAGGCCAGATGGCTTTGCACATATTCGAGATTTTGTAGCAGGATTGTTCGAAGA
CTCAACATCGGCCCCAGTAAAGTGAGAGTTGGGGTCGTGCAGTTTCAGCAATGATGTCTTCCAGAATTCTATCTG
AAAACCTACAGATCCAGGCCCGGTGCTGGACGCCATACGGCGCCTGAGGCTCAGAGGGGGTTCCCCACTGAAC
ACTGGCAAGGCTCTCGAATTTGTGGCAAGAACTCTTTGTTAAGTCTGCGGGAGTCGCATAGAAGACGGGGTG
CCCCAACACCTGGTCTGGTCTGGGTGGAAATCCCAGGACGATGTGTCCAGGTTCCGCCAGGTGATCCGTTCC
TCGGGCATTGTGAGTTTAGGGGTAGGAGACCGGAACATCGACAGAACAGAGCTGCAGACCATCACCATGACCCC
AGACTGGTCTTACAGTGCGAGAGTTTCAGAGAGCTTCCCAACATAGAAGAAAGAATCATGAACTCGTTTGGACCC
TCCGCAGCCACTCCTGCACCTCCAGGGGTGGACACCCCTCCTCCTTACGGCCAGAGAAGAAGAAAGCAGACATT
GTGTTCTGTGGATGGTTCCATCAACTTCAGGAGGGACAGTTTCCAGGAAGTGCTTCGTTTTGTGTCTGAAATA
GTGGACACAGTTTATGAAGATGGCGACTCCATCCAAGTGGGGCTTGTCCAGTACAACCTTGACCCCACTGACGAA
TTCTTCTGAAGGACTTCTCTACCAAGAGGCAGATTATTGACGCCATCAACAAAGTGGTCTACAAAGGGGGAAGA
CACGCCAACACTAAGGTGGGCCTTGAGCACCTGCGGGTAAACCCTTTGTGCCTGAGGCAGGCAGCCGCCTGGAC
CAGCGGGTCCCTCAGATTGCCTTTGTGATCACGGGAGGAAAGTCGGTGGAAAGATGCACAGGATGTGAGCCTGGCC
CTCACCAGAGGGGGGTCAAAGTGTTTGTGTTGGAGTGAGGAATATCGACTCGGAGGAGGTTGGAAAGATAGCG
TCCAACAGCGCCACAGCGTTCCGCGTGGGCAACGTCCAGGAGCTGTCCGAACAGCGAGCAAGTTTGGAACT
TTGCATGATGCGATGCATGAAACCTTTGCCCTGGTGTAACTGATGCTGCCAAAGCTTGTAATCTGGATGTGATT
CTGGGGTTTGATGGTTCTAGAGACCAGAATGTTTTTGTGGCCAGAAGGGCTTCGAGTCCAAGTGGAGCGCCATC
TTGAACAGAATCAGCCAGATGCACAGGGTCAGCTGCAGCGGTGGCCGCTCGCCACCGTGCCTGTGTGATGGTG
GCCAACACGCCCTCGGGCCCGGTGGAGGCTTTGACTTTGACGAGTACCAGCCAGAGATGCTCGAGAAGTTCCGG
AACATGCGCAGCCAGCACCCCTACGTCTCACGGAGGACACCTGAAGGTCTACCTGAACAAGTTCAGACAGTCC
TCGCCGACAGCGTGAAGGTGGTCATTCTTTACTGATGGAGCAGACGGAGATCTGGCTGATTTACACAGAGCA
TCTGAGAACCTCCGCCAAGAAGGAGTCCGTGCCTTGATCCTGGTGGGCCTTGAACGAGTGGTCAACTTGGAGCGG
CTAATGCATCTGGAGTTTGGGCGAGGGTTTATGTATGACAGGCCCTGAGGCTTAACCTTGCTGGACTTGGATTAT
GAAC TAGCGGAGCAGCTTGACAACATTGCCGAGAAAGCTTGCTGTGGGGTTCCCTGCAAGTGCTCTGGGCAGAGG
GGAGACCGCGGGCCCATCGGCAGCATCGGGCCAAAGGGTATTCTGGAGAAGACGGCTACCGAGGCTATCCTGGT
GATGAGGGTGGACCCGGTGAGCGTGGTCCGCCTGGTGTGAACGGCACTCAAGGTTTCCAGGGCTGCCCGGGCCAG
AGAGGAGTAAAGGGCTCTCGGGGATTCCAGGAGAGAAGGGCGAAGTAGGAGAAATTGGACTGGATGGTCTGGAT
GGTGAAGATGGAGACAAAGGATTACCTGGTTCTTCTGGAGAGAAAGGGAATCCTGGAAGAAGGGGTGATAAAGGA
CCTCGAGGAGAGAAAGGAGAAAGAGGAGATGTTGGGATTTCAGGGGACCCGGGTAAACCCAGGACAAAGACGCCAG
GAGAGAGGACCCAAAGGAGAAACCGGTGACCTCGGCCCATGGGTGTCCAGGGAGAGATGGAGTACCTGGAGGA
CCTGGAGAACTGGGAAGAATGGTGGCTTTGGCCGAAGGGGACCCCGGAGCTAAGGGCAACAAGGGCGGTCTCT
GGCCAGCCGGGCTTTGAGGGAGAGCAGGGGACCAGAGGTGCACAGGGCCAGCTGGTCTGTGCTGGTCTCCAGGG
CTGATAGGAGAAACAAGGCATTTCTGGACCTCGGGGAAGCGGAGGTGCCGCTGGTGTCTCTGGAGAACGAGGCAGA
ACCGGTCCACTGGGAAGAAAGGGTGAGCCCGGAGAGCCAGGACCAAAGGAGGAATCGGGAACCGGGGCCCTCGT
GGGGAGACGGGAGATGACGGGAGAGACGGAGTTGGCAGTGAAGGACGCAGAGGCCAAAAAGGAGAAAGAGGATTT

WO 2004/030615

PCT/US2003/028547

1103/6881
FIGURE 1028C

CCTGGATACCCAGGACCAAAGGGTAACCCAGGTGAACCTGGGCTAAATGGAACAACAGGACCCAAAGGCATCAGA
GGCCGAAGGGGAAATTCGGGACCTCCAGGGATAGTTGGACAGAAGGGAGACCCTGGCTACCCAGGACCAGCTXXX
XXXXXXXXGGCAACAGGGGGCGACTCCATCGATCAATGTGCCCTCATCCAAAGCATCAAAGATAAATGCCCTTGCTGT
TACGGGCCCCCTGGAGTGCCCCGTCTTCCCAACAGAACTAGCCTTTGCTTTAGACACCTCTGAGGGAGTCAACCAA
GACACTTTTCGGCCGGATGCGAGATGTGGTCTTGAGTATTGTGAATGACCTGACCATTGCTGAGAGCAACTGCCCA
CGGGGGGGCCCCGGGTGGCTGTGGTCACTACAACAACGAGGTGACCACGGAGATCCGGTTTGCTGACTCCAAGAGG
AAGTCGGTCTCTCTGGACAAGATTAAGAACCTTCAGGTGGCTCTGACATCCAAACAGCAGAGTCTGGAGACTGCC
ATGTCGTTTGTGGCCAGGAACACATTTAAGCGTGTGAGGAATGGATTCCCTAATGAGGAAAGTGGCTGTTTTCTTC
AGCAACACACCCACAAGAGCATCCCCACAGCTCAGAGAGGCTGTGCTCAAGCTCTCAGATGCGGGGATCACCCCC
TTGTTCTTACAAGGCAGGAAGACCGGCAGCTCATCAACGCTTTGCAGATCAATAACACAGCAGTGGGGCATGCG
CTTGTCCTGCTGCGAGGGAGAGACCTCACAGACTTCTGGAGAATGTCTCACGTGTCATGTTTGCTTGACATC
TGCAACATCGACCCATCCTGTGGATTTGGCAGTTGGAGGCCTTCCTTCAGGGACAGGAGCGGCAGGGAGCGAT
GTGGACATCGACATGGCTTTCATCTTAGACAGCGCTGAGACCACCACCCTGTTCCAGTTCATGAGATGAAGAAG
TACATAGCGTACCTGGTCAGACAACCTGGACATGAGCCAGATCCCAAGGCCTCCCAGCACTTCGCCAGAGTGGCA
GTTGTGACAGCACGCGCCCTCTGAGTCCGTGGACAATGCCAGCATGCCACCTGTGAAGGTGGAATTCCTCCTGACT
GACTATGGCTCCAAGGAGAAGCTGGTGGACTTCCTCAGCAGGGGAATGACACAGTTGCAGGGAACCAAGGGCCTTA
GGCAGTGCCATTGAATACACCATAGAGAATGTCTTTGAAAGTGCCCCAAACCCACGGGACCTGAAAATTGTGGTC
CTGATGCTGACGGGCGAGGTGCCGGAGCAGCAGCTGGAGGAGGCCAGAGAGTCATCCTGCAGGCCAAATGCAAG
GGCTACTTCTTCGTGGTCTCTGGGCATTGGCAGGAAGGTGAACATCAAGGAGGTATACACCTTCGCCAGTGAACCA
TTGCCATCCTTCGTGACAGTGAATGCTTTTTTACTTGTCCCCAGATATCAGGAAACAGTGTGATTGGTTCCAA
GGGGACCAACCCACAAAGAACCTTGTGAAGTTTGGTCACAAACAAGTAAATGTTCCGAATAACGTTACTTCAAGT
CCTACATCCAACCCAGTGACGACAACGAAGCCGGTGACTACGACGAAGCCGGTGACCACCACAACAAAGCCTGTA
ACCACCACAACAAAGCCTGTGACTATTATAAATCAGCCATCTGTGAAGCCAGCCGCTGCAAAGCCGGCCCCCTGCG
AAACCTGTGGCTGCCAAGCCTGTGGCCACAAAGACGGCAGCTGTAGACCCCCAGTGGCGGTGAAGCCAGCAACG
GCAGCGAAGCCTGTAGCAGCAAAGCCAGCAGCTGTAAGACCCCCCGCTGCTGCTGCAAACAGTGGCGACCAAG
CCTGAGGTCCCTAGGCCACAGGCAGCCAAACCAAGCTGCCACCAAGCCAGCCACCACTAAGCCCATGGTTAAGATG
TCCCGTGAAGTCCAGGTGTTTGAGATAACAGAGAACAGCGCCAAACTCCACTGGGAGAGGCCTGAGCCCCCGGT
CCTTATTTTTATGACCTCACCGTCACCTCAGCCATGATCAGTCCCTGGTTCTGAAGCAGAACCTCACGGTCACG
GACCGCTCATTGGAGGCCTGCTCGCTGGGCAGACATACCATGTGGCTGTGGTCTGCTACCTGAGGTCTCAGGTG
AGAGCCACCTACCATGGAAGTTTCAGTACAAAGAAATCTCAGCCCCACCTCCACAGCCAGCAAGGTGAGCTTCT
AGTTCAACCATCAATCTAATGGTGAGCACAGAACCATTGGCTCTCACTGAAACAGATATATGCAAGTTGCCGAAA
GACGAAGGAACCTGCAGGGATTTTCATATTAATAATGGTACTATGATCCAAACACCAAAAGCTGTGCAAGATTCTGG
TATGGAGGTTGTGGTGGAAACGAAAACAAATTTGGATCACAGAAAGAATGTGAAAAGGTTTGCGCTCCTGTGCTC
GCCAAACCCGGAGTCATCAGTGTGATGGGAACCTAAGCGTGGGTGGCCAACATCATATACCTCTTGAAGAAGAAG
GAGTCAGCCATCGCCAACTTGTCTCTGTAGAAGCTCCGGGTGTAGATTCCCTTGCACTGTATCATTTTCATGCTTT
GATTTACACTCGAACTCGGGAGGGAACATCCTGCTGCATGACCTATCAGTATGGTGCTAATGTGCTGTGGACCC
TCGCTCTCTGTCTCCAGGCAGTTCTCTCGAATACTTTGAATGTTGTGTAACAGTTAGCCACTGCTGGTGTGTTATG
TGAACATTCTATCAATCCAAATTCCTCTGGAGTTTCATGTTATGCCTGTTGCAGGCÀAATGTAAAGTCTAGAA
AATAATGCAATGTACGGCTACTCTATATACTTTTGCTTGGTTTCAATTTTTTTTTCCCTTTTAGTTAAGCATGACT
TTAGATGGGAAGCCTGTGTATCGTGGAGAAACAAGAGACCAACTTTTTTATTCCCTGCCCCCAATTTCCAGACT
AGATTTCAAGCTAATTTTTCTTTTTCTGAAGCCTCTAACAATGATCTAGTTCAGAAGGAAGCAAAATCCCTTAAT
CTATGTGCACCGTTGGGACCAATGCCTTAATTAAGAATTTAAAAAGTTGTAATAGAGAATATTTTTGGCATTG
CTCTAATGTTGTGTGTTTTTTTTTTTTGTGTGCTGGAGGGAGGGGATTTAATTTTAATTTTAAATGTTTAGGAA
ATTTATACAAAGAACTTTTTAATAAAGTATATTGAAAGTTT

WO 2004/030615

PCT/US2003/028547

1104/6881
FIGURE 1029

AGCCCAGCGAGGCCTGTGCTGTGAGGGGCTGTGCTGTGCCAGGGGAGGCCCCGCACCCGGGAAGCCCAGAGGAGA
GTGTGCACTCACGGAGCCCTCCTGGCAGGGCCGCGTCTCTGGAGCAGCAGACCCGTGTCCCTCTGGGAGGTCAAC
TGCGGCCCTCACAGCTGGGCCTGTCCCAGCACAGCCCTTGTTGGAGGGCGCACCCCGTGTCTCTAGCACCCAGT
GTTGAGTGCCTTGACCTGCAGAGGGGAGCCTGTGCTGGTCCCGGGCGTCTGTGTGGCTCCTGGGTGCCATCTGC
ACCCCTGGCCCTGCTCTGGGCTTCAGTGGAGCCGTGCCACCGTGGGAGTGTCCAGGGTCCTGACGTAGCCCTGAG
ACGTGGCCAGCTCCCTGGCCTGCTGCCCCGCACAGTGGGCCCTTGCTCTGCTCTGGGTGAGGCGAGGCAGCCACC
CATGATGAGCTCTGCAGCCTTCCCAAGGTGGCTGAGCATGGGGGTCCCTCGTACCCCTTCACGGACAGTGTCTT
CGAGCGGGAGAGGACGGGCCTGACCTACCGCGTGCCCTCGTTGCTCCCGTGCCCCCGGGGCCACCCTGCTGGC
CTTTGTGGAGCAGCGGCTCAGCCCTGACGACTCCACGCCCCACCGCTGGTGCTGAGGAGGGGCACGCTGGCCGG
GGGCTCCGTGCGGTGGGGTGCCCTGCACGTGCTGGGGACAGCAGCCCTGGCGGAGCACCGGTCCATGAACCCCTG
CCCTGTGCACGATGCTGGCACGGGCACCGTCTTCTCTTCTTCATCGCGGTGCTGGGCCACACGCCTGAGGCCGT
GCAGATCGCCACGGGAAGGAACGCCGCGCGCCTCTGCTGTGTGGCCAGCCGTGACGCCGGCCTCTCGTGGGGCAG
CGCCCGGGACCTCACCGAGGAGGCCATCGGTGGTGCCGTGCAGGACTGGGCCACATTGCTGTGGGTCCCGGCCA
CGGCGTGACGTGCCCTCAGGCCGCCTGCTGGTACCGGCCTACACCTACCGCGTGGACCGCCGAGAGTGTTTTG
CAAGATCTGCCGGACAGCCCTCACTCCTTCGCCTTCTACAGCGATGACCACGGCCGCACCTGGCGCTGTGGAGG
CCTCGTGCCCAACCTGCGCTCAGGCGAGTGCCAGCTGGCGGCGGTGGACGGTGGGCAGGCCGGCAGCTTCTCTA
CTGCAATGCCCCGAGCCCACTGGGCAGCCGTGTGCAGGCGCTCAGCACTGACGAGGGCACCTCCTTCTGCCCCG
AGAGCGCGTGGCTTCCCTGCCCCGAGACTGCCTGGGGCTGCCAGGGCAGCATCGTGGGCTTCCAGCCCCGCC

WO 2004/030615

PCT/US2003/028547

1105/6881
FIGURE 1030

GAATTGGCAGCCAACATGGCGGCGGAACGCGGCGCGGGGCAGCAACAGTCGCAGGAGATGATGGAGGTTGACAGG
CGGGTCGAGTCTGAAGAATCCGGCGATGAAGAAGGGAAGAAACACAGCAGTGGCATCGTGGCCGACCTCAGTGAA
CAGAGCCTGAAGGATGGGGAGGAGCGGGGGGAGGAGGACCCAGAAGAAGAACATGAGCTGCCTGTGGACATGGAA
ACCATCAACCTGGACAGAGATGCAGAGGATGTTGATTTGAATCACTATCGCATAGGGAAGATTGAAGGATTTGAG
GTACTGAAGAAAGTGAAGACTCTCTGCCTCCGCCAAAATTTAATTAAATGCATTGAGAATCTGGAGGAGCTACAG
AGTCTTCGAGAGCTGGATCTTTACGACAACCAGATCAAGAAGATTGAGAATCTGGAGGCGCTAACAGAGCTGGAG
ATTCTAGATATTTCTTTTAATCTGCTGAGAAACATCGAAGGGGTTGACAAGTTGACACGACTGAAAAAACTCTTC
TTGGTCAACAATAAAATCAGTAAATTTGAGAACTTAAGCAACTTACATCAACTACAGATGCTAGAGCTGGGATCT
AACCGCATCCGGGCAATCGAAAATATCGACACCTTAACCAACCTGGAGAGTTTGTTCCTTGGGGAAAAACAAAATT
ACTAAACTTCAGAACCTGGATGCGCTCACCAACCTGACAGTCCTCAGTATGCAGAGCAACCGGCTGACCAAGATC
GAGGGTCTGCAGAACCTGGTGAACCTGCGGGAGCTGTACCTTAGCCACAATGGCATCGAGGTCATCGAGGGCCTG
GAGAACAATAACAACTCACGATGTTGGACATTGCATCAATAGAATCAAAAAGATTGAAAATATCAGCCATCTA
ACAGAGCTGCAAGAGTTCTGGATGAACGACAATCTCCTTGAGAGCTGGAGCGACCTCGACGAGCTGAAGGGAGCC
AGGAGCCTGGAGACAGTGTACCTGGAGCGGAACCCCTTGAGAAGGACCCCAAGTACCGGCGGAAGGTCATGCTC
GCCCTCCCTCCGTGCGGCAGATCGATGCCACGTTCTGTCAGGTTCTGAGTCCTTCTTGGCTCCTCATGTGGTCCC
TCTCTCGGAAGAACTGCCCAGCCACGGGTTTTTAACCCACCTGTTGCTCCTGAGGTCGTCCTATATCAACAGT
CACAAACCAATGGCAATAAAGGCACTGACGATAGCTGGCGCGCGGACGCCACACACCATTTTCAGATGCCGTT
GCAATTAAATCTTGCCACACTGTC

WO 2004/030615

PCT/US2003/028547

1106/6881
FIGURE 1031

MAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKHSSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLD
RDAEDVDLNHYRIGKIEGFVLKKVKTLCRLQNLIKCIENLEELQSLRELDLYDNQIKKIENLEALTELEILDIS
FNLLRNIEGVDKLTRLKKLFLVNNKISKIENLSNLHQLMLELGSNRIRAIENIDTLTNLESFLGKNKITKLQN
LDALTNLTVLSMQSNRLTKIEGLQNLVNLRELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQE
FWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKVMLALPSVRQIDATFVRF

WO 2004/030615

PCT/US2003/028547

1107/6881
FIGURE 1032A

CAAAAGCTGGCAGGCTGACAGAGGCGGCCCTCAGGACGGACCTTCTGGCTACTGACCGTTTTGCTGTGGTTTTCCCG
GGATTGTGTGTAGGTGTGAGATCAACCATGAGTTCCGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGA
AGTGGGCTGGTTCCGCAACAAATCAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCCCTCCAACCTACAAG
GATGCCCTTCCCTCCACTTCCCTGAGAAAGCTGCTTGCCCTGGAAAGTGCCAGGAACCCCTCTGGAGCCTGGGGGAAC
AAGATCCGACCCATCAAGGCTTCTGTTCATCACTCAGGTGTTCCATGTACCCCTGGAGGAGAGAAAATACAAGGAT
ATGAACCAAGTTTGAGAGAAGGTGAACAAGCAAAAAATCTGCCTTGAGATCATGCAGAGAACTGGTGCTCACTTGGAG
CTGTCTTTGGCCAAAGACCAAGGCCCTCTCCATCATGGTGTGAGGAAAGCTGGATGCTGTTCATGAAAGCTCGGAAG
GACATTGTTGCTAGACTGCAGACTCAGGCCTCAGCAACTGTTGCCATTCCCAAAGAACACCATCGCTTTGTTATT
GGCAAAAATGGAGAGAACTGCAAGACTTGGAGCTAAAAACTGCAACCAAAATCCAGATCCCACGCCCAGATGAC
CCCAGCAATCAGATCAAGATCACTGGCACCAAGAGGGCATCGAGAAAGCTCGCCATGAAGTCTTACTCATCTCT
GCCGAGCAGGACAAACGTGCTGTGGAGAGGCTAGAAGTAGAAAAGGCATTCCACCCCTTCATCGCTGGGCCGTAT
AATAGACTGGTTGGCGAGATCATGCAGGAGACAGGCACGCGCATCAACATCCCCCACCAGCGTGAACCGGACA
GAGATTGTCTTCACTGGAGAGAAGGAACAGTTGGCTCAGGCTGTGGCTCGCATCAAGAAGATTTATGAGGAGAAG
AAAAAGAAGACTACAACCATTGCAGTGGAAAGTGAAGAAATCCCAACACAAGTATGTCAATTGGGCCCCAAGGGCAAT
TCATTGCAGGAGATCCTTGAGAGAACTGGAGTTTCCGTTGAGATCCCACCCTCAGACAGCATCTCTGAGACTGTA
ATACTTCGAGGCGAACCTGAAAAGTTAGGTGAGGCGTTGACTGAAGTCTATGCCAAGGCCAATAGCTTCACCGTC
TCCTCTGTGCGCGCCCTTCTGGCTTCACCGTTTCATCATTGGCAAGAAAGGGCAGAACCTGGCCAAAATCACT
CAGCAGATGCCAAAGGTTTACATCGAGTTCACAGAGGGCGAAGACAAGATCACCCCTGGAGGGCCCTAGAGAGGAT
GTCAATGTGGCCCAGGAACAGATAGAAGGCATGGTCAAAGATTTGATTAAACCGGATGGACTATGTGAGATCAAC
ATCGACCACAAGTTCCACAGGCACCTCATTGGGAAGAGCGGTGCCAACATAAACAGAATCAAAGACCAGTACAAG
GTGTCCGTGCGCATCCCTCCTGACAGTGAGAAAGAGCAATTTGATCCGCATCGAGGGGGACCCACAGGGCGTGCAG
CAGGCCAAGCGAGAGCTGCTGGAGCTTGATCTCGCATGGAAAATGAGCGTACCAAGGATCTAATCATTGAGCAA
AGATTTTCATCGACAATCATTGGGCAGAAGGGTGAACGGATCCGTTGAGCTCAGAGGACCTAAGAATGAGGTGGAATAATGC
ATAAAATACATGCAGAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAG
TTTCAAGAATATCATTGGGAAAGGAGGCGCAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAAATCGAC
CTTCAGCAGAGAATAGCAATTCAGAGACCATTTATCATCACAGGCAAGCGAGCCAACCTGCGAAGCTGCCCGGAGC
AGGATTCTGTCTATTAGAAAGACCTGGCCAAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAAC
TCCCTCATTGGCACCAAGGGCCGTCTGATCCGCTCCATCATGGAGGAGTGCGGCGGGGTCCACATTCACTTTCCC
GTGGAAGGTTCAGGAAGCGACACCGTTGTTATCAGGGGCCCTTCTCGGATGTGGAGAAGGCCAAGAAGCAGCTC
CTGCATCTGGCGGAGGAGAAGCAAAACCAAGAGTTTTCACTGTTGACATCCGCGCCAAGCCAGAATACCACAAATTC
CTCATCGGCAAGGGGGCGGCAAAATTCGCAAGGTGCGCGACAGCACTGGAGCACGTGTCTCTTCCCTGCGGCT
GAGGACAAGGACCAGGACCTGATCACCATCATTGGAAGGAGGACGCCGTCCGAGAGGCACAGAAGGAGCTGGAG
GCCTTGATCCAAAACCTGGATAATGTGGTGGAAAGACTCCATGCTGGTGGACCCCAAGCACCACCGCCACTTCGTC
ATCCGAGAGGCCAGGTCTTGCGGGAGATTGCTGAAGAGTATGGCGGGGTGATGGTCAGCTTCCCACGCTCTGGC
ACACAGAGCGACAAAGTCAACCCTCAAGGGCGCCAAGGACTGTGTGGAGGCAGCCAAGAAACGCATTACGGAGATC
ATTGAGGACCTGGAAGCTCAGGTGACATTAGAATGTGCTATACCCCAGAAATTCATCGATCTGTCTATGGGCCCC
AAAGGTTCCAGAATCCAGCAGATTACTCGGGATTTAGTGTCAAATTAATTCAGACAGAGAGGAGAACGCA
GTTACAGTACAGAGCCAGTTGTCCAGGAGAATGGGGACGAAGCTGGGGAGGGGAGAGAGGCTAAAGATTGTGAC
CCCGGCTCTCCAAGGAGGTGTGACATCATCATCTCTGGCCGAAAGAAAAGTGTGAGGCTGCCAAGGAAGCT
CTGGAGGCATTGGTTCTGTGACCATTTGAAGTAGAGGTGCCCTTTGACCTTCACCGTTACGTTATTGGGCAGAAA
GGAAGTGGGATCCGCAAGATGATGGATGAGTTTGAAGTGAACATACATGTCCCGGCACCTGAGCTGCAGTCTGAC
ATCATCGCCATCACGGGCTCGCTGCAAAATTTGACCGGGCCAAGGCTGGACTGCTGGAGCGTGTGAAGGAGCTA
CAGGCCGAGCAGGAGGACCGGGCTTTAAGGAGTTTTAAGCTGAGTGTCACTGTAGACCCCAATACCATCCCAAG
ATTATCGGGAGAAAAGGGGGCAGTAATTACCCAAATCCGGTTGGAGCATGACGTGAACATCCAGTTTCTGATAAG
GACGATGGGAACAGCCCCAGGACCAATTACCATCACAGGGTACGAAAAGAACAGAAAGCTGCCAGGGATGCT
ATACTGAGAATTGTGGGTGAACCTGAGCAGATGGTTTCTGAGGACGTCCCGCTGGACCACCGGTTACGCCCCG
ATCATTGGTGGCCGCGCAAGCCATTCGCAAAATCATGGACGAATTCAAGGTGGACATTTCGCTTCCCACAGAGC

WO 2004/030615

PCT/US2003/028547

1108/6881
FIGURE 1032B

GGAGCCCCAGACCCCAACTGCGTCACTGTGACGGGGCTCCCAGAGAATGTGGAGGAAGCCATCGACCACATCCTC
AATCTGGAGGAGGAATACCTAGCTGACGTGGTGGACAGTGAGGCGCTGCAGGTATACATGAAACCCCCAGCACAC
GAAGAGGCCAAGGCACCTTCCAGAGGCTTTGTGGTGCGGGACGCACCCTGGACCGCCAGCAGCAGTGAGAAGGCT
CCTGACATGAGCAGCTCTGAGGAATTTCCAGCTTTGGGGCTCAGGTGGCTCCCAAGACCCTCCCTTGGGGCCCC
AAACGATTAATGATCAAAAAGAACAGAACCCCTCTCCAGCCTGCTGACCCAAACCCAACCACACAATGGTTTGTCTC
AATCTGACCCAGCGGCTGGACCCTCCGTAAATTGTTGACGCTCTTCCCCCTTCCCGAGGTCCCGCAGGGAGCCTA
GCGCCTGGCTGTGTGTGCGGCCGCTCCTCCAGGCCTGGCCGTGCCCGCTCAGGACCTGCTCCACTGTTTAACACT
AAACCAAGGTCATGAGCATTTCGTGCTAAGATAACAGACTCCAGCTCCTGGTCCACCCGGCATGTCAGTCAGCACT
CTGGCCTTCATCACGAGAGCTCCGCAGCCGTGGCTAGGATTCCACTTCCTGTGTTCATGACCTCAGGAAATAAAGC
TCCTTGACTTTATAAAAGCC